The Proteostasis Function of the *Saccharomyces cerevisiae* metacaspase Yca1

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Abstract

In addition to apoptosis, metacapases function to regulate various other processes that promote and sustain life. For example, the *Saccharomyces cerevisiae* metacaspase Yca1 promotes cellular fitness by regulating insoluble protein levels. However, the mechanism(s) that regulate this proteostasis function for Yca1 have remained elusive. Here, using proteomics coupled to protein interaction studies, we describe a role for Yca1 in restraining deposition to the insoluble proteome and further identify a post-translational regulatory mechanism for modulating Yca1 function. Our initial analyses uncovered a role for Yca1 in aggregate assembly where Yca1, in coordination with the Cdc48 chaperone, regulates the composition of the insoluble proteome. Interestingly, loss of Yca1 was correlated with reduced sequestration of proteins related to ribosomal and translational processes in the insoluble protein fraction during heat stress. Subsequent proteomic analyses identified a regulatory mechanism for Yca1 mediated by the ubiquitin system, a feature that was instrumental for limiting insoluble protein content. Specifically, we noted K355 ubiquitination and S346 phosphorylation as key modifications that directed Yca1 function to maintain proteostasis. Loss of function mutations at these sites led to increased retention of insoluble protein and increased vacuolar structures. Surprisingly, loss of Yca1 also affected ubiquitin homeostasis *in vivo* as observed by reduced levels of low molecular weight free ubiquitin. Upon further analysis, we observed that the ubiquitin precursor protein Rsp31 was cleaved by Yca1 suggesting a possible role for Yca1 in *de novo* ubiquitin synthesis. Together, these analyses suggest that post-translational modifications of Yca1 are critical regulatory features for this protease, and that this enzyme regulates cell proteostasis in combination with other chaperone and protein degradation machinery.

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* Tables S1-S4 have been compiled together into an excel worksheet and provided along with this thesis as a separate electronically accessible document. Description for these supplementary tables are available in Appendix I.

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List of Abbreviations

2D	Two dimensional
3D	Three dimensional
AAA+	ATPases associated with diverse cellular activities
Ac	Acetyl
ADH1	Alcohol dehydrogenase 1
ADP	Adenosine diphosphate
ALS	Amyotrophic lateral sclerosis
AMC	7-Amino-4-methylcoumarin
Apaf1	Apoptotic peptidase activating factor 1
Atg	Autophagy related gene
AtMC1-9	*Arabidopsis thaliana* metacaspase 1-9
ATP	Adenosine triphosphate
AVG	Average
Bax	Bcl2 associated X protein
Bag3	Bcl2 associated athanogene 3
BF	Bright field
Bid	BH3 interacting-domain death agonist
Bir1	Baculoviral IAP repeat-containing protein 1
Boc	*tert*-butyloxycarbonyl
C	Cysteine
C297A	Catalytic inactive Yca1 mutant
CaMCA1	*Candida albicans* metacaspase
CARD	Caspase recruitment domain
CASA	Chaperone assisted selective autophagy
CC	Catalytic core
CCCP	Carbonyl cyanide *m*-chlorophenyl hydrazine
CCT	Chaperonin-containing TCP-1
Cdc	Cell division cycle
Cdk1	Cyclin-dependent kinase 1

Chc1	Clathrin heavy chain 1
CHF	Caspase hemoglobinase fold
CHIP	C-terminal of Hsc70 interacting protein
CID	Collision induced dissociation
CK1/2	Casein kinase 1/2
CMA	Chaperone-mediated autophagy
Cue5	Coupling of ubiquitin conjugation to ER degradation 5
CUET	Cue5-Tollip proteins
CytC	Cytochrome C
CytoQ	Cytoplasmic quality control
D	Aspartate
DAPI	4,6-Diamidino-2-phenylindole
DAVID	Database for annotation, visualization and integrated discovery
dcbmk	Dichlorobenzylmethyl ketone
DED	Death effector domain
Ded1	Defines essential domain 1
DegAB	Degron AB
DIC	Differential interference contrast
DISC	Death induced signalling complex
DMSO	Dimethyl sulfoxide
DNA	Deoxyribose nucleic acid
dNTP	deoxyribonucleotide triphosphate
DTT	Dithiothreitol
DUB	Deubiquitinase
DVAD	Asp-Val-Ala-Asp
Ecm29	Extracellular mutant 29
Edc3	Enhancer of mRNA decapping 3
EDTA	Ethylenediaminetetraacetic acid
emPAI	exponentially modified protein abundance index
Eno1/2	Enolase 1/2
ER	Endoplasmic reticulum

ERAD	ER associated degradation
Erb1	Eukaryotic ribosome biogenesis 1
EVD	Glu-Val-Asp
Fas	First apoptotic signal
FIP200	Focal adhesion kinase family interacting protein 200
FL	Full length
Fmk	Fluoromethyl ketone
FTMS	Fourier transform mass spectrometry
G	Glycine
GG	Diglycine tag
GAPDH	Glyceraldehyde 3-phosphate dehydrogenase
GFP	Green fluorescent protein
GO	Gene Ontology
GRR	GlyArgArg
H2B	Histone 2B
H_2O_2	Hydrogen peroxide
hBax	Human Bax
HDAC6	Histone deacetylase 6
HECTD3	Homologous to E6-AP C-terminus domain containing protein D3
HEPES	4-4-hydroxyethyl-1-piperazineethanesulfonic acid
HCl	Hydrochloric acid
His	Histidine
HPLC	High-performance liquid chromatography
HRP	Horse radish peroxidase
HS	Heat shock
HSG	Heat stress granule
Hsp	Heat shock protein
HsTSN	*Homo sapiens* tudor staphylococcal nuclease
IAP	Inhibitor of Apoptosis
ICE	Interleukin-1β-converting enzyme
IgG	Immunoglobin G

IL1β	Interleukin-1β
INS	Insoluble
INQ	Intranuclear quality control
IPOD	Insoluble protein deposit
iTRAQ	Isobaric tag for relative and absolute quantitation
JUNQ	Juxtanuclear quality control
K	Lysine
KCl	Potassium chloride
KH_2PO_4	Potassium phosphate
KO	Knockout
LC3	Light chain 3
LC-MS	Liquid chromatography mass spectrometry
LOG	Logarithmic growth at 30°C
LRGG	Leu-Arg-Gly-Gly
LSD1	Lesion stimulating disease
M1	Methionine at position 1
Mca1	Metacaspase 1
mAb	Monoclonal antibody
mcII-Pa	Metacaspase II of *Picea albies*
$MgCl_2$	Magnesium chloride
mRNA	messenger RNA
mtHtt	Mutant huntingtin protein
MTOC	Microtubule organizing centre
NaCl	Sodium chloride
NAD	Nicotinamide adenine dinucleotide
NADPH	NAD phosphate
Na_2HPO_4	Disodium phosphate
NaOH	Sodium hydroxide
NEDD4	Neural precursor cell expressed developmentally down-regulated protein 4
NEF	Nucleotide exchange factor

New1	Non-prion protein form of [NU+]
Nop12	Nucleolar protein 12
NP-40	Nonidet P-40
[NU+]	Prion form of New1
OD	Optical density
PaMCA1	*Podospora anserina* metacaspase 1
PARP	Poly(ADP-ribose) polymerase
PAS	Preautophagosomal structure
PAGE	Polyacrylamide gel electrophoresis
PBS	Phosphate buffered saline
Pca1	Pombe caspase 1
PCD	Programmed cell death
PCR	Polymerase chain reaction
PDB	Protein Database
PE	Phosphatidylethanolamine
PEG	Polyethylene glycol
Pfk1/2	Phosphofructokinase 1/2
[PIN+]	Prion forms of the Rnq1 protein
Pgk1	3-Phosphoglycerate kinase 1
Plk3	Polo-like kinase 3
PN	Proteostasis network
polyQ/N	Polyglutamine and asparagine rich region
ppm	parts per million
PS	Phosphatidylserine
[PSI$^+$]	Prion form of the Sup35 protein
PTM	Post-translational modification
PVDF	Polyvinylidene fluoride
R	Arginine
RAC	Ribosome-associated complex
RC	Regulatory core
REC	Recovery growth condition

RFP	Red fluorescent protein
RING	Really interesting new gene
RIPA	Radioimmunoprecipitation assay buffer
RNA	Ribonucleic acid
ROS	Reactive oxygen species
RPM	Rotations per minute
Rpn11	Regulatory particle non-ATPase 11
Rps31	Ribosomal protein S31
Rpt	Regulatory particle triple-A protein
Rnq1	Rich in asparagine (N) and glutamine (Q) 1
rRNA	Ribosomal ribonucleic acid
Rsp5	Reverses Spt- phenotype 5
RSLC	Rapid separation liquid chromatography
S	Serine
SCX	Strong cation exchange chromatography
SDS	Sodium dodecyl sulfate
Sec63	Secretory 63
SEM	Standard error of mean
sHsp	small heat shock protein
Sik1	Suppressor of I kappa b 1
Sis1	Sit4 suppressor 1
SLGS	Ser-Leu-Gly-Ser
SOL	Soluble
SPG	Stationary phase granule
Src	Sarcoma kinase
Ssa1/2	Stress-seventy subfamily A 1/2
Ssb1/2	Stress-seventy subfamily B ½
SSE	Secondary structural element
SUMO	Small ubiquitin-like modifier
tBid	Truncated BH3 interacting-domain death agonist
TBST	TRIS buffered saline containing Tween-20

TCEP	Tris(2-carboxyethyl) phosphine
TCP-1	Tailless complex polypeptide-1
TbMCA	*Trypanosoma brucei* metacaspase
TcMCA	*Trypanosoma cruzi* metacaspase
TDP-43	Tar DNA binding protein 43
tGnd1	Truncated 6-phosphoGlucoNateDehydrogenase
TOR	Target of Rapamycin
TRAIL	TNF-related apoptosis inducing ligand
TriC	TCP-1 ring complex
TRIS	Tris(hydroxymethyl)aminomethane
tRNA	Transfer RNA
TSN	Tudor staphylococcal nuclease
TUB	Tubulin
Ub	Ubiquitin
Ubc9^{ts}	Ubiquitin conjugating 9 temperature sensitive mutant
Ubp14	Ubiquitin specific protease 14
ULK1	unc-51 like autophagy activating kinase
UPS	Ubiquitin proteasome system
Vma2	Vacuolar membrane ATPase 2
VCP	Valosin containing protein
WT	Wildtype
XIAP	X-linked inhibitor of apoptosis
Y	Tyrosine
Yca1	Yeast caspase 1
Ydj1	Yeast DNAJ 1
YPD	Yeast peptone dextrose
Ypk1	Yeast protein kinase 1
z	Benzyloxycarbonyl
Zuo1	Zuotin 1

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Preface

Parts of the work described in this thesis were conducted in collaboration with Dr. Lawrence G. Puente at the Proteomics Core Facility in the Ottawa Hospital Research Institute. Specifically, the proteomic analysis of the insoluble protein fraction and bioinformatic analysis described in Chapter 3 and depicted in Tables S1-S4 are part of his contribution to the collaboration. Additionally, the results generated from this data along with results described in Chapter 3 and the discussion in 5.1 are parts of a published work (Appendix III). Additionally, subsequent proteomic analysis of the FL-RFP immunoprecipitation (Tables S5 and S6) and the cleavage assay fragments were also conducted by Dr. L. G. Puente. All other works described here were conducted solely by the author of the thesis.

CHAPTER 1

1. General Introduction

1.1. Caspases

Caspases are cysteine dependent aspartate specific proteases that possess a catalytic dyad comprised of conserved cysteine and histidine residues, which is responsible for cleaving substrates at aspartate (D) residues (Fuentes-Prior and Salvesen 2004). These proteases belong to the clan CD family that are characterized by the presence of a unique α/β structural fold termed the caspase hemoglobinase fold (CHF) (Walker, Talanian et al. 1994, Wilson, Black et al. 1994). Caspases are synthesized as inactive zymogens containing a N-terminal prodomain followed by the large (p20) and small (p10) caspase subunits that are separated by a linker region. Additionally, some caspases, termed 'initiators', possess specialized motifs, such as the caspase recruitment domain (CARD) and the death effector domain (DED) within their prodomain that mediate protein interactions, which initiate the apoptosis cascade. Alternatively, caspases lacking such motifs, termed 'effectors', are activated by the initiator caspases downstream and are responsible for proteolytic events that lead to the apoptotic phenotype (Nhan, Liles et al. 2006, Parrish, Freel et al. 2013). Caspases are highly conserved and present in all metazoans. Interleukin-1β-converting enzyme (ICE) was the first recognized caspase involved in proteolytic maturation of IL1β (Cerretti, Kozlosky et al. 1992). Its homolog in *Caenorhabditis elegans*, ced-3 along with ced-4 were observed to regulate cell death (Yuan and Horvitz 1990, Yuan, Shaham et al. 1993). Subsequently numerous caspases have been identified with varying distribution within species, but conserved in their role as regulators of apoptosis (Thornberry 1998, Lamkanfi, Declercq et al. 2002).

Apoptosis is a regulated form of programmed cell death (PCD) that was first described in 1972 by Kerr, Wyllie and Curie. This phenomenon was observed to be critical for normal embryonic development and was accompanied by specific structural changes within the cell that distinguishes it from other forms of PCD (Kerr, Wyllie et al. 1972). These features include chromatin condensation, phosphatidylserine (PS) externalization, cytoplasmic shrinkage and membrane blebbing (Leist and Jaattela 2001). Furthermore, caspase activity is not limited to apoptosis and is required for cellular differentiation, spermatogenesis, dendritic pruning and immune response, which highlights the multifunctionality of these proteases (Fernando and Megeney 2007, Fuchs and Steller 2011, Bell and Megeney 2017).

To become active, the procaspase zymogen must undergo post-translational processing at specific sites that separates the two catalytic subunits followed by the removal of the N-terminal region. The active protease is a heterodimeric complex with a central active site containing the catalytic cysteine for substrate cleavage (Degterev, Boyce et al. 2003, MacKenzie and Clark 2012). *In vivo*, caspases are activated via extrinsic and intrinsic pathways, which lead to the recruitment of initiator caspases via their prodomain motifs to multimeric protein complexes such as the death induced signalling complex (DISC), where they undergo dimerization and proximity induced activation (Kischkel, Hellbardt et al. 1995, Boatright, Renatus et al. 2003). Activated initiator caspases in turn, amplify the apoptotic signal by cleaving and activating inactive zymogens of effector caspases. A substantial activation of effector caspases, such as caspase 3, is considered to be a ‘point of no return’ that commits the cell to the apoptotic fate (Boatright and Salvesen 2003). Thus, regulation of apoptosis via modulation of caspase activity is essential to balance its apoptotic and non-apoptotic functions to ensure proper development. Accordingly, caspase activity is regulated by the inhibitor of apoptosis (IAP) family, which interact with active caspase enzymes and suppress their catalytic activity (Gyrd-Hansen and Meier 2010). Additionally, post-translational modifications, such as phosphorylation and ubiquitination, have also been reported to regulate caspase activity (Zamaraev, Kopeina et al. 2017).

1.2. Metacaspases

The discovery that single celled organisms such as the yeast, *Saccharomyces cerevisiae,* can undergo apoptotic cell death, argued that such organisms may possess caspase like proteases. For example, when mutating critical residues in Cdc48 or when overexpressing mammalian Bax in yeast, the cells displayed hallmark features of apoptosis such as phosphatidylserine externalization and chromatin condensation (Madeo, Frohlich et al. 1997, Ligr, Madeo et al. 1998). Subsequently, using a bioinformatic survey, caspase related proteases, termed metacaspases, were discovered in plants, fungi and protozoa that were similar in sequence and structure to caspases, particularly the presence of the cysteine-histidine catalytic dyad (Uren, O'Rourke et al. 2000). Further investigations using the characteristic CHF fold as a unifying feature, led to the discovery of various structurally related proteases including the identification of metacaspases in multiple bacterial lineages (Aravind and Koonin 2002). To date, other than animals, metacaspases are known to be present in numerous prokaryotic and eukaryotic organisms (McLuskey and Mottram 2015, Minina, Coll et al. 2017).

Metacaspases have been grouped into various categories based on their domain architecture, which echo the caspase classification scheme. Type I metacaspases contain an extended N-terminal prodomain that is rich in proline residues and possess a zinc finger motif. These regions lack any consensus motifs, such as the CARD and DED, however, these domains in metacaspases have been observed to possess functional importance (Uren, O'Rourke et al. 2000, Aravind and Koonin 2002). For example, the prodomain of the *Trypanosoma brucei* metacaspase TbMCA2 is suggested to regulate its activity by restricting access to the active site of the enzyme (McLuskey, Rudolf et al. 2012). In plants, the zinc finger domain in the *Arabidopsis thaliana* type I metacaspase AtMC1 was observed to interact with the lesion stimulating disease 1 (LSD1) protein that was inhibitory to its function (Coll, Vercammen et al. 2010). Alternatively, type II metacaspases, which have been primarily discovered in plants, have a short N-terminal extension that is devoid of any functional motifs. Instead, they possess a large conserved linker region between the two catalytic subunits; p20 (large) followed by p10 (small) subunit (Uren, O'Rourke et al. 2000). More recently, species belonging to plankton were observed to possess metacaspases with similar sequence organization to the type II, but with a reversed arrangement of the subunits; p10 followed by p20. These metacaspases were denoted as type III and their biochemical properties are not yet known (Choi and Berges 2013). In addition to the catalytic conserved cysteine residue, type I and type II metacaspase are known to possess an additional catalytic cysteine, which is positioned upstream of the p20 subunit and has been shown to have functional importance; as evidenced by the C29A/C147A double mutant for AtMC9, which does not exhibit any proteolytic activity (Szallies, Kubata et al. 2002, Belenghi, Romero-Puertas et al. 2007).

Additionally, the distribution and frequency of metacaspase expression between species is widely varied. The genome of yeast such as *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe* contain only a single type I metacaspase named yeast caspase 1 (Yca1) and pombe caspase 1 (Pca1) respectively (Madeo, Herker et al. 2002, Zhang, Chieu et al. 2003); whereas the genome of the protist *Trypanosoma brucei* encodes for five type I metacaspases denoted as TbMCA1-5; two of which, TbMCA1 and 4, are inactive as they possess a serine residue in place of a cysteine residue within the catalytic dyad (Szallies, Kubata et al. 2002, Mottram, Helms et al. 2003). Alternatively, the plant species *Arabidopsis thaliana* expresses nine metacaspases; AtMC1-3 are grouped as type I and the remaining AtMC4-9 are grouped as type II (Vercammen, van de Cotte et al. 2004, Watanabe and Lam 2005, Tsiatsiani, Van Breusegem et al. 2011).

Recent structural studies show that in addition to the CHF, the active site is conserved between caspases and metacaspases (Figure 1). Furthermore, these proteases also share a large proportion of secondary structural elements (SSE) including the structure of the active site and the position of the catalytic dyad within (McLuskey and Mottram 2015). However, differences in the internal architecture suggests that metacaspase are activated via an alternate mechanism. These differences include the presence of two additional β-strands in both type I metacaspases TbMCA2 and Yca1, which allows them to exist as stable monomeric structures. Furthermore, the location of the processing site that separates the two subunits was observed to differ between in TbMCA2 and caspase 7 (Figure 1B and D). In addition, the presence of calcium binding sites in metacaspases suggested calcium to be an activator/regulator of metacaspase activity (Watanabe and Lam 2005, McLuskey, Rudolf et al. 2012, Wong, Yan et al. 2012). These studies also provided a unique regulatory role for the N-terminal prodomain of TbMCA2. Structurally, this region was observed to traverse around the protein and span across the active site. Furthermore, the Y31 residue in the prodomain was bound to residues within the active site. Mutation of this residue (Y31A) led to increased processing of the metacaspase

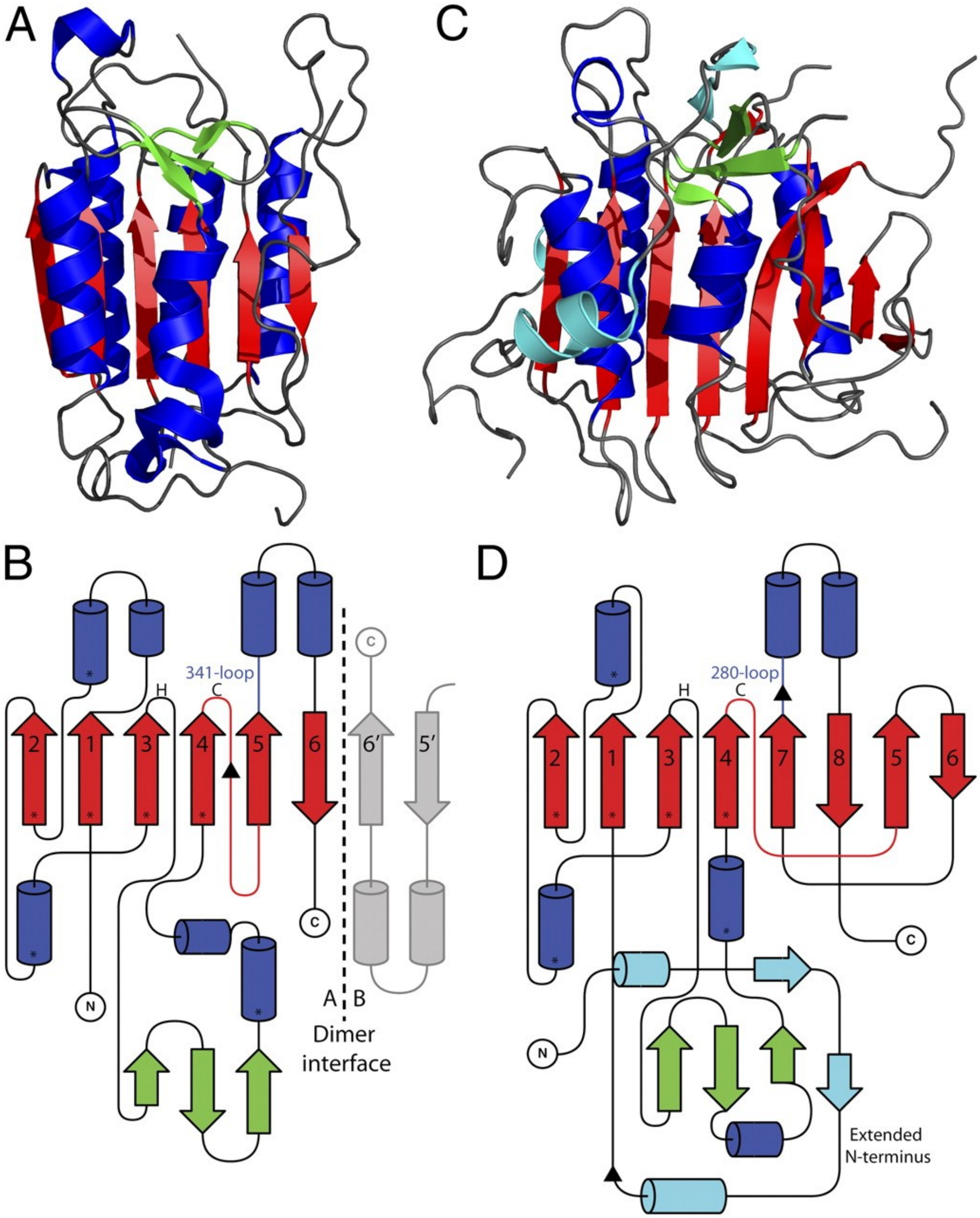

A
C
B
341-loop
H
C
2
1
3
4
5
6
6′
5′
C
N
C
A
B
Dimer
interface
D
280-loop
H
C
2
1
3
4
7
8
5
6
C
N
Extended
N-terminus

Figure 1. Comparison of TbMCA2 and caspase-7. Ribbon diagram of caspase-7 (*A*) and metacaspase (*C*). General loops are colored gray/black, the main β-sheet is colored red, surrounding α-helices are shown in blue, and a small section of the β-sheet at the C terminus of β3 is shown in green. In TbMCA2, secondary structural elements found on the N-terminal domain are colored cyan. (*B*) Topology diagram of caspase-7. The 341-loop and the position of the catalytic dyad are highlighted, and the β-strands are numbered from the N terminus. The intersubunit linker is drawn as a red line with the cleavage site highlighted (▲). (*D*) Topology diagram of TbMCA2, with the catalytic loop shown in red. The 280-loop affected during the Ca^{2+} activation of TbMCA2 and known autoprocessing sites (▲) are shown. The CHF core secondary structural elements are highlighted (*) in *B* and *D*. Adapted from McLuskey et al. 2012. PNAS 109:7469-74 (McLuskey, Rudolf et al. 2012).

suggesting that Y31 association with the active site limits substrate access (McLuskey and Mottram 2015). The presence of this feature has yet to be determined in other metacaspases or caspases.

The processing sites reported for metacaspases also differ to that for caspases. Metacaspases undergo processing at arginine (R) and lysine (K) residues instead of aspartic acid (D) residues, which are preferred by caspases. For instance, generation of recombinant type II AtMC9 identified R183 as a processing site (Vercammen, van de Cotte et al. 2004). Furthermore, structural analyses identified processing at the K55 and K268 residues for TbMCA2 (McLuskey, Rudolf et al. 2012). Similarly, numerous other metacaspase have also been reported to undergo processing at R/K residues (Watanabe and Lam 2005, Minina, Coll et al. 2017). This difference in cleavage site specificity is not limited to autoprocessing and is also evident in substrate processing by metacaspases. Plants and yeast metacaspases have been shown to cleave R/K based synthetic peptides such as Boc-GRR-AMC *in vitro* (Watanabe and Lam 2005). Furthermore, assessing the degradome of the plant metacaspase AtMC9, led to the identification of numerous substrates that were cleaved at R/K sites (Tsiatsiani, Timmerman et al. 2013).

However, despite the difference in cleavage site specificity, metacaspase and caspases have been observed to cleave the same substrate. For instance, the tudor staphylococcal nuclease (TSN) was the first identified substrate for the Norway spruce metacaspase mcII-Pa during developmental and stress-induced PCD. Of note, human TSN (HsTSN) was also shown to be a phylogenetically conserved substrate for caspase 3 during apoptosis (Sundstrom, Vaculova et al. 2009). Additionally, the well-known caspase substrate poly(ADP-ribose) polymerase (PARP), which is cleaved by caspase 3 during apoptosis to prevent NAD and ATP depletion for apoptosis progression (Boulares, Yakovlev et al. 1999), was also shown to be a substrate of the fungal metacaspase PaMCA1 in *Podospora anserina* (Strobel and Osiewacz 2013).

1.3. Yeast caspase 1 (Yca1)

The genome of *Saccharomyces cerevisiae* encodes for a single metacaspase denoted Yeast caspase 1 (Yca1), which is also referred to as Metacaspase 1 (Mca1). Yca1 is the most extensively characterized metacaspase to date, with numerous studies investigating its physiologic as well as biochemical regulation. The presence of a N-terminal prodomain categorizes Yca1 as a type I metacaspase. This region is rich in proline residues that flank a unique polyglutamine rich region (polyQ/N), which has been suggested to confer prionogenic properties to Yca1 (Uren, O'Rourke et al. 2000, Alberti, Halfmann et al. 2009). Additionally, the prodomain has been shown to be involved in directing the metacaspase to the aggregate fraction of the proteome, most likely by establishing protein interactions (Lee, Brunette et al. 2010). Structural analyses of Yca1 suggested that the prodomain of Yca1 is not required for activity and similar to the N-terminal region in TbMCA2, may be inhibitory (Wong, Yan et al. 2012, McLuskey and Mottram 2015).

Structurally, Yca1 conforms to the caspase fold and is superimposable onto caspase structures (Figure 2). Residues involved in substrate binding and in calcium binding are conserved between Yca1 and TbMCA2 (Wong, Yan et al. 2012). Furthermore, the catalytic cysteine at position 297 is required for processing of Yca1, as the C297A mutant was unable to undergo processing (Madeo, Herker et al. 2002). More recently, four tentative processing sites of Yca1 were identified; R93 and K107 residues at the N-terminus and K352 and K355 residues downstream in the caspase subunit, which confirmed its R/K cleavage specificity like other metacaspases (Tsiatsiani, Van Breusegem et al. 2011, Wong, Yan et al. 2012). Additionally, GAPDH isoforms Tdh2/3 have been reported to be a substrate of Yca1 under apoptotic conditions (Silva, Almeida et al. 2011), which is also a target of caspase 1 (Shao, Yeretssian et al. 2007). Furthermore, Yca1 was shown to cleave a portion of the Bir1 protein *in vitro,* which was greatly enhanced by calcium binding (Wong, Yan et al. 2012). However, neither study could determine if Yca1 also targets R/K residues on its substrates. Bir1 belongs to the inhibitor of apoptosis protein family, which are targeted by caspases during apoptosis (Yoon and Carbon 1999, Gyrd-Hansen and Meier 2010). Thus, cleavage of Bir1 by Yca1 reinforces the functional overlap that exists between caspases and metacapases, despite differences in cleavage site specificity.

1.3.1. Yeast apoptosis and Yca1

The original observation that yeast can undergo apoptosis was perplexing as the retention of a cell death process in a single celled organism argues against evolutionarily principles i.e. retention of a death only protein in a single cell organism would reduce fitness rather than improve it. Nonetheless, the basis for yeast apoptosis is suggested to be the altruistic nature of the organism, where aged cells undergo apoptosis to improve the odds of survival for younger cells. Furthermore, the tractability of the yeast system has been influential in understanding various fundamental processes, including apoptosis (Carmona-Gutierrez, Eisenberg et al. 2010, Shrestha and Megeney 2012).

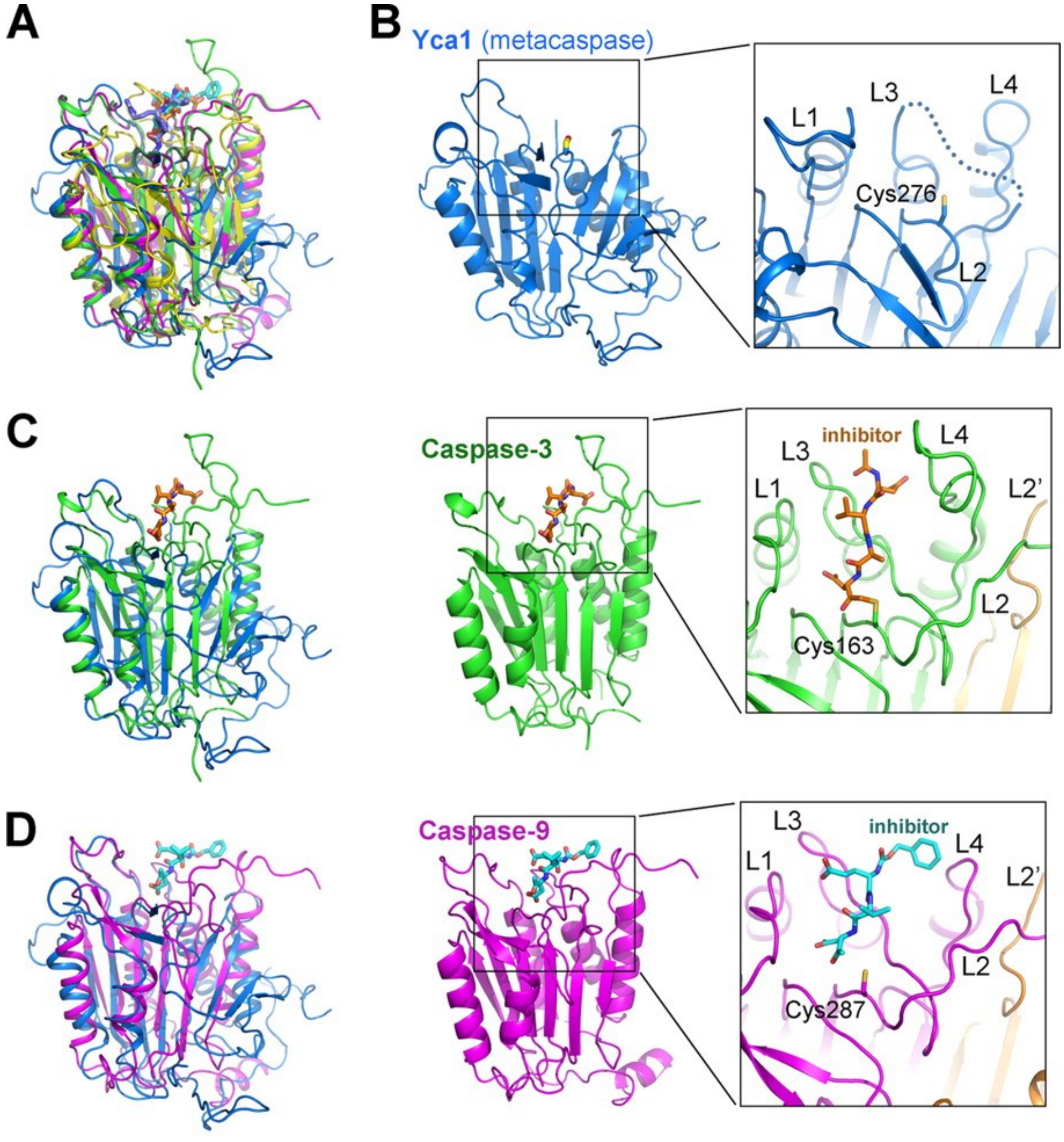

A
B
Yca1 (metacaspase)
L1
L3
L4
Cys276
L2
C
Caspase-3
inhibitor
L3
L4
L1
L2'
L2
Cys163
D
Caspase-9
L3
inhibitor
L4
L1
L2'
L2
Cys287

Figure 2. Structural comparison of Yca1 with caspases. (A) Structural overlay of Yca1 (*blue*), caspase-3 (*green*) and caspase-9 (*magenta*). (B) A close-up view of the active site of Yca1. Among the four active site loops, L1, L2, and L4 exhibit well defined conformation. A large portion of the L3 loop (*dotted line*), however, is disordered, likely due to its flexible nature in the absence of substrate binding. (C) Comparison of Yca1 (PDB code 4F6O) with caspase-3 (PDB code 1CP3). A close-up view on the caspase-3 active site is shown. The covalently bound inhibitor acetyl-Asp-Val-Ala-Asp-fluoromethyl ketone (Ac-DVAD-fmk) is highlighted in *orange.* (D) Comparison of Yca1 with caspase-9 (PDB code 1JXQ). A close-up view on the caspase-9 active site is shown. The covalently bound inhibitor benzyloxycarbonyl-Glu-Val-Asp-dichlorobenzylmethyl ketone (z-EVD-dcbmk) is highlighted in *cyan.* Adapted from Wong et al. 2012. J. Biol. Chem. 287:29251-59 (Wong, Yan et al. 2012).

In yeast, Yca1-mediated apoptosis can occur under various conditions. Reports suggests that exposure to various external stressors such as lethal doses of salts, acids, metals and viral toxins result in the induction of apoptotic cell death. Additionally, defects in key cellular processes such as mRNA stability and mitochondrial metabolism or the expression of human disease-related proteins such as alpha-synuclein can also lead to an apoptotic cell death, as triggered by Yca1 activation (Mazzoni and Falcone 2008, Madeo, Carmona-Gutierrez et al. 2009). However, the intermediate signals that transduce apoptosis in yeast have yet to be extensively explored and to date, no death receptors or ligands that lead to metacaspase activation analogous to metazoans have been reported for Yca1 or any other metacaspase.

The generation and accumulation of reactive oxygen species (ROS) is a common factor that underlines metacaspase-dependent apoptosis in *S. cerevisiae*. Upon external insults such as H_2O_2 treatment or internal stressors that augment ROS such as expression of a mutant Cdc48 (S565G), results in Yca1-dependent apoptosis. Ablation of Yca1 led to reduced sensitivity to ROS, which suggested that ROS mediates Yca1-dependent apoptosis (Madeo, Frohlich et al. 1997, Madeo, Herker et al. 2002, Khan, Chock et al. 2005). ROS-mediated regulation of metacaspase-dependent apoptosis has also been observed for other yeast species, such as *Candida albicans* where the mRNA decapping protein Edc3, was observed to drive ROS accumulation and regulate expression of the metacaspase CaMCA1 (Jung and Kim 2014, Jeong, Lee et al. 2016). Expression of Yca1 during ROS-induced apoptosis in *S. cerevisiae* may involve a similar mechanism, although additional experimentation will be required to determine this hypothesis. Similarly, ROS is also a driver of apoptosis in metazoans. Uncoupling of oxidative phosphorylation in human carcinoma cell lines by carbonyl cyanide *m*-chlorophenylhydrozone (CCCP) led to ROS production, which in turn led to TRAIL induced apoptotic activation of caspase 3 (Izeradjene, Douglas et al. 2005). Together, these observations suggest that both caspases and metacaspases can be triggered by ROS during apoptosis and that ROS regulation is a conserved feature of apoptosis in metazoans and yeasts.

In addition to ROS, the mitochondrial factor cytochrome C (CytC) has also been observed to be involved in Yca1-mediated apoptosis. In the absence of ATP/ADP carrier proteins, acetic acid treated yeast release CytC due to impairment in the permeabilization of the mitochondrial outer membrane (Pereira, Camougrand et al. 2007). However, downstream effects of CytC release in yeast are not as well defined as in metazoans, where this event signals the formation of the apoptosome and activation of the caspase 9-mediated intrinsic apoptotic cascade (Parrish, Freel et al. 2013). Additionally, homologs of apoptotic peptidase activating factor 1 (Apaf1) or other components of the apoptosome have yet to be identified in yeast. Thus, whether CytC is an ancestral proapoptotic protein or represents a conservation of the intrinsic apoptotic machinery in yeast, remains to be determined (Carmona-Gutierrez, Eisenberg et al. 2010).

Despite the established role for Yca1 in apoptotic signaling, numerous forms of regulated cell death occur independent of Yca1 (Madeo, Carmona-Gutierrez et al. 2009). For example, cells treated with external stressors such as formic acid or copper, undergo cell death with hallmark features of apoptosis, but without the involvement of Yca1 (Liang and Zhou 2007, Du, Su et al. 2008). More surprisingly, proapoptotic proteins such as human Bax (hBax) and truncated Bid (tBid) promote cell death when expressed in yeast and do so without the involvement of Yca1 (Guscetti, Nath et al. 2005). Such observations argue against the role of Yca1 as an exclusive executioner of apoptosis in yeast or suggests a limited conservation of apoptotic function for Yca1, despite it being the only structurally caspase-related protease in *S. cerevisiae*. On the other hand, this may also suggest that, like caspases, the functional paradigm of metacaspases such as Yca1 may also include involvement in non-death related processes.

1.3.2. Non-death roles of Yca1

As observed for caspases, metacaspases of various fungal species and protozoa have been shown to promote cell survival and fitness (Tsiatsiani, Van Breusegem et al. 2011, Shrestha and Megeney 2012). Specifically, in *S. cerevisiae*, Yca1 is required for proper cellular growth, by actively regulating cell cycle dynamics. Loss of Yca1 or its activity led to a delayed G1 to S transition as Δ*yca1* cells remained in the G1 phase for a prolonged period compared to wildtype (Lee, Puente et al. 2008). A similar observation was also noted for the *Trypanosoma* metacaspase TcMCA3, which when overexpressed, led to the complete block of the G1/S transition and severe growth reduction (Laverriere, Cazzulo et al. 2012). These cell cycle functions of metacaspases have paralogous activities in mammalian caspases. For example, caspase 3 is required for B cell homeostasis, which is mediated by caspase 3 cleavage of the cell cycle regulator p21 (Woo, Hakem et al. 2003) More specifically, caspase 8 was reported to regulate the G1/S transition to promote hepatocyte proliferation (Gilot, Serandour et al. 2005). Taken together, these observations suggest a conserved role for metacaspase and caspases in regulating the G1/S transition.

In addition to the G1/S transition, Yca1 was also shown to be involved in establishing the G2/M checkpoint. Microtubule disruption by nocodazole treatment induces cell cycle arrest at the induced G2/M checkpoint in wildtype cells, yet nocodazole treated Δ*yca1* cells were observed to continue cell cycle progression (Lee, Puente et al. 2008). Similarly, caspase 3 activity in human hepatoma cells is required for the establishment of this nocodazole induced checkpoint suggesting a functional conservation between caspases and metacaspases in regulating the G2/M checkpoint (Hsu, Yu et al. 2006). Overall, regulation of cell cycle dynamics represents a non-apoptotic, prosurvival function that is conserved in caspase and metacaspase proteases.

Subsequent molecular analysis of Yca1 revealed that this metacaspase acts to limit the accumulation of protein aggregates within the cell. First, Yca1 was observed to interact with various chaperones such as the Cdc48, Ssa1/2 and Hsp42 that are involved in protein folding and degradation. Furthermore, in stationary aged cultures, Yca1 colocalized with the chaperone Hsp104, which is a marker for aggregated material within the cell. The loss of Yca1 led to an increased retention of insoluble protein within the cell, which was accompanied by an increase in vacuolar peptidase levels and vacuole abundance (Lee, Brunette et al. 2010). Taken together, these observations suggest that Yca1 ensures protein homeostasis or proteostasis (in part) by regulating the level of insoluble protein material. The ablation of this function led to the compensatory upregulation of the autophagic response as observed by the increase in vacuolar processes. The proteostasis control exerted by Yca1 may originate from precise subcellular targeting events, as Yca1 directs misfolded proteins to specific protein quality control sites, namely the juxtanuclear quality control (JUNQ) and insoluble protein deposit (IPOD) (Hill, Hao et al. 2014). This subcellular distribution of Yca1 was also associated with the capacity to extend the replicative lifespan of the cell, where Yca1 facilitated the removal of protein aggregates in coordination with the Hsp104 disaggregase and the general proteasome (Hill, Hao et al. 2014). Together, these observations suggest that Yca1 confers a fitness advantage, which in turn is dependent on its capacity to maintain proteostasis.

The proteostasis function of Yca1 has also been speculated for the plant metacaspase AtMC1. Loss of AtMC1 leads to early senescence in plants, which was characterized by the presence of increased protein aggregates. Furthermore, the full length AtMC1 was observed to localize to the insoluble aggregates. Thus, in the context of aging, a similar role for AtMC1 in mediating aggregate clearance may occur, which in turn has been suggested to limit premature senescence (Coll, Smidler et al. 2014). Additionally, there may be an analogous function in specific caspase proteases. For example, caspases have been implicated in regulating levels of toxic disease associated proteins, where caspase 3 activity has been reported to cleave the amyotrophic lateral sclerosis (ALS)-associated tar DNA binding protein 43 (TDP-43) to reduce its toxicity. Indeed, blocking this cleavage event led to increased toxicity of TDP-43 compared to the wildtype protein (Suzuki, Lee et al. 2011). More recently, caspase 2 has also been implicated in regulating age-associated proteome changes. Proteome profiling suggested that premature aging observed in caspase 2 deficient mice was due to specific proteomic changes such as reduced NADPH, ribosomal and respiratory complex protein levels (Wilson, Shalini et al. 2015). Therefore, emerging data suggests that both caspases and metacaspases may balance their respective proteomes through engagement of global proteostasis regulatory events.

1.4. Protein folding and aggregation

The regulation of cellular protein levels is an indispensable feature which ensures the fidelity of key fundamental processes within the cell. (Balch, Morimoto et al. 2008). For a protein to be functional, the newly synthesized linear nascent polypeptide chain must fold into a three-dimensional (3D) functional structure termed the native fold. *In vitro* folding experiments have shown that the information required for a nascent peptide to adopt a native fold is present within the primary sequence (Dobson and Ellis 1998). Protein folding is initiated as the nascent peptide emerges from the ribosome and is dependent on various intramolecular dynamics that leads to the formation of various structural intermediates before the functional structure is acquired (Dobson 2003). The generation of these structural intermediates increases the risk of aggregation as hydrophobic residues that are normally buried within the protein structure, are often found to be exposed in these partially folded intermediates (Rajan, Illing et al. 2001, Chiti and Dobson 2006). Additionally, some proteins are inherently disordered and only achieve their functional structure by associating with other partners (Dunker, Silman et al. 2008). Furthermore, the crowded cellular environment also poses a risk for protein folding *in vivo* as it restricts the liberty with which nascent polypeptide chains might fold, increasing the probability of non-specific interactions leading to protein aggregation (Ellis and Minton 2006, Hartl and Hayer-Hartl 2009). Thus, the cell invests in sophisticated quality control mechanisms comprising of various chaperone proteins that act to oversee the folding/refolding of proteins as well as degradation machineries that facilitate the removal of unwanted misfolded conformers and aggregated material (Hartl 1996, Bukau and Horwich 1998, Goldberg 2003, Rubinsztein 2006). Together, these components form a coordinated

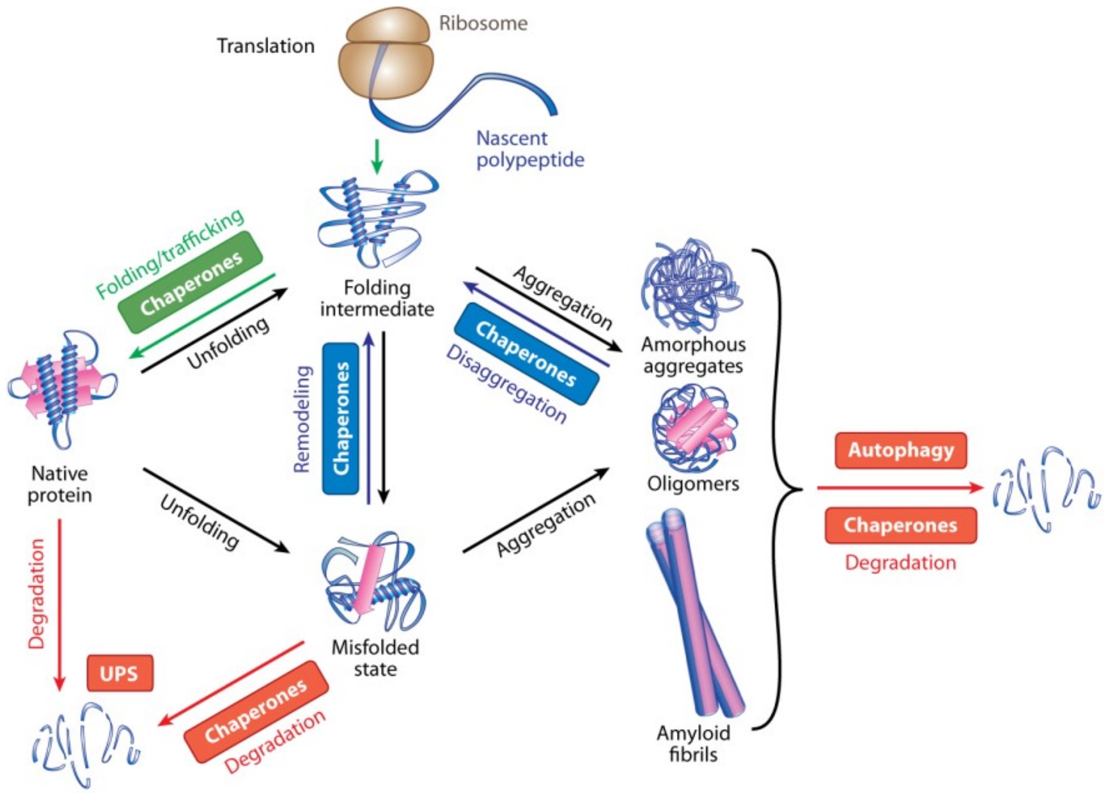


Figure 3. Protein fates in the proteostasis network (PN). The PN integrates chaperone pathways for the folding of newly synthesized proteins, the remodeling of misfolded states, and disaggregation with protein degradation. Adapted from Kim et al. 2013. Annu. Rev. Biochem. 82:323-55 (Kim, Hipp et al. 2013).

network that act to limit protein aggregation and ensure proteostasis (Figure 3), which is fundamental for proper cellular and organismal functioning (Balch, Morimoto et al. 2008, Powers, Morimoto et al. 2009).

Protein misfolding increases when these proteostasis components are overwhelmed or exhausted by various factors such as, mutations, errors in transcription/translation, environmental stress and age-related decline. Such cellular dysfunction has been attributed to various disorders termed 'conformational diseases' (Kopito and Ron 2000, Ross and Poirier 2004). Furthermore, when the degree at which misfolding occurs surpasses the cellular refolding and degradation capacity, misfolded proteins tend to accumulate, which leads to their ordered incorporation into larger structures termed aggregates. These aggregates are ordered structures with varying levels of β-sheet organization (Dobson 2003). The presence of such aggregates in dysfunctional neurons was originally hypothesized to be the pathological trigger for a variety of neurodegenerative disorders. However, more recent evidence suggest that these structures may serve as a secondary protective mechanism (Chiti and Dobson 2006). For instance, inclusion body formation of mutant huntingtin (mtHtt) was positively correlated with neuronal survival compared to the diffused oligomeric soluble form (Arrasate, Mitra et al. 2004). Furthermore, a similar role was also described for aggregates formed upon overexpression of alpha-synuclein and synphilin-1 (Tanaka, Kim et al. 2004).

This spatial sequestration of misfolded proteins has also been observed in yeast cells (Kaganovich, Kopito et al. 2008). Upon heat shock coupled to proteasome inhibition, misfolded proteins partitioned into two distinctly localized cytoplasmic inclusions. The slower forming inclusion colocalized with Atg8 and the pre-autophagosomal structure

(PAS) and was observed to be enriched for aggregates of the amyloidogenic prion protein Rnq1 and thus named IPOD (for insoluble protein deposit). The other inclusion displayed a perinuclear localization which was encapsulated by the endoplasmic reticulum (ER) marker Sec63 and named JUNQ (for juxtanuclear quality control compartment) (Kaganovich, Kopito et al. 2008). However, the precise localization of the JUNQ has been questioned as the same substrates used to define the JUNQ were also confined within nucleopore rings. Thus, the authors of the latter study renamed the JUNQ as INQ (for intranuclear quality control compartment) (Miller, Ho et al. 2015). The distinct localization of the JUNQ/INQ and IPOD, has led to the suggestion that proteins which localize to the JUNQ/INQ are those targeted for degradation via the proteasome and ER associated degradation (ERAD), whereas the aggregate clearance of IPOD may involve a bulk degradation process such as autophagy (Kaganovich, Kopito et al. 2008). These compartments were observed to be physically tethered to the vacuole and the nucleus which results in the asymmetric retention of the aggregate within the aged mother cell; a feature that has been shown to ensure that nascent daughter cells are generated free of aggregate associated toxicity (Liu, Larsson et al. 2010, Spokoini, Moldavski et al. 2012). In addition to the IPOD and JUNQ/INQ, further investigation recognized that misfolded proteins are initially incorporated into smaller stress foci, referred to as CytoQ which limits aberrant aggregation and allows for future sorting into the larger structures (Spokoini, Moldavski et al. 2012, Miller, Ho et al. 2015).

Sorting of misfolded substrates into either compartment was first suggested to be dependent on their ubiquitination state, where ubiquitinated proteins were observed to localize solely to the JUNQ (Kaganovich, Kopito et al. 2008). However, subsequent studies have revealed that ubiquitin is rather a general signal as ubiquitinated substrates were also observed to be directed to the IPOD (Shiber, Breuer et al. 2013, Miller, Ho et al. 2015, Miller, Mogk et al. 2015). Overall, the formation of such structures suggests that protein aggregation is an ordered process with multiple defense strategies that allows for efficient proteostasis maintenance across a wide variety of stress events.

1.5. Chaperone proteins

One of the main regulatory components of the proteostasis network (PN) are chaperone proteins. These proteins are defined as those which interact with respective substrates and aid in their assembly into a functionally active conformation (Hartl 1996). A defining characteristic of chaperone proteins is their elevated expression under stress conditions during which the likelihood of misfolding and aggregation increases. The identification of this feature by Ferruccio Ritossa in the 1960s led to the concept and discovery of chaperone proteins and the heat shock response (Ritossa 1964, Ritossa 1996). Subsequently, chaperone proteins were demonstrated to be present in all organisms and broadly responsive to stress conditions, using heat shock treatment. These proteins have been aptly named heat shock proteins (Hsp) and are grouped based on molecular weight; Hsp40, Hsp60, Hsp70, Hsp90, Hsp100 and small Hsps (Lindquist and Craig 1988, Hartl 1996). These chaperones network with each other to ensure proper protein folding, as well as to regulate protein trafficking and turnover, which allows for the maintenance of a healthy proteome (Gong, Kakihara et al. 2009, Fujiwara, Ishihama et al. 2010).

Chaperones mediate *de novo* folding at multiple levels (Figure 4). Upon emergence of the nascent polypeptide from the ribosome, specialized Hsp70 chaperones, such as the ribosome-associated complex (RAC) in yeast comprising of Ssz1 (Hsp70) and Zuo1 (Hsp40), interacts with the nascent chain to limit premature folding during translation (Preissler and Deuerling 2012). Additionally, non-ribosome associated Hsp70 along with its Hsp40 co-chaperone, ATP and nucleotide exchange factors (NEFs) actively assist in the post-translational folding of peptide chains and structural intermediates in the cytosol. These chaperones recognize and bind exposed hydrophobic residues on misfolded or partially folded proteins and prevent aggregation. The folding/re-folding process occurs via ATP-dependent cycles of binding and release to the substrate (Kampinga and Craig 2010, Winkler, Tyedmers et al. 2012). Additionally, in some cases, such as nuclear steroid hormone receptors, the Hsp70/Hsp40 chaperones transfer the folding substrate to the Hsp90 system which, also assisted by cofactors and ATP, supports the partially folded protein's bid to reach its functional conformation (McClellan, Xia et al. 2007, Taipale, Jarosz et al. 2010). Alternatively, partially folded proteins can also be transferred to the chaperonins/Hsp60 family members such as TRiC and GroEL-GroES. These chaperones form a multimeric large ring-like structures that contain a central cavity which allows for secluded folding of proteins that possess complex folds, also in an ATP dependent manner (Yam, Xia et al. 2008, Fujiwara, Ishihama et al. 2010).

Members of the small Hsp (sHsp) family act in an ATP-independent manner as 'holdases'. These chaperones form strong contacts with early unfolded or misfolded conformers to limit aggregation which allows for subsequent refolding by other chaperones families (Mogk and Bukau 2017). Furthermore, in yeast, small Hsps have been observed to also function as 'aggregases', where Hsp42 was observed to specifically localize to the

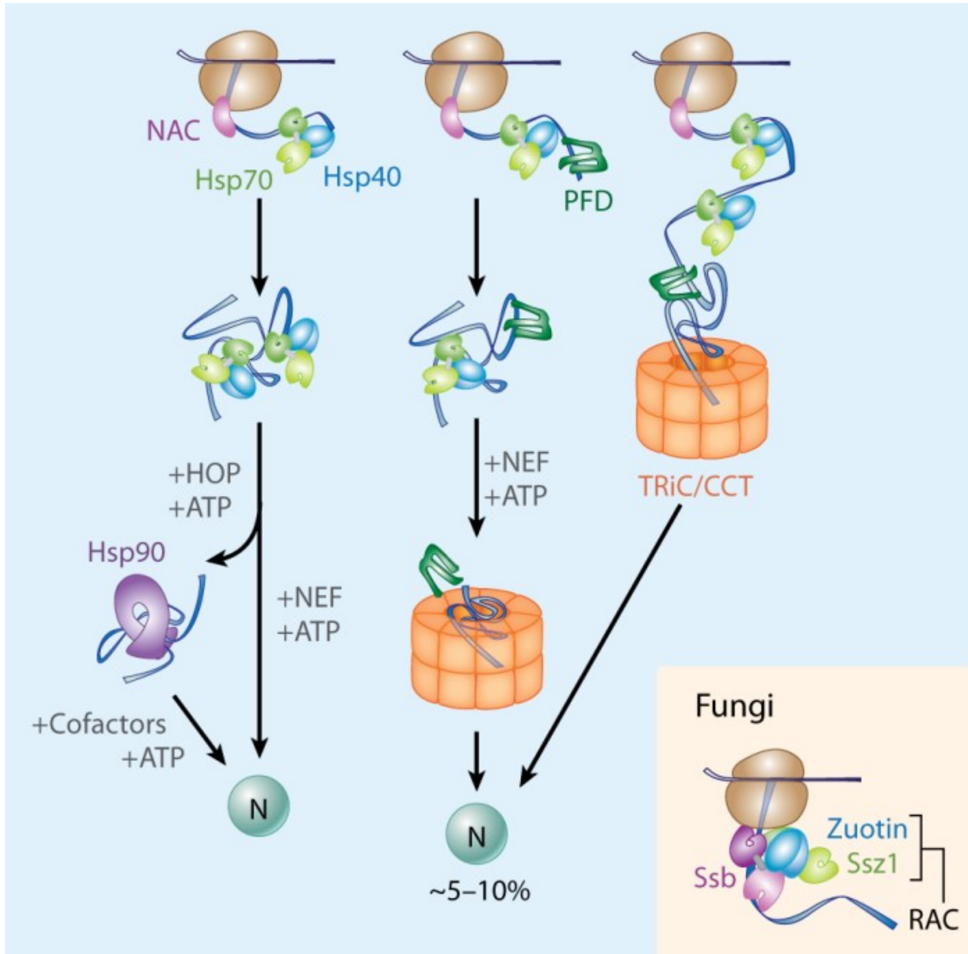


Figure 4. Organization of chaperone pathways in the cytosol in eukaryotes. Ribosome-bound chaperones [nascent-chain-associated complex (NAC)] aid folding co-translationally by binding to hydrophobic segments on the emerging nascent chains. For longer nascent chains, members of the heat shock protein Hsp70 family together with Hsp40s and nucleotide exchange factors (NEFs), mediate co- and post-translational folding. Partially folded substrates may be transferred to the chaperonins [Tailless complex polypeptide-1 (TCP-1) ring complex (TRiC)/chaperonin-containing TCP-1 (CCT)]. The Hsp90 system also receives its substrates from Hsp70 system and mediates their folding with additional cofactors. The insert shows the ribosome-binding chaperone system, the ribosome-associated complex (RAC), in fungi. RAC consists of Ssz1 (a specialized Hsp70) and zuotin (Hsp40) and assists nascent chain folding together with another Hsp70 isoform, Ssb. Percentages indicate the approximate protein flux through the various chaperones. Adapted from Kim et al. 2013. Annu. Rev. Biochem. 82:323-55 (Kim, Hipp et al. 2013).

CytoQ and was required for the formation of this compartment (Miller, Ho et al. 2015). Upon aggregation, members of the Hsp100 family act to reverse the aggregation process. In yeast, the presence of the 'disaggregase' Hsp104 ensures that the organism survives under various stresses (Sanchez, Taulien et al. 1992). Hsp104 in coordination with the Hsp70 system binds to aggregated material, such as amyloid structures of prions, and acts to resolubilize the aggregate in an ATP-dependent manner (Glover and Lindquist 1998, Winkler, Tyedmers et al. 2012). Furthermore in yeast, Hsp104 has been observed to colocalize with the JUNQ and IPOD as well as CytoQ, where it is suggested to act similarly (Kaganovich, Kopito et al. 2008, Miller, Ho et al. 2015).

Thus, chaperones are critical components of the PN that ensure cellular fidelity by regulating protein structure. Furthermore, the presence of multiple families of chaperones allows for protein quality control under various conditions and loss or dysfunction of the chaperone machinery have been linked to numerous diseases (Hishiya and Takayama 2008).

1.6. Protein degradation

In addition to protein folding and re-folding, the PN is also comprised of protein degradation complexes (Figure 3). Removal of unwanted material is also an important feature contributing to proteostasis and perturbations affecting efficient protein turnover have also been linked to various disease conditions (Madeo, Eisenberg et al. 2009, Im and Chung 2016). Within the cell, protein degradation occurs either at the proteasome or in bulk via one of the many autophagy pathways. The degradation process ensures that proteins are structurally accurate and are engaged in cellular processes in a proper manner (Jackson and Hewitt 2016).

1.6.1. The Ubiquitin Proteasome System (UPS)

The ubiquitin proteasome system (UPS) is the primary protein degradation machinery in the cell (Figure 3). This system is dependent on the post-translational attachment of ubiquitin molecules to the protein substrate which is recognized by the proteasome for degradation (Komander and Rape 2012). Ubiquitin is a small 76 amino acid long protein that is generally attached to the substrate protein via a three-step process: (1) the E1 enzyme activates the ubiquitin molecule at the C terminal glycine residue to form a charge molecule, (2) the charged ubiquitin molecule is then conjugated onto a E2 protein, (3) the E3 ligase binds to the protein substrate via its N-terminus and catalyzes the transfer of the ubiquitin molecule via its C-terminal ligase domain onto a K residue on the protein substrate (Hershko and Ciechanover 1998). This process, termed ubiquitination (also referred to as ubiquitylation), is ATP dependent and can be repetitive, leading to the formation of ubiquitin chains anchored onto either one of the seven K residues (K6, K11, K27, K29, K33, K48, K63) or the M1 residue of the ubiquitin moiety. Additionally, the formation of these chains can be homotypic, where the ubiquitin moieties are linked via the same residue. Alternatively chains can also form via linkages with various K residues leading to formation of mixed or branched chains. (Swatek and Komander 2016).

The presence of this post-translational modification has consequences on the fate, function or cellular localization of the substrate (Komander and Rape 2012). For instance, polyubiquitin chains on substrates formed via K48 linkage are marked for proteasome degradation whereas, substrates with K11 and K29 chains are destined for degradation via the ERAD and the endosome respectively (Chastagner, Israel et al. 2006, Zattas and Hochstrasser 2015). On the other hand, tagging of substrate with the K63 polyubiquitin chain is suggested to be non-degradative but rather the K63 polyubiquitin chain has been attributed to form a stage for the assembly of protein complexes involved in immune response signalling (Xu, Duong et al. 2009, Perrett, Lin et al. 2011). Alternatively, monoubiquitination, where a single ubiquitin protein is attached to the substrate is associated with conformational change that alters the protein function and activity in various scenarios such as transcriptional regulation, endocytosis, DNA damage repair and apoptosis (Nakagawa and Nakayama 2015). For instance, monoubiquitination of histone H2B has been correlated with an altered transcriptional elongation rate as well as nucleosome stability and chromatin structure (Fuchs, Hollander et al. 2014, Fuchs and Oren 2014). Additionally, proteins can also undergo monoubiquitination at multiple lysine residues, as observed for membrane receptors which are internalized and degraded (Haglund, Sigismund et al. 2003). Post ubiquitination, the substrates can either directly interact with the proteasome or be delivered to the proteasome by shuttle factors that contain domains that recognize and bind polyubiquitin chains as well as possess proteasome interacting domains. At the proteasome, a substrate destined for degradation needs to undergo unfolding and removal of the ubiquitin chain by deubiquitinases (DUBs) before degradation (Bach and Hegde 2016, Bett 2016).

The proteasome is a large multi-protein complex that consists of two major components; the catalytic core (CC) and the regulatory core (RC). Protein subunits forming the CC are assembled into a double ring cylindrical structure with outer and inner rings.

The inner rings contain subunits for catalytic activity and possess affinity for acidic, basic and hydrophobic residues (Hegde and DiAntonio 2002, Bach and Hegde 2016). The RC consists of a protein complex 'base' that supports a 'lid' structure and is responsible for the activation of the proteasome in an ATP dependent manner. The assembly of the RC to the CC either at one or both ends leads to the formation of the proteasome. The interaction between the base structure of the RC, which contains the AAA+ ATPase subunits, with the CC, activates the CC, forming an 'open' conformation for substrate processing (Sorokin, Kim et al. 2009). The RC interacts with ubiquitinated substrates that undergo deubiquitination, unfolding and translocation into the CC via ATPase activity. Within the catalytic core, the substrate protein undergoes proteolytic processing leading to the generation of small peptide chains (Hegde 2010, Bach and Hegde 2016).

The proteasome is responsible for degrading a broad range of proteins. However, proteins with certain amino acid composition, such as polyglutamine rich proteins, have been observed to resist proteasomal degradation and further incapacitate the UPS leading to cellular dysfunction (Jana, Zemskov et al. 2001, Holmberg, Staniszewski et al. 2004). Furthermore, efficient degradation by the proteasome requires substrate unfolding and not all aggregates are amenable to unfolding, which requires alternate routes of disassembly (Bence, Sampat et al. 2001). In such cases, these proteins are degraded in bulk via autophagy mechanisms.

1.6.2. Autophagy

Autophagy is an alternate degradation process through which the cell can recycle unwanted cellular material (Cuervo 2004). This process is conserved in all cells and contributes towards cell survival as inhibition of autophagy can lead to apoptosis induction (Boya, Gonzalez-Polo et al. 2005). Autophagy can be categorized into three major categories; chaperone-mediated autophagy (CMA), microautophagy and macroautophagy. CMA involves the direct delivery of substrates to the lysosome for degradation by Hsp70, which binds to 'KFERQ'-like pentapeptide sequences on the substrate. Additionally, CMA is a secondary response to the other two constitutive forms of autophagy which is activated during stress conditions to replenish nutrients. This process is well characterized in higher eukaryotes but is absent in yeast (Lynch-Day and Klionsky 2010, Arias and Cuervo 2011). Microautophagy, on the other hand is a poorly understood process which involves the capture of cytosolic cargo by invaginations of the lysosomal membrane. Furthermore, unlike in macroautophagy, the proteins involved in this process are not conserved between yeast and mammals (Tuttle and Dunn 1995, Kaushik and Cuervo 2012).

In contrast, macroautophagy is a highly-conserved process denoted by the engulfing of cytoplasmic material, such as macromolecules and organelles, into a double membraned structure called the autophagosome. This process is constitutively active to ensure a healthy cytoplasm and is upregulated under various stresses such as nutrient starvation (Rubinsztein, Codogno et al. 2012). Macroautophagy is controlled by the conserved protein kinase target of rapamycin (TOR), which ensures a basal level of autophagy in nutrient rich conditions. This repression is carried out in two steps; first by phosphorylation-mediated repression of ULK1-ATG13-FIP200 complex and second by regulating expression levels of proteins involved in the autophagic process also through its kinase activity. Under starvation conditions, the TOR repression on ULK1 complex is relieved which leads to initiation of the autophagy pathway and the downstream formation of the autophagosome. This process involves numerous genes that have been termed autophagy related genes (Atg) which are activated similar to the ubiquitin cascade and are conserved between yeast and mammals (Cuervo 2004, Sarkar 2013).

Originally, macroautophagy was suggested to be non-selective process. However, it now evident that protein aggregates, such as polyglutamine aggregates, that are unable to be degraded by the proteasome can be selectively targeted for degradation via macroautophagy (Carra, Seguin et al. 2008). In this instance, Hsp70 and the sHsp HspB8 interact with the substrate. The co-chaperone Bag3 interact with these substrate-bound chaperones and facilitates the interaction with the E3 ligase carboxyl terminus of Hsp70-interacting protein (CHIP). CHIP ubiquitinates the substrate which is recognized by the p62 autophagy adapter protein. p62 interacts with LC3 leading to autophagosome formation to engulf the polyubiquitinated material and subsequent degradation via the lysosome. This form of autophagy has been termed chaperone assisted selective autophagy (CASA) (Arndt, Dick et al. 2010).

The occurrence of CASA suggests that the UPS and autophagy systems communicate with each other to ensure removal of unwanted material. Indeed, inhibition of the proteasome has been observed to upregulate autophagy as a compensatory stress response. In addition, certain proteins such as HDAC6 and p62 function in both processes and thus act as adapters to link the two degradation machineries. (Ding, Ni et al. 2007, Wojcik 2013). The histone deacetylase HDAC6 is involved in proteostasis where it interacts with ubiquitinated proteins and transports them to the microtubule organizing center (MTOC) on dynein cables where they are incorporated into a larger structure called the aggresome (Kawaguchi, Kovacs et al. 2003). HDAC6 has also been implicated in the autophagosome maturation and its subsequent fusion with the lysosome (Lee, Koga et al. 2010). In addition, HDAC6 interaction with p62 regulates its deacetylase activity (Yan, Seibenhener et al. 2013). Alternatively, p62 has been suggested to undergo phosphorylation by CK2 or ULK1 under conditions of proteotoxic stress. This phosphorylation event disrupts p62 dimerization and increases its affinity to ubiquitin chains (Matsumoto, Wada et al. 2011, Lim, Lachenmayer et al. 2015). p62 has been observed to mediate the removal of polyubiquitinated huntingtin aggregates via autophagy which limits the toxicity associated with mutant huntingtin (Bjorkoy, Lamark et al. 2005). More recently in yeast, a similar selective autophagy was described involving the conserved CUET (Cue5-Tollip) proteins. The yeast protein Cue5 was observed to act as an adapter that interacts with ubiquitinated polyglutamine aggregates and links it to the Atg8-PE complex on the PAS membrane. This function of Cue5 was conserved in its mammalian homolog Tollip (Lu, Psakhye et al. 2014). Taken together, these reports indicated that the crosstalk between the UPS and autophagy pathways is a conserved feature, which allows for alternate modes of protein turnover to ensure proteostasis and survival under proteotoxic stress conditions.

1.7. Yca1 in proteostasis regulation

The newly discovered non-apoptotic role for Yca1 in proteostasis is intriguing as its suggests that Yca1 may be a part of the cellular proteostasis network. However, the network that ensures cellular proteostasis contains a large array of pathways and molecular machines and at this stage it is not entirely clear how Yca1 functions within this broader context. Based on the features of proteostasis described above, the proteolytic activity of

Yca1 could be favourable to limit proteotoxicity. However, questions remain as to how this protease can regulate death and non-death scenarios. The existing evidence suggests that a probable functional mechanism that directs the role of Yca1 in proteostasis would most likely involve cooperation with chaperones. Furthermore, the association of Yca1 with chaperones of multiple families with distinct roles suggests multiple possible functions for Yca1 in proteostasis. For instance, Yca1 has been shown to interact with both cytosolic Hsp70 (Ssa1/2) and ribosome-associated Hsp70 (Ssb1/2), which could imply Yca1 involvement in *de novo* protein folding (Lee, Brunette et al. 2010). Furthermore, Yca1 can also interact with the Hsp70 cofactor, Ydj1 (Hsp40) and also with the disaggregase Hsp104 at recognized quality control compartments (Lee, Brunette et al. 2010, Hill, Hao et al. 2014). Together, Yca1 in synergy with these chaperones may be involved in protein refolding and aggregate disassembly. Yca1 may also be involved in protein sequestration, as it can associate with the sHSP, Hsp42, which is a marker for the recently described CytoQ compartment (Lee, Brunette et al. 2010, Miller, Mogk et al. 2015). Furthermore, the yeast histone deacetylase Hos2 forms reversible protein structures termed stationary phase granules (SPG) in aged cells. These SPGs were enriched for stress response proteins including Hsp42 and Yca1 (Liu, Chiu et al. 2012). Alternatively, regulation of protein degradation may also encompass Yca1, as it interacts with Cdc48; an AAA+ ATPase which is involved in a broad change of cellular processes and particularly well characterized for its role in ubiquitin dependent protein degradation in the ER (Stolz, Hilt et al. 2011). Furthermore, the observed increase in vacuolar peptidase levels and vacuole structures suggest that an alternative degradative process may be upregulated in response to the loss of functional Yca1 (Lee, Brunette et al. 2010). Thus, the scope of Yca1 function within the

PN is indeed vast, and further investigation into this prosurvival role is vital to understand mechanism(s) that contrasts its nonapoptotic and apoptotic functions. Furthermore, such investigations will prove to be inventive to understanding the parallel functions in other metacaspases as well as caspases.

1.8. Hypothesis and Objectives

Thus, to further characterize the role of Yca1 in proteostasis we conducted two studies. Our previous observations showed that Yca1 can be targeted to the insoluble proteome and that the loss of Yca1 resulted in increased retention of insoluble protein (Lee, Brunette et al. 2010). Thus, as a follow up study, first we analyzed the role of Yca1 within the insoluble proteome. We hypothesized that Yca1 is present in the insoluble protein fraction and acts to remodel aggregated material. Our objectives were to (i) identify the constituents of the insoluble proteome, (ii) assess how the loss of Yca1 affected the composition of the insoluble proteome and (iii) identify established protein interactions within the insoluble fraction.

We observed that the insoluble proteome consists of a multitude of proteins of various functions. Specifically, we observed a significant decline in proteins relating to ribosomal and translational control processes in the insoluble fraction of Δ*yca1* compared to wildtype yeast, following exposure to heat stress. Moreover, Yca1 was required to recruit remodeling chaperones such as Cdc48 to the insoluble protein fraction. Together, these results suggest that Yca1 modifies aggregate composition in coordination with known proteostasis regulators.

Subsequently, we conducted protein interactions screens to determine the mechanisms by which Yca1 controls the protein aggregation process. We hypothesized that Yca1-mediated proteostasis may be dependent on protein interactions that direct or manage Yca1 activity.

The proteomic interaction screens determined that Yca1 had a strong affinity to the most prominent proteasome regulatory cascade, i.e. protein ubiquitination. For example, Yca1 displayed robust interactions with both ubiquitin and ubiquitinated proteins. We further identified sites on Yca1 that were directly modified by ubiquitin, confirming the K355 site as critical in establishing interaction with ubiquitinated material. We also noted that the E3 ligase Rsp5 physically interacts with Yca1 and this interaction may involve the phosphorylation of an adjacent site at S346. Loss of function mutations in either the ubiquitination or phosphorylation sites of Yca1 (K355A and S346A respectively) resulted in proteostasis deficits that were synonymous with the Δ*yca1* strain, as demonstrated by increased insoluble protein content and elevated vacuolar processes. Interestingly, observations such as the reduced levels of monomeric ubiquitin upon the loss of Yca1 or its activity and the processing of the ubiquitin precursor Rps31 by Yca1 suggests that Yca1 may be involved in ubiquitin biogenesis. Taken together, these results suggest that Yca1 maintains proteostasis (in part) by directly modifying the ubiquitin-mediated protein degradation system.

CHAPTER 2

2. Materials and Methods

2.1. Yeast strains, media and growth conditions

For the experiments conducted in Chapter 3, the yeast strains, media and growth conditions are as follows: The wildtype BY4741 and Δ*yca1* strains of *S. cerevisiae* (Open Biosystems, ThermoFisher Scientific, USA) were grown in acidified YPD media (1% yeast extract, 2% peptone and 2% glucose, pH 3.5). 5 ml starter cultures of YPD were inoculated with a single colony and grown overnight. Larger YPD cultures were then inoculated from the starter cultures and grown to mid-logarithmic phase (OD_{600} 0.5-0.6) at 30ºC with orbital rotation. Cells were then collected via centrifugation at 2800 RPM for 5 minutes, washed with water and re-collected then stored at -80ºC for future processing. For heat shock treatment, mid-logarithmic cultures were further incubated at 42ºC for 1 hour before collection (Shrestha, Puente et al. 2013).

In addition to the strains listed above, we also utilized the Yca1-GFP strain (Invitrogen, USA) and the inactive Yca1 mutant strain C297A, which was generated as previously described (Lee, Puente et al. 2008). Yeast strains were prepared from frozen glycerol stocks on solid medium in either YPD (1% yeast extract, 2% bactopeptone, 2% glucose supplemented with 2% agar) or on synthetic selective media lacking uracil (0.67% yeast nitrogen base without amino acids, 0.192% yeast synthetic dropout media supplement lacking uracil, 2% glucose supplemented with 2% agar) with incubation at 30°C. All final experiments were conducted using cells that were cultured in the acidified YPD media as noted above except for the preparation of transformed yeast cell lines which were performed in unbuffered YPD media. The Δ*yca1* strain was transformed with plasmids expressing full length Yca1 and Yca1 mutants as RFP fusions. The Yca1-GFP strain was transformed with the plasmid expressing the Rsp5-RFP fusion.

In addition to the growth conditions listed above, cells were also subjected to a post-stress recovery growth condition where cultures were incubated at 30°C, 225 RPM for an additional period of 45 minutes after the heat stress treatment. For immunoprecipitation experiments, cultures were grown to OD_{600} between 1.0 and 1.2 at 30°C before collection. For insoluble protein analyses, cell cultures were cultured at 30°C and limited to a maximum cell density between 0.8 and 0.9 at OD_{600} at which point they were washed, collected and frozen.

2.2. Cloning, plasmids and PCR

The FL construct expressing the full length Yca1 protein as a RFP fusion under the control of the ADH1 promoter described in Lee et al. (2010), was used as the template for preparing Yca1 mutants and subsequent cloning into the same backbone for expression of these mutants. Mutant Yca1-RFP sequences were generated using site directed mutagenesis PCR and cloned into the *Sal*I/*Xba*I restriction sites in the FL template construct to replace the wildtype Yca1 sequence using the USB® Ligate-IT™ Rapid Ligation Kit (Affymetrix, USA). The primers used to generate the respective single amino acid change in the Yca1 coding sequence are listed in Table 1. The Rsp5-RFP expression plasmid was generated by cloning into the pRS316 plasmid (Creative Biogene, USA). The ADH1 promoter sequence was amplified from the FL template plasmid and ligated into the *Xho*I/*Sal*I restriction sites. The Rsp5 sequence was amplified from BY4741 genomic DNA and cloned into the *Sal*I/*Sma*I site. The mCherry sequence was amplified from the FL plasmid and ligated into the *Sma*I/*Xba*I sites downstream of the Rsp5 coding sequence.

All final constructs were verified by DNA sequencing analysis (StemCore Laboratories, Ottawa, Canada) prior to transformation of yeast strains.

The PCR protocol used for DNA amplification and cloning is described as follows. The reaction mixture for each reaction contained 10 μL of 5X Phusion® HF buffer (New England Biolabs, USA), 200 μM of dNTP mixture (Life Technologies, USA), 0.2 μM of forward and reverse primers and 0.5 unit of Phusion® DNA Polymerase (New England Biolabs, USA). Dimethyl sulfoxide (DMSO) was added to a final concentration of 5% (v/v). 100 ng of plasmid DNA or 500 ng of genomic DNA was used as templates. Sterile water was used to generate a final volume of 50 μL. The reaction was carried out in a thermal cycler using the following parameters: 1) 98°C for 5 minutes, 2) 98°C for 1 minute, 3) 50°C for 1 minutes, 4) 72°C for 1 minute, 5) Steps 2-4 were repeated 29 times, 6) 72°C for 20 minutes and 7) hold the reaction at 4°C. The annealing temperature of 50°C (step 3) was adjusted based on the primer composition used for each reaction to enhance specificity. Additionally, the elongation step (step 4) was extended to accommodate the amplification of DNA fragments that were larger than 1.5 kb. Following PCR, the resulting DNA products were resolved on 1% agarose gels containing 0.2 μg/mL of ethidium bromide.

2.3. Yeast transformation

Cells were grown in 50 mL of unbuffered YPD media (1% yeast extract, 2% peptone and 2% glucose) to OD_{660} of 1.0 at 30°C, 225 RPM. Cells were collected via centrifugation at 2800 RPM for 5 minutes. The media was discarded and the cells were

Name	Sequence
Yca1-K158A-F	ACTGGGCGTAGAGCGGCTTTGATTATC
Yca1-K170A-F	TACATAGGTTCAGCAAATCAACTGCGT
Yca1-K352A-F	GGTTCTATATTCGCGACCGTTAAGGGA
Yca1-K355A-F	TTCAAGACCGTTGCGGGAGGTATGGGC
Yca1-K384A-F	ATGTTATCAGGTTCGGCGGATAATCAAACTTCT
Yca1-S346A-F	GCTGCTTTGATTGGTGCTTTAGGTTCTATA
Yca1-RFP-SalI-F	TTT*GTCGAC*ATGAAGATGAGCCTCGAAG
RFP-XbaI-R	GCGC*TCTAGA*TTAGGCGCCGGTGG
XhoI-ADH1-F	TTT*CTCGAG*AAGGTGAGACGCGCATAACCG
SalI-ADH1-R	AAA*GTCGAC*GTGATATGAGATAGTTGATTG
SalI-Rsp5-F	TT*GTCGAC*ATGCCTTCATCCATATCCGTC
SmaI-Rsp5-R	TT*CCCGGG*TTCTTGACCAAACCCTATGGT
SmaI-RFP-F	TT*CCCGGG*GCCTCCTCCGAGGACGTC

Table 1. List of primers used in this study. Primers used to prepare RFP fusions of Yca1 mutants and the Rsp5-RFP fusion are depicted above in 5'→3' order. The nucleotide mismatches within the primer sequences have been underlined. The restriction site sequences within the primers are denoted with italics.

washed with 10 mL of sterile water. The cells were recollected via centrifugation at 2800 RPM for 5 minutes. The cell pellet was resuspended in 1 mL of 0.1 M lithium acetate and incubated further at 30°C, 150 RPM for 20 minutes. Cells were recollected via centrifugation and resuspended in 300 µL of fresh 0.1 M lithium acetate. This cell suspension was used to generate multiple 50 µL aliquots for individual transformations. The cells in the aliquots were pelleted via centrifugation at 10,000 RPM for 5 seconds and the supernatant was removed. Reagents were added to the aliquot of cells in the following order: 240 µL of 50% polyethylene glycol 3350 (PEG), 36 µL of 1 M lithium acetate, 50 µL of carrier DNA (2 mg/mL DNA sodium salt from salmon testes; Sigma, USA) and 36 µL of sterile water containing 6-8 µg of plasmid DNA. The cell pellet was resuspended by maximal vortex for 1 minute followed by incubation at 42°C for 1 hour. Cells were collected via centrifugation at 5000 RPM for 2 minutes. The supernatant was discarded and the cells were resuspended in 1 mL of YPD and allowed to recover at 30°C, 225 RPM for 30 minutes. 25 µL of the cell culture was plated on solid synthetic media lacking uracil (0.67% yeast nitrogen base without amino acids, 0.192% yeast synthetic dropout supplement, 2% glucose, 2% agar) and incubated further at 30°C to obtain transformed cells.

2.4. Protein extraction

The procedure used to extract protein for mass spectrometry analyses of insoluble protein and immunoblotting in Chapter 3 is as follows: Frozen cell pellets were suspended in modified RIPA buffer (50 mM TRIS-HCl, 1 mM EDTA, 1% glycerol, 1% NP-40, pH 7.4) containing protease inhibitors (Calciobiochem, Darmstadt, Germany) and added to

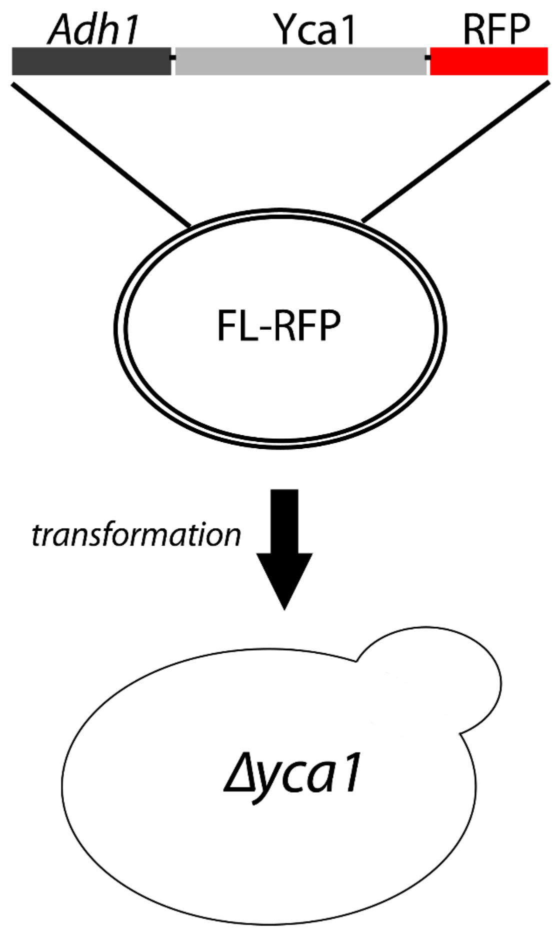


Figure 5. Experimental system utilized for isolating proteins interacting with Yca1. The plasmid expressing the full length Yca1 sequence fused to the mCherry sequence under the control of the Adh1 promoter was transformed in the Δ*yca1* strain. The transformed cell strain was used to isolated and identify protein interacting with Yca1 via the RFP tag. This plasmid also served as template for point mutations corresponding to post-translational modification sites. Additionally, this strategy was also utilized to identify Rsp5 interacting proteins in Yca1-GFP cells.

tubes containing 0.6 gm of glass beads (Sigma USA). Cells were lysed using the Disruptor Genie (Scientific Industries, USA) at 4ºC with six alternating 1-minute cycles of breaking and 1 minute on ice for a total of 12 minutes. The cell lysate was further cleared by centrifugation at 2000 RPM for 1 minute followed by centrifugation at 3000 RPM for another minute. The final protein lysate was aliquoted and stored at -80ºC (Shrestha, Puente et al. 2013).

Subsequent assays that required extraction of protein from cells were prepared using the procedure described above with alternate buffers. For immunoprecipitation analyses, cells were lysed in buffer A (20 mM HEPES-NaOH, pH 7.4, 2 mM $MgCl_2$, 300 mM NaCl and 0.1% Tween-20). For assessing differences in ubiquitin levels, the cells were lysed in buffer B (50mM TRIS-HCl, pH 7.4, 150 mM NaCl, 1 mM EDTA, 1% NP-40, 1% glycerol). For preparation of the insoluble protein fraction, cells were lysed in buffer C (50 mM TRIS-HCl, pH 7.4, 0.1% NP-40, 1 mM EDTA, 1% glycerol). All buffers were supplemented with 1X Halt™ Protease Inhibitor Cocktail (ThermoFisher Scientific, USA) before the cell lysis step.

2.5. Immunoprecipitation

50 µL of antibody conjugated magnetic beads were added to equal amounts of total protein extract, ranging between 4000-5000 µg, for all samples. The volume was normalized using the respective lysis buffer. Anti-RFP mAb-magnetic beads (Medical & Biological Laboratories, Japan) were used to isolate proteins interacting with either RFP tagged full length Yca1 or Yca1 single mutants as well as those interacting with Rsp5-RFP fusion protein. Anti-Multi Ubiquitin mAb-magnetic beads (Medical & Biological

Laboratories, Japan) were used to isolate the ubiquitinated proteins in Yca1-GFP cells. Mouse Anti-IgG (Santa Cruz Biotechnology, USA) and Dynabeads Proteins G (ThermoFisher Scientific USA) were used as controls. The total protein extract samples were incubated overnight with the beads at 4°C with end over end rotation. Following incubation, samples were placed on a magnet (Life Technologies, USA), to separate the lysate from the beads. The lysate was discarded and beads were further washed 5 times with ice cold buffer A without protease inhibitors. After the final wash, the Anti-RFP mAb-magnetic beads were resuspended in 1X laemmli buffer (63mM TRIS-HCl, pH 7.4, 2% SDS, 12.5% Glycerol, 0.005% Bromophenol Blue, 0.16% β-mercaptoethanol), whereas the Anti-Multi Ubiquitin mAb-magnetic beads were resuspended in 1X laemmli buffer lacking β-mercaptoethanol for 2-3 minutes. β-mercaptoethanol was added to the sample containing Anti-Multi Ubiquitin mAb-magnetic beads before the samples were boiled at 100°C for 5 minutes. The magnetic beads were separated from the laemmli buffer by placing the sample on the magnet for 1 minute. The eluted proteins suspended in laemmli buffer were separated via SDS-PAGE and either resolved by silver nitrate staining or transferred to PVDF membranes for western hybridization as described (Shrestha, Puente et al. 2013).

2.6. Sample preparation for mass spectrometry

For the assessment of the insoluble protein fraction described in Chapter 3, the total protein extracts were fractioned into soluble and insoluble via centrifugation as described in (Cashikar, Duennwald et al. 2005). Equal amounts of total protein extract were subjected to centrifugation at 15,000 x *g* for 15 minutes. For the 2D LC-MS analysis the supernatant (soluble fraction) was discarded and the resulting protein pellet (insoluble fraction) was further washed in modified RIPA buffer and re-collected via centrifugation. The modified RIPA buffer was discarded and the final pellet containing the insoluble protein fraction was solubilized in buffer consisting of 8M urea, 2% dithiothreitol (DTT) and 50 mM Tris-HCl pH 8.0 via vortex (Shrestha, Puente et al. 2013).

For identification of proteins bound to FL-RFP, the resulting post immunoprecipitation eluate was subjected to electrophoretic separation on a 15% polyacrylamide gel followed by silver nitrate staining of the proteins following guidelines described in (Shevchenko, Wilm et al. 1996). Each sample lane on the gel was cut out into strips and each gel strips was further divided into 0.5-1 cm^2 pieces for LC-MS/MS analysis.

2.7. Mass spectrometry

Proteomics analysis by mass spectrometry was performed at the Ottawa Hospital Research Institute Proteomics Core Facility (Ottawa, Canada). For identification of proteins in the insoluble protein fraction described in Chapter 3, the following procedure was used for protein digest. Proteins were reduced by addition of DTT and alkylated by the addition of iodoacetamide before dilution of the sample in 100 mM ammonium bicarbonate to reduce the concentration of urea to < 2 M. Proteins were digested using trypsin (Promega, USA). The resulting peptides were purified by ZipTip (Millipore, USA), concentrated by vacufuge (Eppendorf, Germany), and resuspended in 0.1% trifluoroacetic acid (Shrestha, Puente et al. 2013).

For identification of FL-RFP bound proteins, the reagents used for reduction and alkylation were altered to prevent false recognition of artifacts as protein modifications.

Proteins were reduced using 5 mM Tris(2-carboxyethyl)phosphine hydrochloride (TCEP) and alkylated using 5 mM 2-chloroacetamide. Proteins were digested and concentrated as described above without the need for ZipTip purification. The final digested peptides were resuspended in 1% formic acid.

For analysis of proteins within the insoluble fraction examined in Chapter 3, we used a two-dimensional liquid chromatography-tandem mass spectrometry approach (2D LC-MS/MS). Peptides were analyzed by 2D LC-MS/MS on an LTQ Orbitrap XL hybrid mass spectrometer with nanospray source (ThermoFisher Scientific, USA) and an UltiMate 3000 RSLC nano HPLC (Dionex, USA). Peptides were loaded onto a POROS 10S (Dionex, USA) and eluted using ammonium acetate salt steps (0 mM, 10 mM, 20 mM, 50 mM, 100 mM, 500 mM) onto a PepMap C18 trap column (Dionex, USA) for 5 minutes at 15 μL per minute, then eluted over a 60-minute gradient of 3% - 45% acetonitrile with 0.1% formic acid at 0.3 μL per minute onto a 10-cm analytical column (New Objective Picofrit self-packed with Agilent Zoran C18), and nanosprayed into the mass spectrometer. MS scans were acquired in the Orbitrap module and MS^2 scans were acquired in the ion trap module using data-dependent acquisition of the top 5 ions from each MS scan. Total data acquisition time = 9 hours. Between samples, the system was washed three times with 1 M ammonium acetate salt injection on the SCX column and a 60-minute acetonitrile gradient over the C18 columns (Shrestha, Puente et al. 2013).

For identification of proteins bound to FL-RFP, the peptides were analyzed by liquid chromatography – tandem mass spectrometry (LC-MS/MS) on the same system as described above. The system was controlled by Xcalibur software version 2.0.7 (ThermoFisher Scientific, USA). Peptides were loaded by autosampler onto a C18 trap column (Agilent Technologies, USA) in 3% acetonitrile, 0.1% formic acid at a flow rate of 15 µL per minute for 5 minutes. Peptides were eluted over a 100-minute gradient of 5.6% - 25.6% acetonitrile at a flow rate of 250 nL per minute (Keilhauer, Hein et al. 2015), through a 10-cm analytical long column with integrated emitter tip (Picofrit PF360-75-15-N-5 from New Objective packed with Zorbax SB-C18, 5 micron from Agilent Technologies, USA), and nanosprayed into the mass spectrometer. Nano-pump HPLC solvents contained 0.1% formic acid and 5% DMSO (Hahne, Pachl et al. 2013). MS scans were acquired in FTMS mode at a resolution setting of 60,000. MS/MS scans were acquired in ion trap CID mode using data-dependent acquisition of the top 5 ions from each MS scan.

2.8. Protein identification using MASCOT

The following procedure describes how proteins listed in Table S1 were identified. MASCOT 2.3.01 software (Matrix Science) was used to infer peptide and protein identities from the mass spectra. The observed MS/MS spectra were matched against *S. cerevisiae* (6,973 sequences) from the SwissProt database (version 57.15) and against 248 sequences from a Contaminants database (downloaded from maxquant.org, June 9th, 2011). Mass tolerance parameters were MS tolerance of ± 5 ppm and MS/MS tolerance of 0.6 Da. Enzyme specificity was set to 'Trypsin/P'. Oxidation of methionine, carbamidomethylation of cysteine, protein N-terminal acetylation, deamidation, and/or conversion of Glu or Gln to Pyro-Glu were allowed as variable modifications. The emPAI scores reported by Mascot were used as estimates of protein abundance. Mascot's Decoy

Search function was used to calculate False Discovery Rate (FDR; Table S4) (Shrestha, Puente et al. 2013).

For identification of proteins in the FL-RFP immunoprecipitation analyses, MASCOT software version 2.5 (Matrix Science, UK) was used to infer peptide and protein identities from the mass spectra. The observed MS/MS spectra were matched against *S. cerevisiae* sequences from SwissProt (version 2014-08) and against a database of common contaminants. Mass tolerance parameters were MS ± 10 ppm and MS/MS ± 0.6 Da. Enzyme specificity was set to 'Trypsin' with <=2 miscuts. GlyGly modification of lysine, LeuArgGlyGly modification of lysine, oxidation of methionine, protein N-terminal acetylation, and conversion of glutamine to pyroglutamate were allowed as variable modifications. In some searches, phosphorylation of serine or threonine, formylation of serine, dimethylation of methionine and/or oxidation of tryptophan or histidine were also used as variable modifications. Error-tolerant search was also used in some cases. The data was exported to Scaffold and Scaffold PTM software (Proteome Software, USA), for further viewing and validation.

2.9. Bioinformatics

Data was summarized and basic comparisons performed using the Excel spreadsheet program (Microsoft, USA). GO terms annotation was performed using the Functional Annotation Chart tool of the web service DAVID (Dennis, Sherman et al. 2003, Huang da, Sherman et al. 2009). Relative enrichment of GO terms was determined using the web service FunSpec (http://funspec.med.utoronto.ca/) (Shrestha, Puente et al. 2013).

2.10. Polyacrylamide gel electrophoresis (PAGE)

The following protocol was used for the analysis of protein levels within the soluble and insoluble protein fractions described in Chapter 3. The total protein extract was fractioned into soluble and insoluble as described above. The insoluble protein pellet was dissolved in modified RIPA buffer via vortex and loaded onto a 10% acrylamide gel containing SDS (0.1% w/v) with equal volume of sample buffer. The electrophoretic separation of the insoluble protein fraction was conducted at 100 volts for 10-14 hours. The corresponding soluble fraction was also separated similarly on separate gels. After separation, the proteins were either stained using the silver stain method (Shevchenko, Wilm et al. 1996), or transferred onto a membrane for western hybridization (Lee, Brunette et al. 2010). Subsequent experiments requiring SDS-PAGE based separation were conducted as described above but using gels ranging between 12-15% polyacrylamide.

2.11. Silver nitrate staining

SDS containing polyacrylamide gels were stained with silver nitrate using the following guidelines (Shevchenko, Wilm et al. 1996). Post electrophoretic separation of proteins within the gel, the gel was fixed in 45% ethanol, 10% acetic acid for 30 minutes. The gel was washed in 50% ethanol for 10 minutes followed by 2 washes with water for 10 minutes each. The gel was sensitized in 0.02% sodium thiosulfate for 5 minutes followed by 2 washes with water for 5 minutes each. The gel was stained using 0.2% silver nitrate solution for 30 minutes followed by a quick wash with water for 2 minutes to remove excess stain. The protein bands were resolved using the developing solution (2% sodium carbonate containing 0.04% formalin). Once the desired staining intensity was achieved the developing solution was discarded and the reaction was halted by incubating the gel in 5% acetic acid for a minimum for 15 minutes. Post staining the gels were stored in 1% acetic acid at 4°C.

2.12. Protein transfer and immunoblotting

The following procedure was used to assess protein distribution between the soluble and insoluble protein fractions in Chapter 3. Proteins fractioned via SDS-PAGE were transferred to 0.45 μM PVDF membrane (Millipore, USA) on the TRANS-BLOT SD apparatus (Bio-Rad, USA). Membranes were blocked with tris buffered saline containing tween (TBST; 10 mM TRIS-HCl, pH 8.0, 150 mM NaCl, 0.1% Tween 20) containing 5% skim milk for minimum of 1 hour after which they were supplemented with primary antibody and further incubated at 4º C overnight. Bands were detected using primary antibodies specific for Cdc48 (Dr. Thomas Sommer, Max Delbruck Institute, Germany) as well as for Ydj1 and Ssa2 (Abcam, USA) and β-tubulin (Developmental Studies Hybridoma Bank, USA). Densitometry analysis of the resulting bands was conducted using ImageJ software (Shrestha, Puente et al. 2013).

Subsequent immunoblotting experiments were conducted as described above with the following changes to the upgrades to the transfer procedure. The transfer was carried out as per the manufacturer's suggestions where the gels alone were equilibrated in the transfer buffer (48 mM Tris, 39 mM Glycine, 1.3 mM SDS, 20% methanol) for 30 minutes followed by an additional 10 minutes with the PVDF membrane and filter paper. The transfer sandwich was setup as directed; two sheets of filter paper upon which the membrane was placed. The gel was placed upon the membrane followed by another two sheets of filter paper atop the gel. Air bubbles in between the layers were removed using a blotting roller. The transfer was carried out at 15 volts for 1 hour using the PowerPac™ HC High-Current Power Supply (Bio-Rad, USA).

Furthermore, antibodies used in subsequent experiments in Chapter 4 are described below. To detect ubiquitin, we used the polyclonal rabbit anti-Ubiquitin antibody (ab19247; Abcam, USA). The goat anti-Rsp5 (sc-26193; Santa Cruz Biotechnology, USA) polyclonal antibody was used to detect presence of Rsp5. Yca1-GFP presence was detected using the chicken polyclonal to GFP antibody (ab13970; Abcam, USA). Tubulin levels were detected using monoclonal rat anti-tubulin antibody (ab6160; Abcam, USA). IgG levels were detected using the goat anti-rat IgG HRP conjugate antibody (STAR113P; Bio-Rad, USA). RFP fusions were detected using monoclonal mouse anti-RFP antibody (M155-3; Medical & Biological Laboratories, Japan). Secondary HRP conjugated antibodies used to detect the primary antibodies in this study are as follows: goat anti-mouse (170-6516), goat anti-rabbit (170-6515), rabbit anti-goat (172-1034; Bio-Rad, USA) and goat anti-chicken (ab6877; Abcam, USA)

2.13. Vacuole staining

Cell cultures with OD_{600} between 0.4 - 0.5 were stained with the 2 μM FM® 1-43X lipophilic dye (Molecular Probes, USA). Cells were further incubated with the dye at 30°C, 225 RPM for 1 hour. Following staining, cells were fixed in 5% (v/v) formaldehyde for 15 minutes on ice. Following fixation, cells were collected at 5000 RPM for 2 minutes and washed with 1X PBS (137 mM NaCl, 2.7 mM KCl, 10 mM Na_2HPO_4, 1.8 mM KH_2PO_4, pH 7.4). Cells were recollected and then suspended in fresh 1X PBS. Cells were spotted on microscopy slide and visualized using the Zeiss Observer Z1 microscope fitted with an Axiocam. Multiple images were captured at 63X magnification using the Axio Vision SE64 software.

2.14. Nuclear staining

Cells from cultures with OD_{600} between 0.6 - 0.8 were collected at 5000 RPM for 2 minutes. The media was discarded and the remaining cell pellet was resuspended in ice cold 70% ethanol. The cells were fixed in ethanol for 15 minutes on a nutator (Fisher Scientific, USA) at room temperature. Following fixation, the cells were recollected at 5000 RPM for 2 minutes and suspended in 1X PBS containing 1 μg/mL of 4',6-diamidino-2-phenylindole (DAPI). The cells were stained with DAPI for an additional 10 minutes on the nutator at room temperature. Following staining, the cells were pelleted at 5000 RPM for 2 minutes and the stain was discarded. The cell pellet was resuspended in 1X PBS. Cells were spotted on microscopy slides and viewed under 100X magnification using the Leica DMI 6000 florescent microscope (Leica Microsystems, Germany), equipped with a Sutter DG4 light source (Sutter Instruments, USA), Ludl emission filter wheel with Chroma band-pass emission filters (Ludl Electronic Products, USA) and Hamamatsu Orca AG camera (Hamamatsu Photonics, Japan). Multiple images were captured using Volocity 4.3.2 Build 23 (Perkin-Elmer, USA).

2.15. Insoluble protein quantification

The preparation of the insoluble protein fraction was conducted using guidelines stated in 2.6 with a few modifications. To prepare the insoluble protein fraction, equal amount of the total protein extract for all samples were obtained and the volume was normalized using lysis buffer C as described above. The samples were subjected to centrifugation at 15,000 x *g* for 15 minutes at 4°C to separate soluble and insoluble proteins. The resulting supernatant containing the soluble proteins was discarded. The remaining protein pellet was washed with buffer C supplemented with 2% NP-40 via gentle vortex for 10 seconds. The pellet was reobtained via centrifugation at 15,000 x *g* for 15 minutes at 4°C. The wash step was repeated once more followed by centrifugation to obtain the final insoluble protein pellet. The protein pellet was dissolved in the resolubilization buffer (6 M urea, 2% SDS, 20 mM HEPES-NaOH, 150 mM NaCl, 2 mM EDTA, 1 mM, DTT, pH 7.4; modified from (Wallace, Kear-Scott et al. 2015)) via vortex at 4°C for 25 minutes. The dissolved insoluble protein solution was further diluted 1:3 in 1X PBS. 10 μL of the diluted insoluble fraction was used to determine the insoluble protein concentration spectrophotometrically using the proteins assay reagent (Bio-Rad, USA).

2.16. Genomic DNA extraction

Genomic DNA from BY4741 cells were prepared as described previously (Lee, Brunette et al. 2010). Cells from an overnight culture in YPD media were collected at 2800 RPM for 5 minutes. Cells were washed with water and resuspended in buffer D (2% Triton X-100, 1% SDS, 100 mM NaCl, 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) and transferred to a tube containing acid washed glass beads. Equal volume of phenol:chloroform:isoamyl alcohol (25:24:1) was added to the mixture and cells were lysed via continuous vortex for 5 minutes. The lysate was cleared at 10,000 RPM for 5 minutes at room temperature and the supernatant was transferred to a new tube containing 3X (v/v) of ice cold 100% ethanol.

The DNA was precipitated at 4°C for 1 hour followed by centrifugation at 12,000 RPM for 5 minutes at room temperature. The ethanol was discarded and the DNA pellet was dried at room temperature. The dried DNA pellet was dissolved in TE buffer (10 mM TRIS-HCl, 1 mM EDTA, pH 8.0) and stored at -20°C.

2.17. *in vitro* cleavage assay

Recombinant 6XHis-SUMO tagged Rps31 and Yca1 (ABclonal, USA) were incubated together or alone in the reaction buffer (20mM TRIS-HCl, 150 mM NaCl, pH 8.0). Calcium chloride was added to a final concentration of 15 mM for metacaspase activation (Wong, Yan et al. 2012). Reaction was incubated at 25°C for 2 hours and followed by SDS-PAGE separation and silver nitrate staining as described previously (Shevchenko, Wilm et al. 1996). Protein bands were excised from the gel and analysed by LC-MS/MS for identification as described in 2.7.

2.18. Statistical analysis

Densitometry, insoluble protein concentration and proportion of multivacuolated cell data was subjected to t-Test analysis using Excel software (Microsoft, USA). The paired two sample means was used to compare each experimental group to the control. A p value of ≤ 0.05 was considered to be significant and denoted by an asterisk (*).

CHAPTER 3

3. The role of Yca1 in proteostasis. Yca1 regulates the composition of the insoluble proteome

3.1. Composition of the insoluble protein fraction

Here, we used a proteomic approach to examine the composition of the insoluble protein fraction as a surrogate to model/understand protein aggregate formation in yeast. The metacaspase Yca1 has been implicated in regulating levels of protein aggregates and hence we further validated this hypothesis by comparing the composition of the insoluble protein fraction of the wildtype BY4741 (WT) to the Δ*yca1* (KO) strain under normal and heat stressed conditions by using a two-dimensional liquid chromatography – tandem mass spectrometry (2D LC-MS) approach and used the emPAI scores as estimates of relative protein abundance[†]. In this study, we altered our approach for obtaining the insoluble fraction than reported previously (Lee, Brunette et al. 2010). Initial experimentation of the insoluble fraction after conducting the NP-40 detergent washes resulted in low yield with regards to protein identification in comparison to what was observed from a silver stained acrylamide gel of the same fraction (Figure 6). We postulated that the presence of NP-40 as well as glycerol in the suspension buffer may be interfering with the 2D LC-MS and hence opted to use an alternate buffer that was known to be compatible with this form of online MS analysis. Importantly, similar results using this NP-40 buffer for insoluble protein isolation have been reported by other groups for LC-MS analysis (Yeung, Nieves et al. 2008). Therefore, we reverted to the original method as described in (Cashikar, Duennwald et al. 2005), where the insoluble fraction was simply obtained by high speed centrifugation. Here, we included an additional wash step with the same buffer used for

[†] Conducted by Dr. L. G. Puente at the Proteomics Core Facility of the Ottawa Hospital Research Institute.

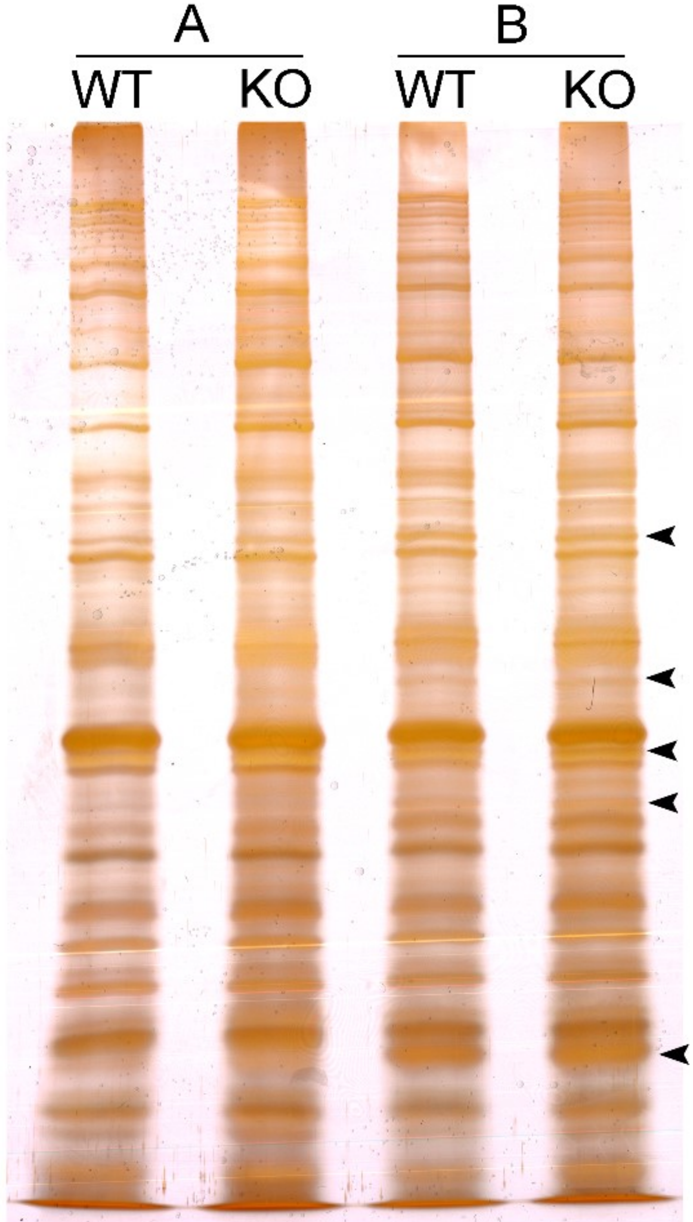


Figure 6. Insoluble protein composition differs with induction of heat stress. Silver stained gel depicting the protein profile within the wildtype (WT) and knockout (KO) strains during normal growth (A) and with heat stress treatment (B). Arrows indicate the differences in the electrophoretic profile during heat stress in comparison to normal growth (Shrestha, Puente et al. 2013).

lysis and suspension and eliminated the NP-40 rich detergent washes to minimize interference during the LC-MS analysis. Furthermore, this method yielded the insoluble fraction in its entirety without any exclusion that may have resulted from repeated detergent washes and have not been accounted for previously.

Within the total 2120 proteins that were observed by the MASCOT search engine, a proportion of these proteins were exclusive to either condition. In the first data set we detected 678 proteins in normal growth conditions and 1178 proteins in heat stress conditions for the wildtype BY4741 strain. For the Yca1 knockout strain we detected 880 proteins in normal growth conditions and 1180 proteins during heat stress. In the second data set we detected 573 proteins in normal growth conditions and 876 proteins during heat stress for the BY4741 strain and 1181 proteins in normal conditions and 1015 proteins during heat stress for the knockout mutant (Table S1). This increase in proteins levels is similar to what we have previously observed (Lee, Brunette et al. 2010). Furthermore, functional clustering using the DAVID software resulted in the identification of 592 categories for proteins within the insoluble fraction for the wildtype while the Yca1 knockout showed 518 categories (Table S2)[‡]. Additionally, we also included the insoluble protein fraction of the catalytically inactive mutant of Yca1, C297A, in our 2D LC-MS analysis and the corresponding data is also included in Table S1. However, we chose to primarily focus on the data generated from the wildtype and knockout strains for this study.

‡ Conducted by Dr. L. G. Puente at the Proteomics Core Facility of the Ottawa Hospital Research Institute.

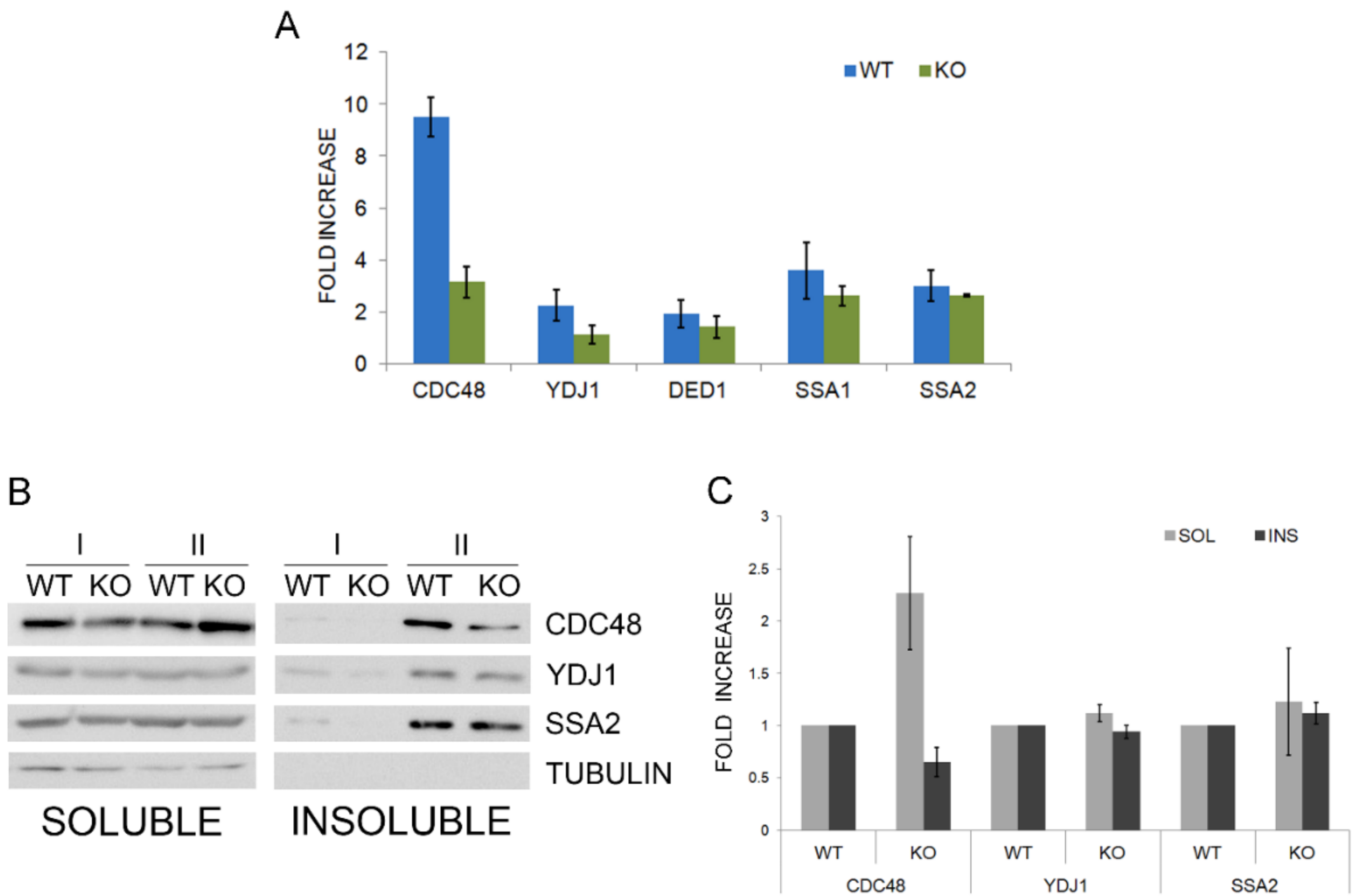

A
FOLD INCREASE
WT
KO
CDC48
YDJ1
DED1
SSA1
SSA2
B
I
II
WT KO WT KO
CDC48
YDJ1
SSA2
TUBULIN
SOLUBLE
INSOLUBLE
C
FOLD INCREASE
SOL
INS
CDC48
YDJ1
SSA2

Figure 7. Cdc48 recruitment to the insoluble protein fraction is Yca1-dependent. (A) A graphical representation of the average fold increase observed for each of the Yca1-interacting protein upon the induction of heat stress in the two strains obtained from the 2D LC-MS analysis (*n*=2; AVG ± SEM). (B) Western blot showing the levels of Cdc48, Ydj1 and Ssa2 within the soluble and insoluble fractions during normal (I) and heat stress (II) and the respective enrichment determined by densitometry analysis, normalized to the wildtype (C, *n*=3; AVG ± SEM; SOL - soluble, INS - insoluble). β-tubulin levels in the respective soluble fraction served as a loading control (Shrestha, Puente et al. 2013).

3.2. Enrichment analysis of proteins interacting with Yca1

Prior observations by our group suggest that Yca1 can interact with Cdc48 and proteins of the Hsp40 and Hsp70 family (Lee, Brunette et al. 2010). Furthermore, these Yca1-interacting proteins are also active members of protein re-solubilization/degradation machinery, acting to limit the occurrence of misfolded proteins (Tyedmers, Mogk et al. 2010). However, what remains unknown is whether these proteins control aggregate deposition by remaining within the soluble or insoluble fraction. For example, one may predict a number of scenarios whereby the aggregate control machinery resides within the soluble fraction of the proteome to limit aggregate deposition. Alternatively, such Yca1 interacting proteins may reside largely within the insoluble fraction to dissolve aggregate composition. To address for alternate functional scenarios, we examined the relative abundance of these proteins during normal conditions and assessed enrichment following the induction of heat stress. As shown in Figure 7A, the induction of heat stress led to a dramatic 9-fold increase in levels of Cdc48 in the wildtype while the loss of Yca1 only showed a modest 3-fold increase. Surprisingly, we did not observe any significant increase in the levels of Ydj1, Ssa1 and Ssa2, which are active components of the re-solubilization machinery as well as for Ded1. We further verified the LC-MS data by western hybridization (Figure 7B) and assessed the change in levels of Cdc48, Ydj1 and Ssa2 following heat stress by densitometry (Figure 7C). We observed that Cdc48 levels were reduced in the insoluble fraction of the knockout strain compared to the wildtype while Ydj1 and Ssa2 levels were similar in both strains, which are in agreement with the data generated from LC-MS. We also examined the changes in the level of these proteins upon

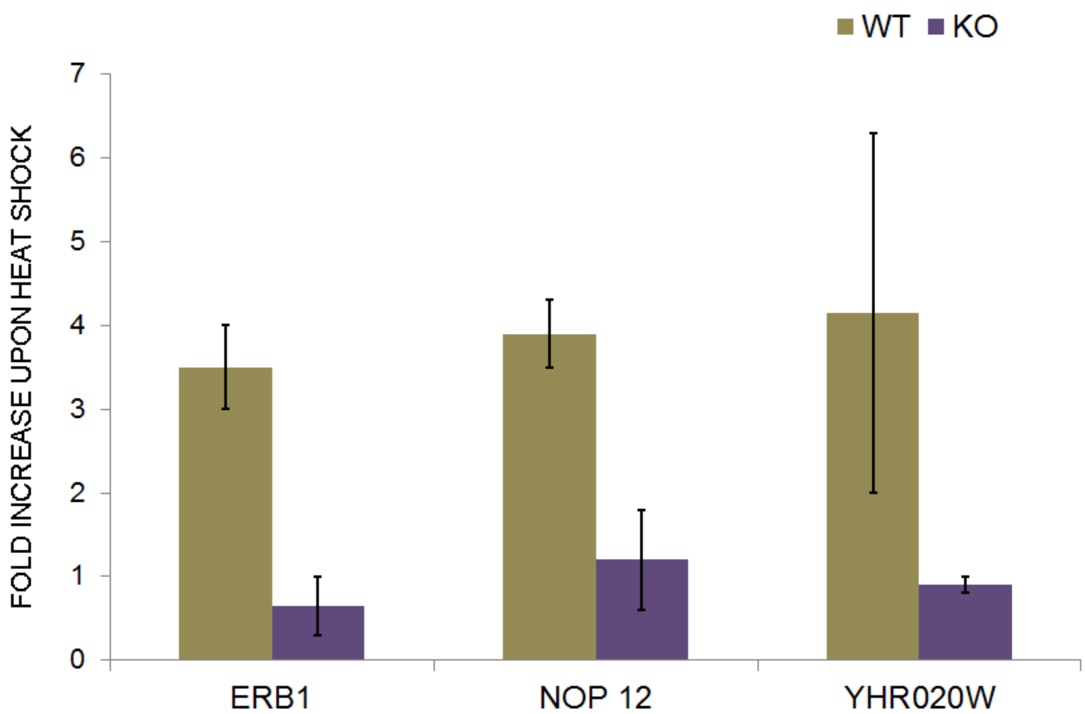


Figure 8. Heat stress induces enrichment of proteins of the translational machinery. A diagrammatic depiction of the fold increase in ribosomal processes related proteins during heat stress induction in the wildtype and knockout strains (*n*=2; AVG ± SEM) (Shrestha, Puente et al. 2013).

Category	Term	Rank in WT	Rank in KO
GOTERM_CC_FAT	GO-0030686_90S preribosome	140	498
GOTERM_BP_FAT	GO-0043039_tRNA aminoacylation	91	325
GOTERM_BP_FAT	GO-0043038_amino acid activation	92	326
SP_PIR_KEYWORDS	ribosome biogenesis	62	264

Table 2. GO term ranking for ribosomal and protein synthesis related processes in wildtype and Yca1 knockout strains under heat stress.

heat stress within the soluble fraction. In both the wildtype and Yca1 knockout strains, Ydj1 and Ssa2 levels were observed to be similar between the soluble and insoluble fractions. Interestingly, in the Yca1 knockout strain, the reduced level of Cdc48 observed in the insoluble fraction was accompanied by an increased localization of Cdc48 within the soluble fraction in comparison to the wildtype. Thus, Cdc48 enrichment within the insoluble fraction is dependent on the presence of Yca1.

3.3. Loss of Yca1 influences ribosomal protein function in the insoluble fraction during stress

We have previously observed that the electrophoretic profile of the insoluble protein fraction is variable and not specific to a single or a few protein species (Lee, Brunette et al. 2010). To further validate this observation, we used the DAVID software to retrieve the Gene Ontology (GO) terms associated with the proteins that were observed to be enriched as a result of heat shock in both Yca1 backgrounds. We noted that the GO term ranking for processes relating to protein synthesis/translational machinery showed a large decrease in the knockout strain (Table 1). Thus, we furthered our analysis on four of the affected GO terms; "GO:0030686~90S preribosome", "GO:0043039~tRNA aminoacylation", "GO:0043038~amino acid activation" and "SP-PIR Ribosome biogenesis". We generated a non-overlapping list of 73 proteins associated with these GO terms that are affected by the induction of heat stress (Table S3)[§]. To identify proteins that

[§] Conducted by Dr. L. G. Puente at the Proteomics Core Facility of the Ottawa Hospital Research Institute.

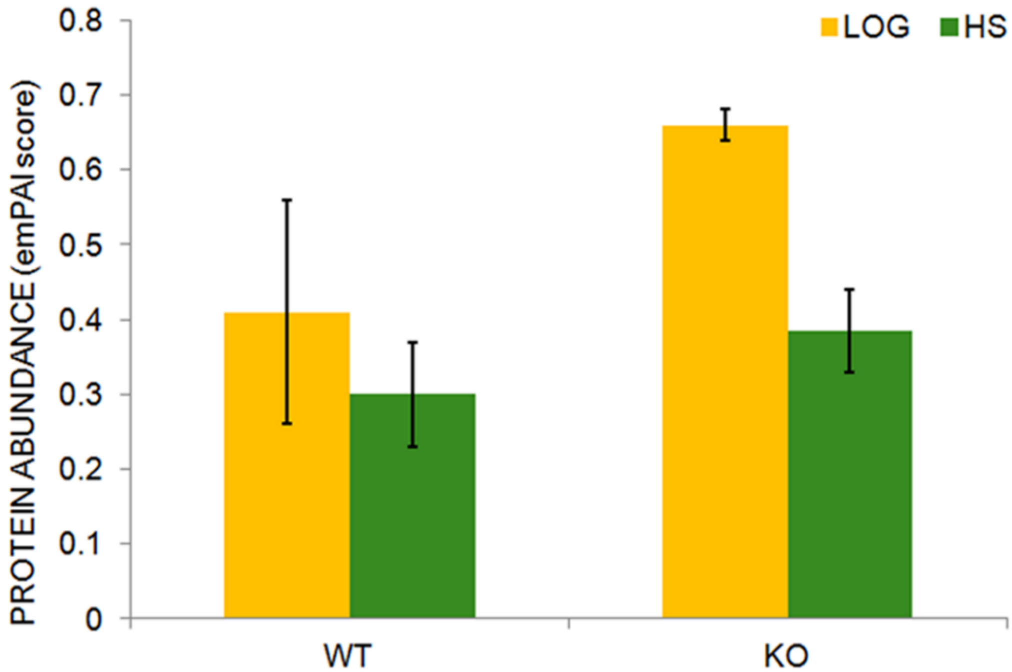


Figure 9. [NU+] prion protein level is Yca1 independent. The relative abundance of the [NU+] protein as represented by the emPAI score in each strain is depicted above for the two conditions (n=2; AVG ± SEM) (Shrestha, Puente et al. 2013).

showed a fold increase in the wildtype, suggesting a requirement for Yca1, we chose to highlight three proteins of significant interest ERB1, NOP12 and YHR020W (Figure 8). Erb1 is a constituent of the 66S pre-ribosomal complex required for the maturation of the 5.8S and 25S rRNAs (Pestov, Stockelman et al. 2001). Nop12 is a nucleolar protein involved in the large subunit biogenesis and 25S rRNA maturation (Wu, Wu et al. 2001). YHR020W is an uncharacterized essential protein in yeast which shares similarity with proline-tRNA ligase and is postulated to interact with ribosomes (Tatusov, Galperin et al. 2000, Fleischer, Weaver et al. 2006). All three proteins were considerably enriched during heat stress in the wildtype amounting to larger than threefold, whereas within the knockout strains their levels either remained the same or were reduced.

3.4. Prion protein levels are unaffected in Δ*yca1* cells

In yeast, aggregates of prionogenic proteins, such as [PSI^{+}], are known to be cytoplasmically inherited by daughter cells which ensure the transfer of epigenetic traits (Serio and Lindquist 2000). To assess for a role of Yca1 in regulating levels of such misfolded proteins we searched our protein list for known prions that may be present in the insoluble protein fraction. Our data generated from the 2D LC-MS analysis included the [NU+] prion protein form of New1 and the prion form of Rnq1 protein, [PIN+]. We analyzed the relative abundance using emPAI scores of [NU+] which is depicted in Figure 9. Under normal growth circumstances, [NU+] levels were more abundant in the knockout strain. Consequently, the induction of heat stress led to a reduction in [NU+] levels.

CHAPTER 4

4. Ubiquitin-mediated regulation of Yca1 function during proteostasis maintenance

4.1. The Yca1 Interactome

Type I metacaspases such as Yca1, contain an N-terminal prodomain; a distinctive feature of initiator caspases that is also present in metacaspases. Furthermore, such domains contain various motifs that allow for protein-protein interactions which are necessary for its function (Uren, O'Rourke et al. 2000, Tsiatsiani, Van Breusegem et al. 2011). Thus, we reasoned that identifying and analyzing proteins that interact with Yca1 could help identify a functional mechanism for Yca1. To accomplish this, we used the plasmid expressed Yca1-RFP system that was previously described (Lee, Brunette et al. 2010). In this experimental system (Figure 5), the Δ*yca1* cell line was transformed with the plasmid that expresses the full length Yca1 sequence tagged with the mCherry sequence (denoted as FL). This fusion protein expression was designed to be expressed under the control of the ADH1 promoter which allowed for constitutive expression of the Yca1-RFP fusion. Of note, our full length Yca1 protein consists of 453 residues as originally described in the founding works of Yca1 (Uren, O'Rourke et al. 2000, Madeo, Herker et al. 2002). However, subsequent studies have referenced a smaller sized protein comprised of 432 residues (Wong, Yan et al. 2012, Hill, Hao et al. 2014), which has led to altered numbering and identification of critical residues such as the catalytic cysteine residue in the literature. Thus, reference to any residues within Yca1 have been and further will be based on the original sequence encoding the 453-residue version of Yca1.

To identify a broad range of protein interactions with Yca1, we conducted immunoprecipitation analyses against the RFP tag using the experimental model described

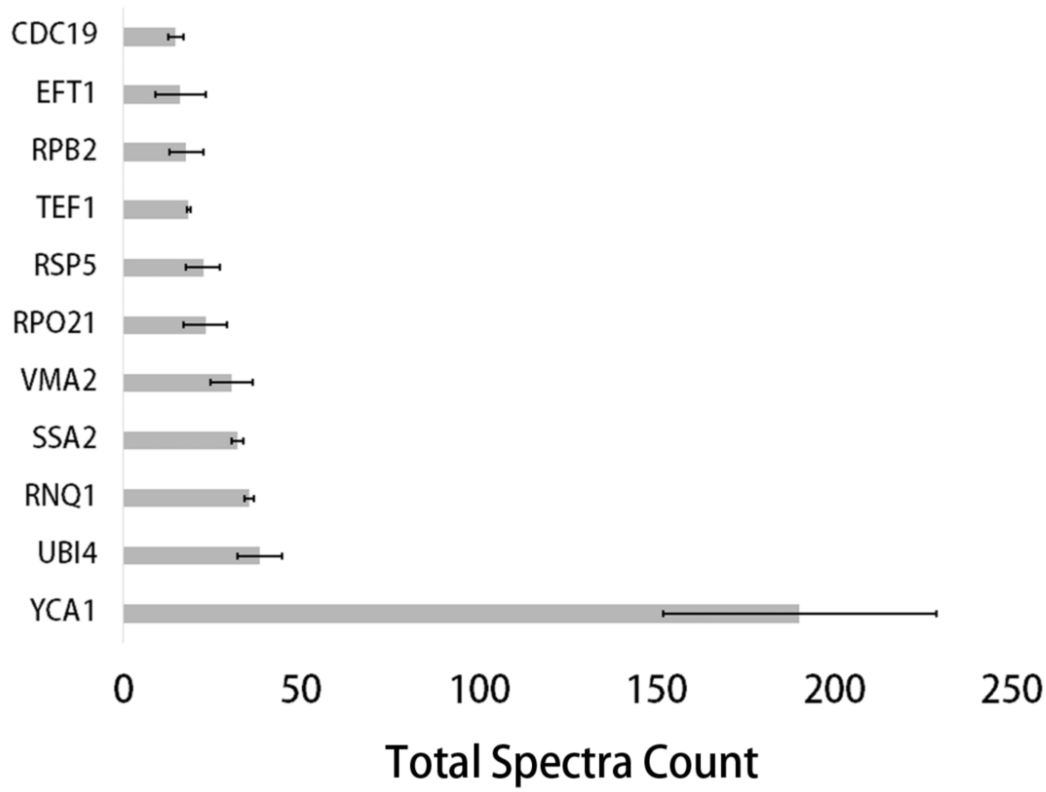


Figure 10. Proteins from the FL-RFP immunoprecipitation ranked on abundance. The total spectra count for each protein in the three replicates of the MS/MS trails were averaged and sorted based on abundance. The top ten most abundant proteins present in the Yca1 interactome along with the bait (Yca1) are depicted above (AVG ± SEM). *n* =3.

above. Proteins interacting with Yca1 were isolated using anti-RFP antibody conjugated magnetic beads, resolved via SDS-PAGE and silver nitrate staining and identified using mass spectrometry. Empty RFP plasmid expressing cells and Δ*yca1* were used as controls. The MS/MS data was analysed using the Scaffold software under the following parameters: 99% protein threshold, 95% peptide threshold and minimum of peptides detected per protein was set to 2. Under these restrictions, we identified 145 proteins that were repeatedly present in the pulldown with Yca1-RFP from three separate MS trials (Table S5). We further sorted this list based on protein abundance (Figure 10), and we noted that ubiquitin (Ubi4) was present within this set and furthermore averaged as one of the most abundant protein within the samples. Additionally, we also observed the presence of the E3 ligase Rsp5, within this subset at a lower abundance compared to ubiquitin.

The presence of these two proteins within the Yca1 interactome was of high interest which suggested a potential interaction between Yca1 and the well characterized ubiquitin system which is involved in determining protein fate and function (Komander and Rape 2012). Thus, we sought to verify these predicted interactions using an immunoprecipitation approach coupled with immunoblotting (Figure 11). To assess the interaction between Yca1 and ubiquitin, protein extracts from endogenously GFP tagged Yca1 (Yca1-GFP) cells were used to isolate the pool of ubiquitinated proteins using anti-multi ubiquitin antibody conjugated beads (Lanes 3-5; Figure 11B). Upon probing the interactome with the anti-GFP antibody, we observed a band corresponding to the estimated size of full length as well as processed versions of Yca1-GFP (Lanes 3-5; Figure 11A). The presence of Yca1 within the ubiquitinated proteome suggested that Yca1 fate and/or function may also dictated by the post-translational modification by ubiquitin.

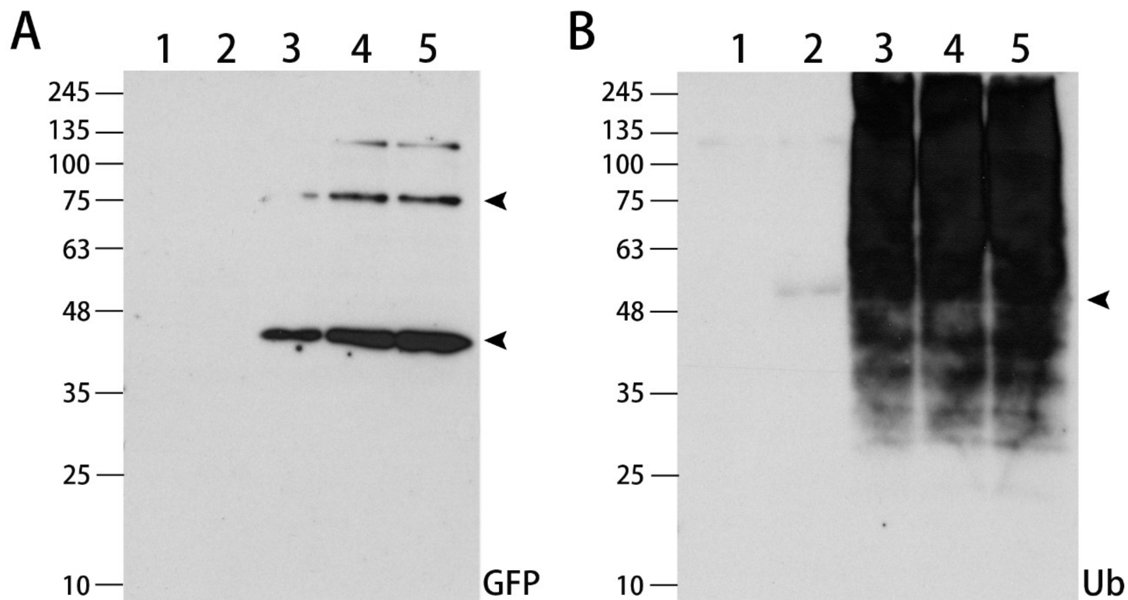


Figure 11. Yca1 interacts with ubiquitin. (A) Ubiquitinated proteins in the Yca1-GFP strain were isolated using anti-multi ubiquitin conjugated magnetic beads and subjected to SDS-PAGE and PVDF isolation. Dynabeads Protein G (Lane 1) and anti-IgG conjugated Dynabeads (Lane 2) were used as interaction controls. Yca1-GFP fusion protein (Lanes 3-5 are three independent replicates) was detected by anti-GFP (GFP) immunoblotting. The estimated size for the full length Yca1-GFP fusion protein is 77 kDa. The arrows indicate the full length and shorter processed forms of Yca1-GFP (estimated at 64 kDa and 37 kDa). *n*=3. (B) Immunoblot showing the presence of ubiquitin (Ub) to verify the bait used to capture Yca1-GFP during immunoprecipitation in A. The arrow highlights the position of the IgG heavy chain.

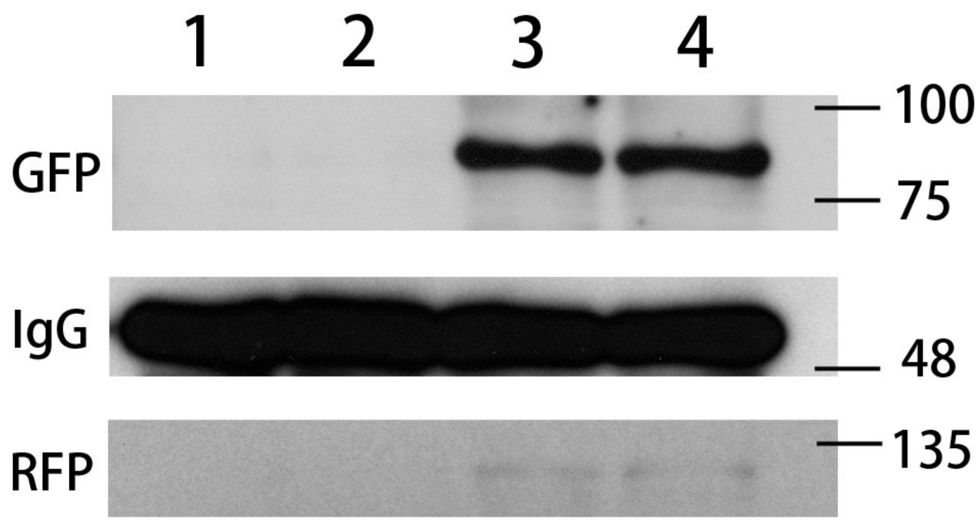


Figure 12. Yca1 interacts with the E3 ligase Rsp5. Yca1-GFP cells were transformed with plasmid expressing the Rsp5-RFP fusion protein (Lanes 3-4). Proteins interacting with Rsp5-RFP in the Yca1-GFP strain were isolated using anti-RFP conjugated magnetic beads and subjected to SDS-PAGE and PVDF isolation. Yca1 presence was detected by anti-GFP immunoblotting (GFP) and Rsp5 presence was detected via anti-RFP blotting (RFP). Untransformed Yca1-GFP cells (Lane 1) and Yca1-GFP cells expressing the RFP vector alone (Lane 2) were used as controls. IgG was used as a reagent/loading control. The estimated size for the full length Yca1-GFP fusion protein is 77 kDa. *n*=4.

A similar approach was taken to verify the interaction between Yca1 and Rsp5. Yca1-GFP cells transformed with the plasmid expressing the Rsp5-RFP fusion protein was used to isolate proteins interacting with Rsp5. Immunoprecipitation was conducted using anti-RFP antibody conjugated beads and the presence of Yca1 within the Rsp5 interactome was detected via anti-GFP immunoblotting (Figure 12). Together, these results confirmed the interactions predicted by the MS data (Figure 10 and Table S5) and suggested an interplay between Yca1 and components of the ubiquitin system; an interaction that may be involved regulating protein homeostasis within the cell.

4.2. Ubiquitin modification sites on Yca1

The validation of the interaction between Yca1 and ubiquitin as well as Yca1 and the E3 ligase, Rsp5 suggested that Yca1 may be post-translationally modified by ubiquitin and that this modification may be mediated by Rsp5. As noted previously, the presence of the ubiquitin tag on proteins provides a signal that results in modification of the protein's fate, function and even cellular localization (Komander and Rape 2012). More specifically, the C-terminus G76 residue of the ubiquitin molecule is conjugated onto specific lysine residues on the protein substrate by an E3 ligase (Hershko and Ciechanover 1998). This linkage can be detected via mass spectrometry to identify sites K sites within the substrate protein to which the ubiquitin moiety is anchored (Wang and Cotter 2005). Thus, we sought to identify such modified residues on Yca1 by examining the MS/MS data for peptides containing lysine residues with modifications corresponding to either the diglycine tag (GG) or the LeuArgGlyGly tag (LRGG) that results from the tryptic cleavage of ubiquitin

Site	Peptide Sequence	Modification	Localization	Ascore
K158	kALIIGINYIGSK	K1 Gly Gly	100%	110.54
K170	ALIIGINYIGSkNQLR	K12 GlyGly	100%	1,000.00
K352	AALIGSLGSIFkTVK	K12 GlyGly	100%	1,000.00
K355	TVkGGMGNNVDR	K3 LeuArgGlyGly	100%	1,000.00
K384	FSAADVVMLSGSk	K13 GlyGly	100%	1,000.00
S346	AALIGsLGSIFK	S6 Phospho	100%	29.64

Table 3. Post-translational modification sites on Yca1. LC-MS/MS data from the FL-RFP immunoprecipitation was scanned for peptides containing modifications corresponding to the LRGG and GG post-tryptic digest remnant of ubiquitin as well as for Ser/Thr phosphorylation modifications. The various modified sites on Yca1 along with the peptide sequence and modification observed are listed above. The localization probability and the Ascore for each site reflects the positional accuracy of the modification. The lowercase letter within the peptide sequence indicates the position of the amino acid residue where the modification was observed.

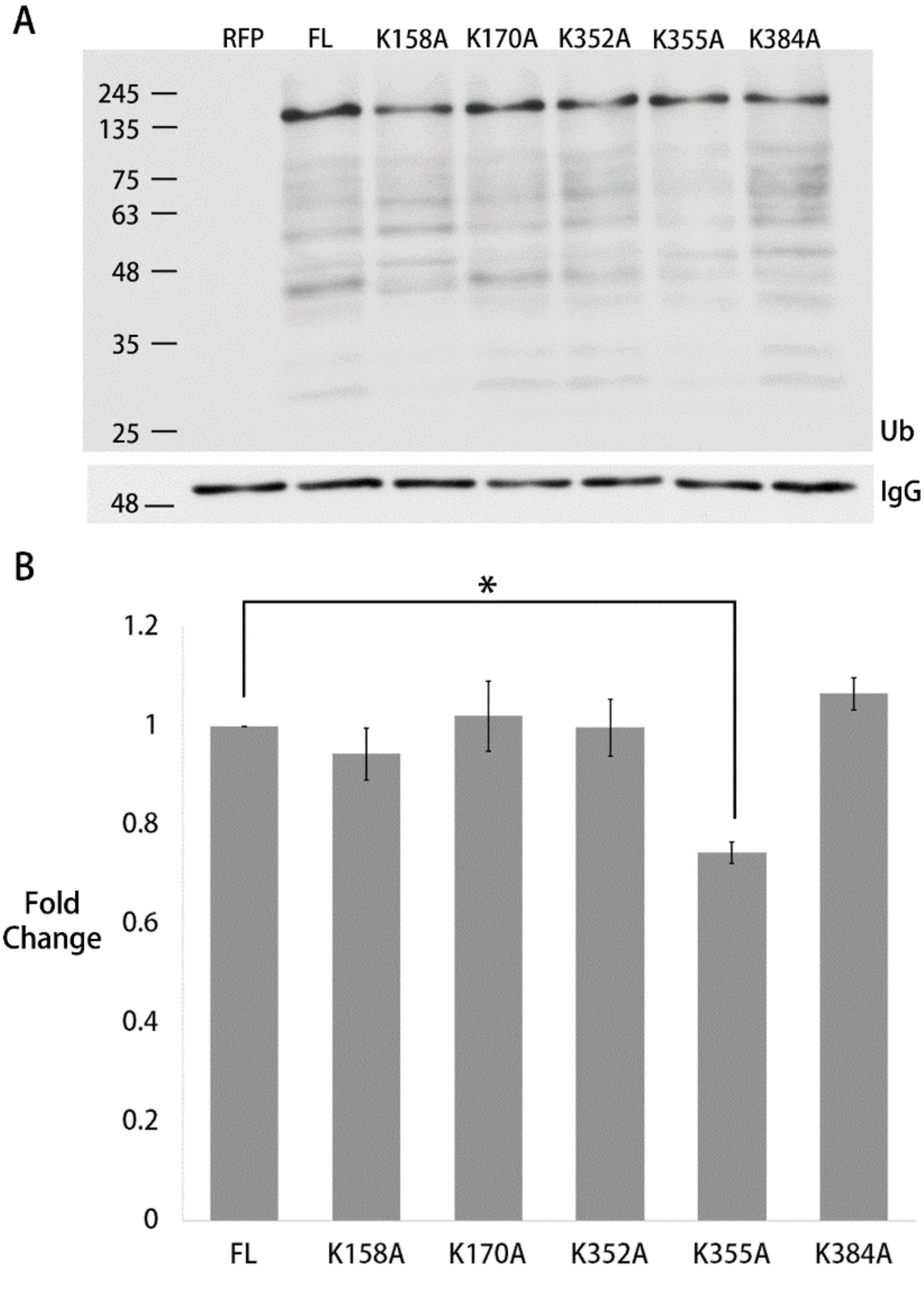

A
RFP
FL
K158A
K170A
K352A
K355A
K384A
245
135
75
63
48
35
25
Ub
48
IgG
B
*
1.2
1
0.8
0.6
0.4
0.2
0
Fold Change
FL
K158A
K170A
K352A
K355A
K384A

Figure 13. The K355A Yca1 mutant shows reduced interaction with ubiquitinated proteins. (A) The full length Yca1 (FL) and the various Yca1 mutants for ubiquitin interaction (K158A, K170A, K352A, K355A and K384A) were expressed as RFP fusions in Δ*yca1* cells. Proteins interacting with these fusion proteins were isolated and subjected to SDS-PAGE separation and PVDF immobilization. Interaction with ubiquitin was assessed via anti-ubiquitin (Ub) immunoblotting. Δ*yca1* cells expressing the RFP vector alone (RFP) was used as a control for interaction. IgG detection was used as a loading/reagent control. (B) The level of interaction with ubiquitin (entire lane for each sample) was quantified via densitometry analysis of the immunoblots using ImageJ software and normalized to the FL sample. The graph above depicts the fold change in the level of interaction with ubiquitin for the various Yca1 K mutants compared to be FL (AVG ± SEM). *n*=3. T-test analysis was conducted to assess statistical significance. * denotes $p \leq 0.05$.

(Wang and Cotter 2005, Denis, Vasilescu et al. 2007). Our analyses using Scaffold PTM predicted five sites on Yca1; K158, K170, K352, K355 and K384, with high probability that were modified with either of the tags mentioned above (Table 3). Moreover, three of these sites; K170, K352 and K355 have been previously reported to be marked by the GG tag upon enrichment with plasmid expressed His-tagged ubiquitin, which affirmed the validity of our data (Swaney, Beltrao et al. 2013). Thus, the presence of these modified sites on Yca1 suggests that Yca1 fate and/or function may also be dictated by ubiquitin binding.

Next, we tested the relevance of these residues as ubiquitin modification sites, by assessing their ability to interact with ubiquitin. Using a site-directed mutagenesis approach we altered the respective lysine (K) residue to an alanine (A) in the Yca1 coding sequence and then expressed these mutants as RFP fusions from plasmids in Δ*yca1* cells as described earlier. We conducted immunoprecipitation against the RFP tag and assessed for the interaction between the Yca1 K mutant and ubiquitin via immunoblotting using anti-ubiquitin antibody (Figure 13).We observed that wildtype full length Yca1 (FL) associated with multiple bands of different sizes that were positive for ubiquitin as observed with the banding pattern that spanned across the entire lane rather than a single band corresponding to ubiquitin or a specific sized polyubiquitin chain (Figure 13A). This suggested that Yca1 interacts with ubiquitin chains as well as multiple different proteins that are ubiquitinated. Of note, the PTM analysis revealed that Yca1 and other ubiquitinated proteins were tagged via either K48 or K63 conjugated ubiquitin chains (Table S6).

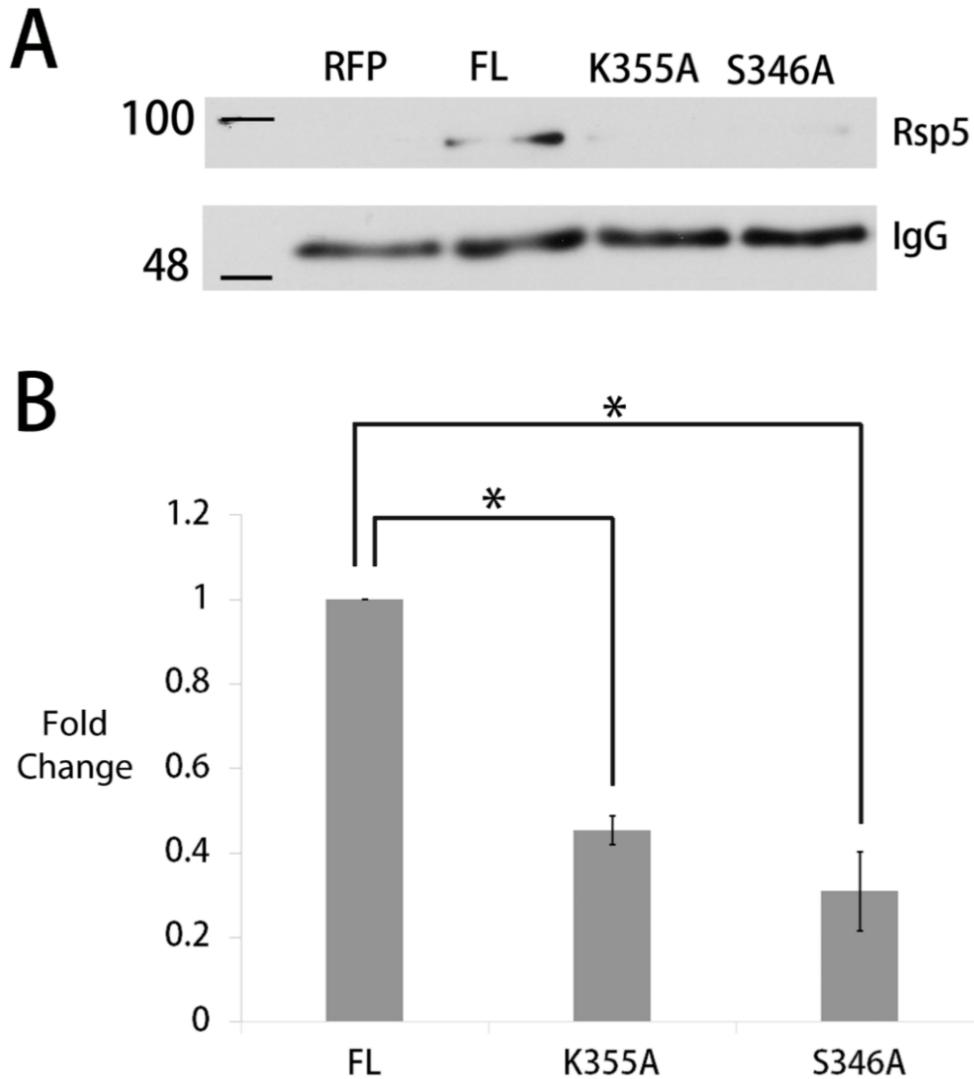


Figure 14. The S346 and K355 residues are involved in mediating the interaction with Rsp5. (A) Proteins interacting with the two Yca1 mutants and full length Yca1 (FL) were isolated and subjected to SDS-PAGE and PVDF immobilization. The presence of Rsp5 within the respective interactome was detected by anti-Rsp5 (Rsp5) immunoblotting. The expected size of Rsp5 is 92 kDa. The vector only cells (RFP) were used as an interaction control. IgG detection served as a loading/reagent control. (B) The fold change in the level of interaction with Rsp5 for the mutants compared to FL was quantified from the immunoblots via densitometry analyses using ImageJ software and statistically analysed using the T-test. The graph depicts the fold change in interaction with Rsp5 for the two mutants compared to FL (AVG ± SEM). n=3. * denotes $p \leq 0.05$.

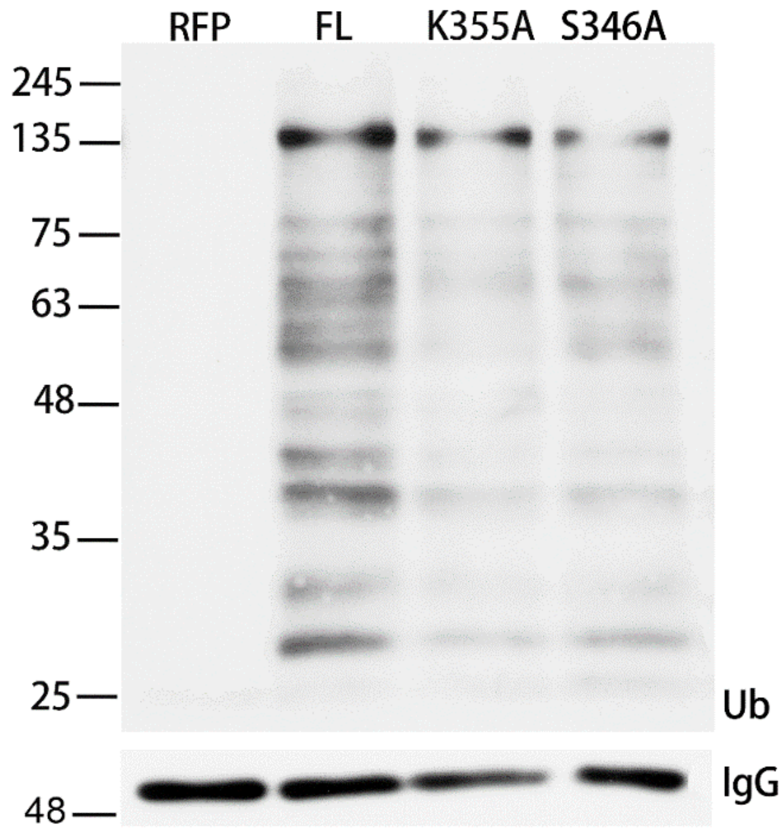
Interestingly, we noted a reduction in the interaction with such ubiquitinated proteins for the K355A mutant. Densitometry analyses revealed that the reduction observed for K355A was significant (p = 0.007) in comparison to the FL. For the remaining four mutants, the level of interaction with ubiquitinated proteins was similar to that observed for the FL (Figure 13B), suggesting that mutation of these sites individually did not affect such interaction. Overall, we identified multiple sites on Yca1 that were modified with ubiquitin and among these the K355 residue was observed to be more influential in establishing this interaction with other proteins modified by ubiquitin.

4.3. Phosphorylation modification on Yca1

The search for post-translational modifications (PTM) on Yca1 also led to the identification of an additional modification. The serine residue at position 346 (S346), which is adjacent to the K352 and K355 ubiquitin modification sites, was observed to be phosphorylated within our MS/MS data as revealed by Scaffold PTM (Table 3). The sequence of the homologous to E6-AP C-terminus (HECT) E3 ligase, Rsp5 is known to contain three WW protein interaction domains between its N-terminal C2 domain and the conserved C-terminal HECT domain (Wang, Yang et al. 1999).

Furthermore, the Rsp5 ligase belongs to the NEDD4 family of E3 ligases (Huibregtse, Scheffner et al. 1995), and the WW domains of the NEDD4 E3 ligase have been shown to recognize and bind substrates in a phosphoserine dependent manner (Lu, Zhou et al. 1999). Thus, we speculated that the phosphorylation event at the S346 residue

A


RFP
FL
K355A
S346A
245
135
75
63
48
35
25
Ub
IgG
48

B

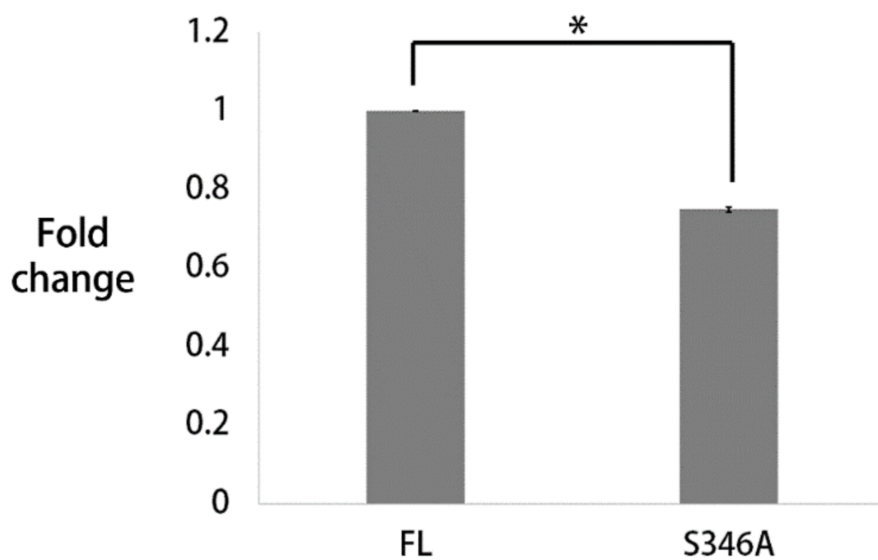

1.2
1
0.8
0.6
0.4
0.2
0
Fold change
*
FL
S346A

Figure 15. Interaction with ubiquitinated proteins is also reduced for the S346A mutant. (A) Proteins interacting with RFP, FL, K355A and S346A were isolated using and subjected to SDS-PAGE followed by immobilization on PVDF membranes. The interaction between ubiquitin and these fusion proteins was resolved via anti-ubiquitin (Ub) immunoblotting. The K355A mutant was included in the analysis as reference for reduction in interaction. IgG detection served as a loading/reagent control. (B) Densitometry analysis of immunoblots was performed using ImageJ software to quantify the level of interaction with ubiquitin (entire lane for each sample). The fold change in the interaction with ubiquitin for the S346A Yca1 mutant compared to FL is depicted above (AVG ± SEM). *n*=3. T-test analysis was conducted to assess statistical significance between the level of interaction with ubiquitin in FL and S346A.* denotes $p \leq 0.05$.

may be involved in the interaction between Yca1 and Rsp5, in a manner that was similar to that described for NEDD4.

We assessed whether the interaction between Yca1 and Rsp5 was dependent on the S346 residue by generating the S346A mutant using a site-directed mutagenesis approach. We expressed this mutant as an RFP fusion from a plasmid in the Δ*yca1* strain as described in 4.2 (Figure 5). Physical interaction between Yca1 and Rsp5 was detected using the previously described immunoprecipitation approach coupled with immunoblotting. We observed that the association with Rsp5 was reduced in the S346A mutant and also in the K355A mutant (Figure 14A). Furthermore, densitometry analysis revealed that this reduced interaction with Rsp5 was statistically significant for the Yca1 mutants; $p = 0.004$ for K355A and $p = 0.01$ for S346A (Figure 14B). This observation suggested that the phosphorylation competent S346 and the ubiquitination competent K355 residues are important for proper interaction between Yca1 and the E3 ligase Rsp5.

Next, we hypothesized that if Rsp5 was responsible for the ubiquitination of Yca1, then disturbing the ability of Yca1 to interact with Rsp5 would in turn affect its ability to interact with ubiquitin, as observed for the K355A mutant (Figure 13). We tested this hypothesis by repeating the immunoprecipitation with the S346A mutant and probed for the levels of ubiquitin via immunoblotting (Figure 15A). We observed that similar to the K355A mutant, the level of interaction between ubiquitinated proteins and Yca1 in the S346A mutant was reduced compared to the FL. Further densitometry and statistical analyses showed that the reduction observed was significant ($p = 0.0006$; Figure 15B) and

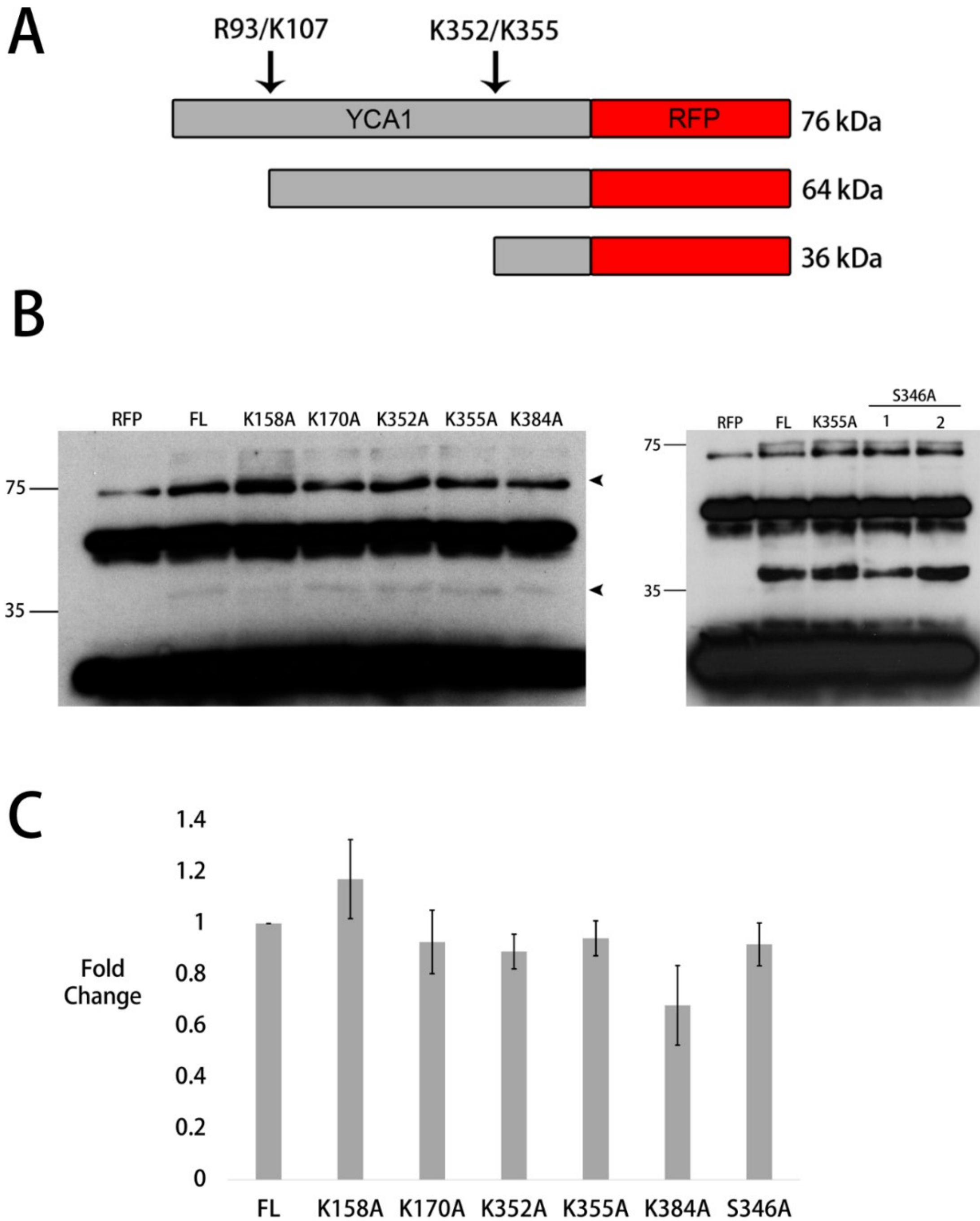

A
R93/K107
K352/K355
YCA1
RFP
76 kDa
64 kDa
36 kDa
B
RFP
FL
K158A
K170A
K352A
K355A
K384A
75
35
RFP
FL
K355A
S346A
1
2
75
35
C
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Fold Change
FL
K158A
K170A
K352A
K355A
K384A
S346A

Figure 16. Comparison of RFP fusion protein isolated during immunoprecipitation. (A) Different sizes on Yca1-RFP fusion observed on a gel corresponding to full length and processed versions of the fusion protein. (B) Representative immunoblots depicting the RFP profile for extracts results from the immunoprecipitation reactions. The arrows highlight the bands corresponding to the RFP fusion proteins. (C) Graph depicting the level of each fusion protein recovered during immunoprecipitation normalized to the FL. (AVG ± SEM) *n*=3.

at a level, similar to that observed for the K355A Yca1 mutant. Taken together, these results suggest a possible mechanism for the ubiquitination of Yca1 at the K355 residue by Rsp5 that is influenced by the upstream phosphorylation competent S346 residue.

Furthermore, we also assessed the level of bait (RFP) captured from the immunoprecipitation reactions to further validate our findings and our methodology (Figure 16). Quantification of the bands corresponding to the three fragments of Yca1 suggested that the levels of the fusion proteins captured during the immunoprecipitation procedure were not different from the FL. The K384A did show a slightly reduced level of RFP fusion. However, statistical analysis suggested that this reduction as well as the changes observed in the other mutants were not significant (p = 0.38 for K158A, p = 0.62 for K170A, p = 0.25 for K352A, p = 0.48 for K355A, p = 0.18 for K384A and p = 0.43 for S346A). Thus, this finding further validates our quantitative analysis for interaction with ubiquitinated proteins and Rsp5 (Figures 13-15).

4.4. Insoluble protein content analysis of Yca1 mutants

A defining observation for Yca1's function in maintaining proteostasis was its ability to regulate the insoluble material within the cell, whereby the loss of Yca1 or its catalytic activity led to an increase in levels of insoluble material retained within the cell (Lee, Brunette et al. 2010). To understand if the above observed post-translational modifications influence this role of Yca1, we examined the levels of insoluble protein in the K355A and S346A Yca1 mutants in comparison to the FL and the internal control

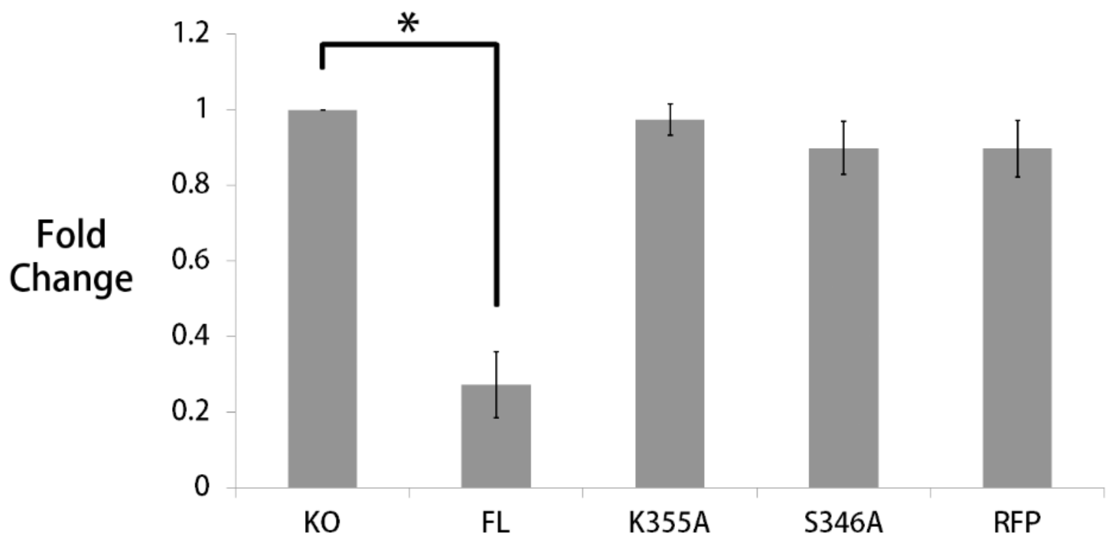


Figure 17. The K355A and the S346A mutants show increased retention of insoluble material. Equal amounts of total protein extract from Δ*yca1*(KO), FL, K355A, S346A and RFP (vector control) cells were used to prepare the insoluble protein fraction. The final insoluble pellet was resolubilized and quantified via spectrophotometry. The protein concentrations were normalized to the KO sample. The fold change (AVG ± SEM) in insoluble protein concentration compared to the KO is depicted above. n=3. The t-test was used to assess statistical significance within the dataset. * denotes $p \leq 0.05$.

Δ*yca1*. The insoluble protein pellet was obtained from total cellular extract and further washed to remove membrane proteins (Lee, Brunette et al. 2010). The final pellet was solubilized in a detergent concentrated buffer (Wallace, Kear-Scott et al. 2015) and protein concentration within this pellet was determined spectrophotometrically (Figure 17). For the FL, the analyses revealed a reduction in the levels of insoluble material; an observation which is in agreement with that observed by other groups (Hill, Hao et al. 2014), and was also statistically significant ($p = 0.01$) compared to Δ*yca1* (KO). In comparison to the FL, the Yca1 mutants K355A and S346A displayed increased levels of insoluble protein retention that was not significantly different from the level observed for the Δ*yca1* (KO) strain (*p* values - K355A = 0.5 and S346A = 0.5). Thus, we conclude that the ability of Yca1 to limit insoluble material within the cell is influenced by post-translational modifications on K355 and S346 residues.

4.5. Vacuole morphology of Yca1 mutants

In addition to the alteration in insoluble protein content in Δ*yca1* cells, prior iTRAQ MS studies also defined a notable increase in levels of vacuolar peptidases in the Δ*yca1* strain. The iTRAQ results were also supported by increased vacuole number in the absence of Yca1, suggesting a compensatory autophagic response to combat the loss of the proteostasis safeguard (Lee, Brunette et al. 2010). Thus, we conjectured that the loss of proteostasis observed by the increase in levels of insoluble protein in the K355A and S346A Yca1 mutants may also be accompanied by a similar compensatory autophagic response. We investigated this supposition by assessing the levels of vacuolar structures in

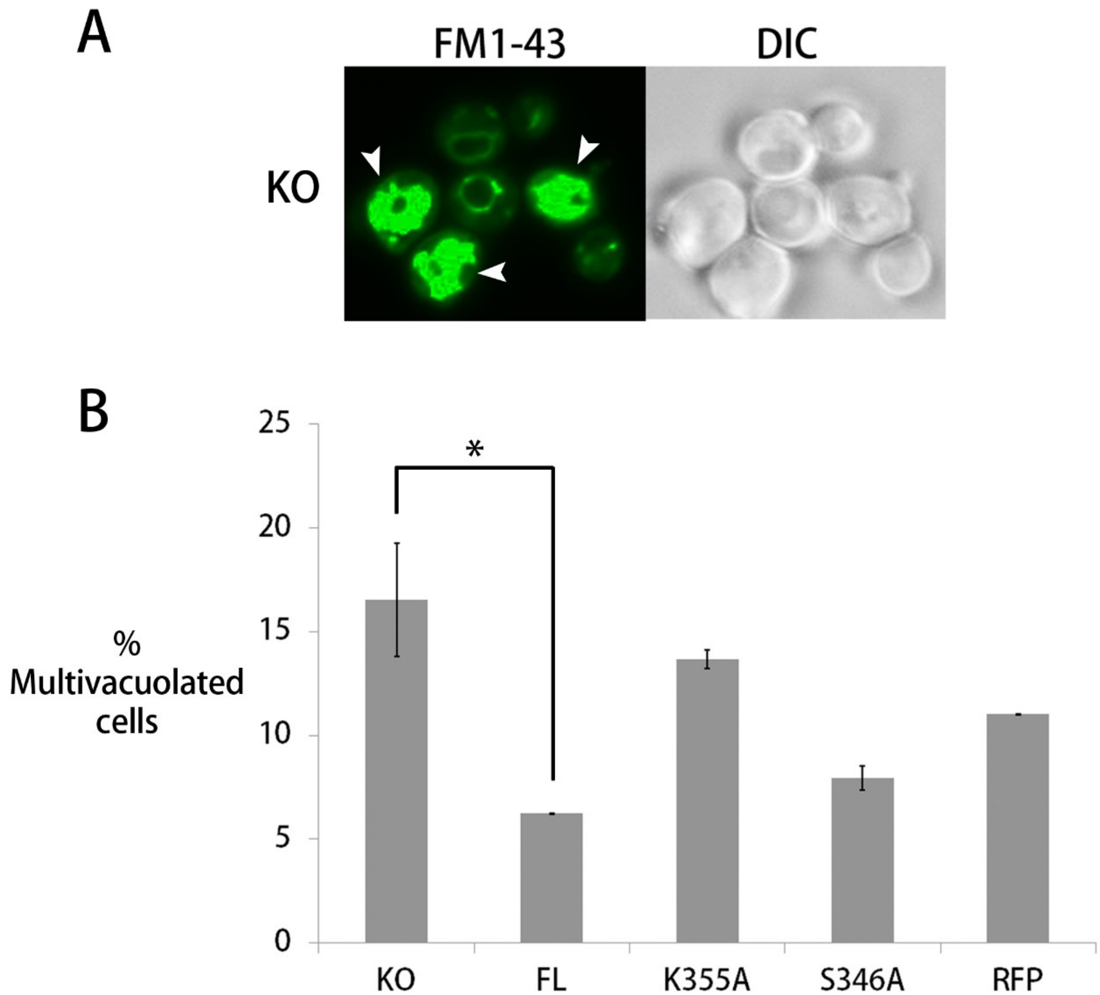


Figure 18. The K355A mutant has increased proportion of multivacuolated cells. (A) Δ*yca1* (KO), FL, K355A and S346A cells were cultured to mid-logarithmic phase and stained with the FM 1-43X fluorescent dye to mark vacuoles. Stained cells were fixed and analyzed at 63X magnification using the Zeiss Axiocam fitted Zeiss Observer Z1 fluorescent microscope in light (DIC) and fluorescent (FM1-43) channels. Multiple images were captured and analyzed using Axio Vision SE64 software. The white arrows mark KO cells that are multivacuolated (>3 vacuoles/cell). (B) The proportion of multivacuolated cells (marked with white arrows in A) are represented as a percentage of the whole in the graph (AVG ± SEM). n=3. The t-test analysis was conducted to assess statistical significance within the dataset. Samples with $p \leq 0.05$ are highlighted with *.

these cells. Yca1 knockout (KO), FL, K355A, S346A and RFP cultures were stained using the lipophilic dye FM® 1-43X as a marker for vacuoles under normal conditions.

The cells were analysed via fluorescence microscopy and captured images were used to quantify the proportion of multivacuolated cells. (Figure 18). We observed a significant reduction in multivacuolated cells in the FL strain ($p = 0.03$) compared to the KO cells. Additionally, statistical analysis revealed that both, the K355A and the S346A Yca1 mutant expressing cells, possessed elevated number of multivacuolated cells that was not significantly different from the level observed in KO cells ($p = 0.3$ and 0.1 respectively). Thus, this analysis suggests that the loss of insoluble protein level regulation incurred by the K355A and S346A mutations on Yca1 is accompanied by an increase in the cellular abundance of vacuoles.

4.6. Impact of ubiquitination on Yca1 localization

As mentioned previously, a consequence of protein ubiquitination is the change in the cellular localization of the targeted protein. Specifically, using the temperature sensitive Ubc9 (Ubc9^{ts}), it was shown that the misfolding of this protein under high temperatures leads to its compartmentalization at distinct cellular deposition sites in yeast, and that this substrate sorting was dependant on the ubiquitinated state of the protein (Kaganovich, Kopito et al. 2008). Furthermore, Yca1 has been shown to localize to these depositions sites, namely the IPOD and the JUNQ compartments, the latter of which is known to consist of polyubiquitinated proteins (Kaganovich, Kopito et al. 2008, Hill, Hao et al. 2014).

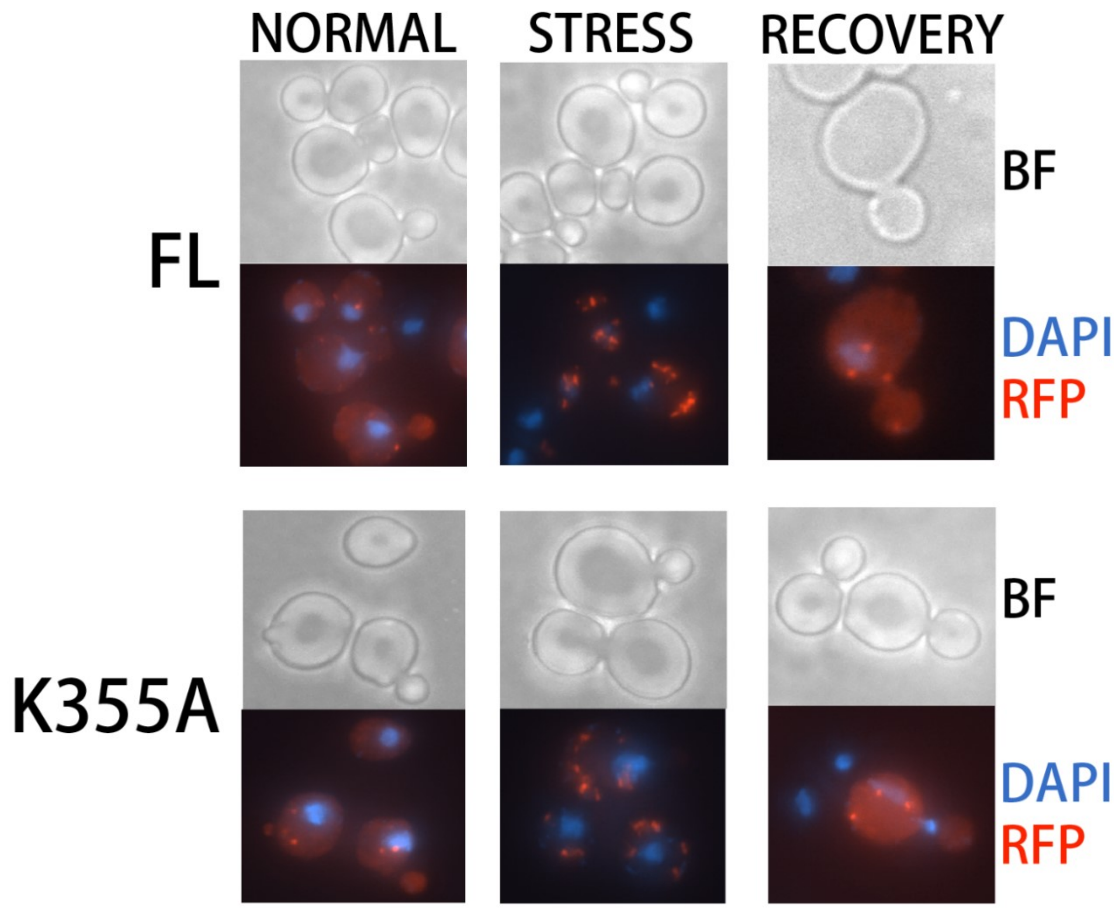


Figure 19. Juxtanuclear localization of Yca1 is unaffected for the K355A mutant. FL and K355A mutant cells were cultured under normal, heat stress and post-stress recovery conditions. Cells were fixed in ethanol and then stained with DAPI to mark the nucleus. Images were captured at 100X magnification using the Leica DMI 6000 fluorescent microscope under bright field (BF) as well as under blue (DAPI) and red (RFP) fluorescent channels. Images were analyzed using the Volocity 4.3.2 software. *n*=3.

However, it is not known how Yca1 is recruited to these deposition sites. Therefore, we reasoned that ubiquitination of Yca1 may serve as a translocation signal that spurs Yca1 recruitment to the JUNQ compartment.

We assessed for the ubiquitin-mediated targeting of Yca1 to quality control sites by examining the localization of the FL and the K355A mutant with respect to the nucleus, as the JUNQ compartment has been shown to form adjacent to the nucleus (Spokoini, Moldavski et al. 2012). Δ*yca1* cells expressing the FL and K355A-RFP fusions were stained with DAPI to mark the nucleus under normal growth conditions as well as heat stress and post-stress recovery conditions. These cells were analyzed for juxta-nuclear localization via fluorescence microscopy (Figure 19). The analyses revealed that both full length Yca1 (FL) and the K355A mutant formed distinct foci under normal, heat stress and post-stress recovery conditions. Furthermore, these foci in both FL and K355A Yca1 cells were observed to be present at the nuclear periphery in all conditions that were assessed. Therefore, these analyses suggest that the ubiquitination at the K355 residue does not serve to recruit Yca1 to nuclear quality control sites such as the JUNQ compartment.

4.7. Profiling ubiquitin levels *in vivo*

So far, our results show a dependence on ubiquitin as a driver of Yca1 function. Furthermore, mutations that abrogated this post-translational modification of Yca1, exhibited behaviour characteristic of the Δ*yca1* strain. Accordingly, we speculated that if Yca1 and the ubiquitin system are synergistically linked for proteostasis maintenance, then the loss of Yca1 would affect the crosstalk between these two systems. Thus, we explored

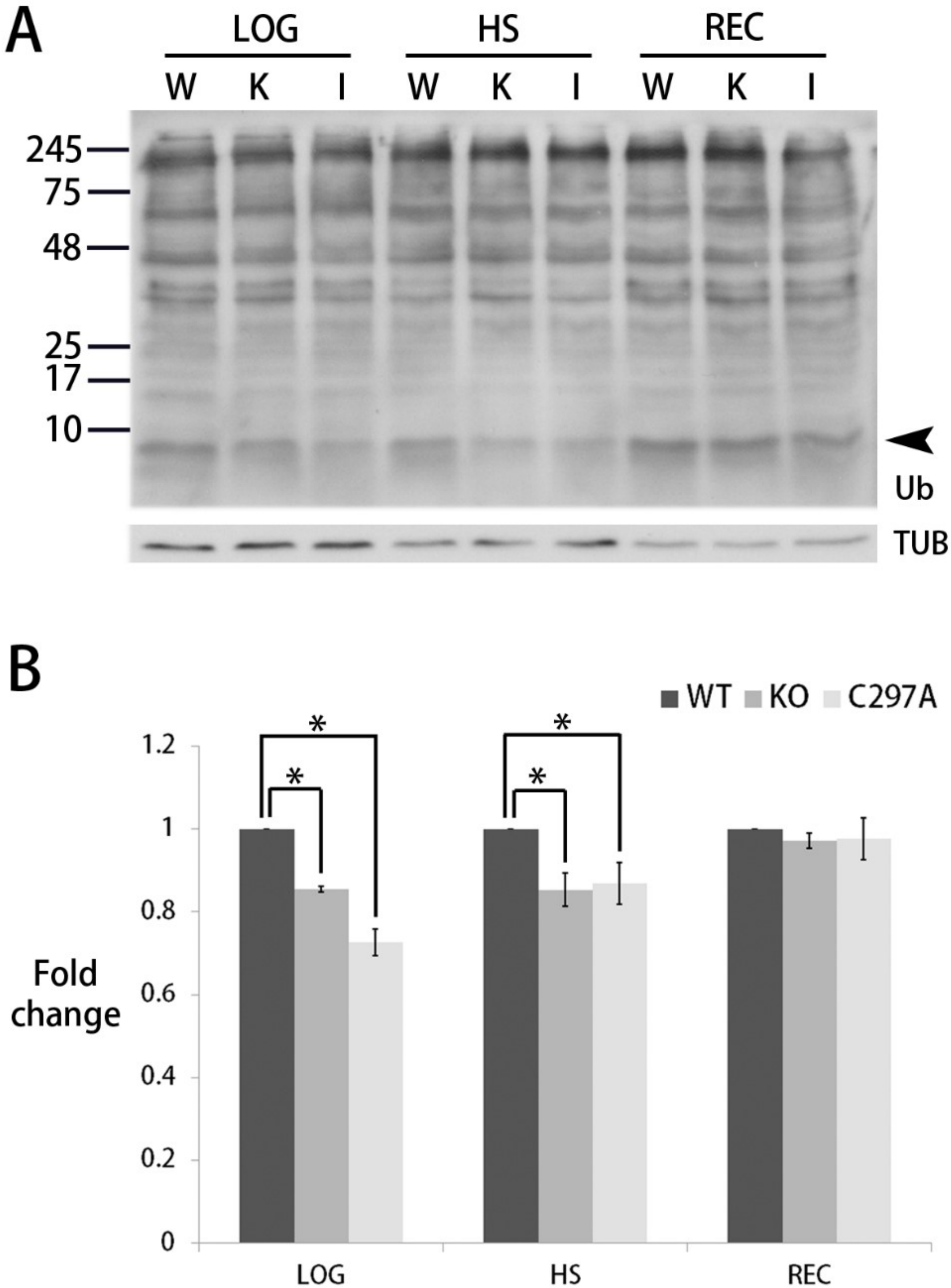
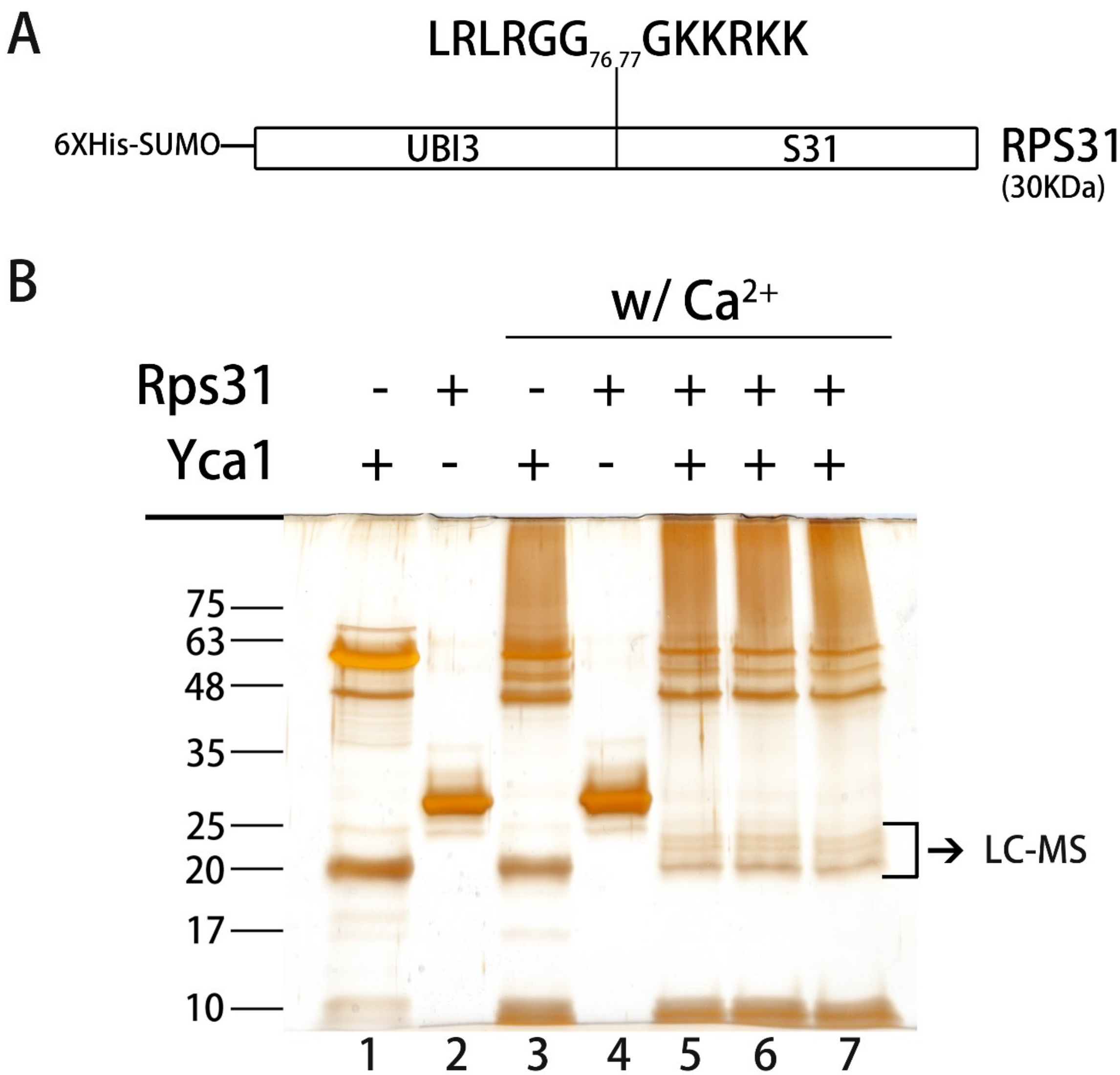

A
LOG
HS
REC
W K I W K I W K I
245
75
48
25
17
10
Ub
TUB
B
WT KO C297A
1.2
1
0.8
0.6
0.4
0.2
0
Fold change
*
*
*
*
LOG
HS
REC

Figure 20. Loss of Yca1 affects ubiquitin abundance *in vivo*. (A) Total protein extracts from wildtype BY4741 (W), Δ*yca1* (K) and inactive Yca1 (C297A; I) cells cultured under normal (LOG), heat stress (HS) and post-stress recovery (REC) conditions were prepared and subjected to SDS-PAGE and immobilized on to PVDF membranes. The ubiquitin levels were detected via immunoblotting with anti-ubiquitin antibody (Ub). Tubulin (TUB) served as a loading control (B) Densitometry analyses were performed on immunoblots using the ImageJ software for the lowest MW band (denoted with an arrow). The fold change (AVG ± SEM) in the levels of this band in Yca1 knockout (KO) and C297A cells compared to the wildtype (WT) is represented in the graph for each of the three conditions. n=4. The t-test was conducted to assess for statistical significance between the strains in each of the conditions. Samples marked with * denote a p value of ≤ 0.05.

this hypothesis by examining the profile of ubiquitin in the wildtype BY4741, Δ*yca1* and the inactive Yca1, C297A cells *in vivo*. Protein extract from cells cultured under normal, heat stress and post-stress recovery conditions was subjected to SDS-PAGE and immobilised on PVDF membranes. The ubiquitin profile for each strain in the differing conditions were resolved via immunoblotting with anti-ubiquitin antibody (Figure 20).

Examining the banding pattern for ubiquitin from the immunoblot analysis, we noticed alterations in the levels of a lower molecular weight (MW) band (Figure 20A; indicated with an arrow). This band corresponded roughly to the size of a single ubiquitin moiety, which is approximately 8 kDa. Densitometry and statistical analysis of this band between the different cells types in each condition showed that under normal conditions (LOG) the intensity of this band was significantly reduced in the KO cells (p = 0.0002) compared to the WT. Upon curbing the catalytic activity of Yca1 (C297A), the reduction was observed to be even greater than that observed for the KO, and also statistically significant (p = 0.003) compared to the WT (Figure 20B). Furthermore, upon the advent of heat stress, both the KO and the C297A cells showed similarly reduced levels compared to the WT cells, which was also significant (p = 0.03 and 0.05 respectively). However, under post-stress recovery conditions, this band was observed to be present at comparable levels in all the three endogenous strains (p = 0.2 for KO and 0.6 for C297A). Therefore, we observed that loss of Yca1 or its catalytic activity was associated with alteration in the cellular ubiquitin composition.



C

RS27A_YEAST (100%), 17,216.6 Da
Ubiquitin-40S ribosomal protein S31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS31 PE=1 SV=3
12 exclusive unique peptides, 15 exclusive unique spectra, 33 total spectra, 66/152 amino acids (43% coverage)

```
MQIFVKTLTG KTITLEVESS DTIDNVKSKI QDKEGIPPDQ QRLIFAGKQL
EDGRTLSDYN IQKESTLHLV LRLRGGGKKR KKKVYTTPKK IKHKHKKVKL
AVLSYYKVDA EGKVTKLRRE CSNPTCGAGV FLANHKDRLY CGKCHSVYKV
NA
```

Figure 21. Rps31 is cleaved by Yca1 *in vitro*. (A) Schematic representation of the 6XHis-SUMO-Rps31 precursor protein substrate which contains the N-terminal ubiquitin domain and C-terminal S31 ribosomal protein of the small subunit. The schematic also depicts the sequence of the junction of these two domains which includes the G76 residue via which ubiquitin is anchored onto protein substrates. (B) Silver stained gel on the cleavage assay. Recombinant 6XHis-SUMO tagged Yca1 and Rps31 were incubated either alone or in combination with or without calcium. The resulting reaction was resolved by SDS-PAGE and silver nitrate staining. The expected size for Yca1 is 64 kDa and for Rps31 is 30kDa. The bracket highlights the area on the gel with the resulting cleavage products which was further identified via mass spectrometry analysis. (C) Protein coverage of the cleavage products observed in B as depicted in Scaffold. The peptides corresponding to Rps31 detected via LC-MS/MS is highlighted in yellow.

4.8. Processing of the ubiquitin precursor protein Rps31

We speculated that the observed reduction in the levels of the low molecular weight ubiquitin could be a consequence of compromised *de novo* ubiquitin synthesis. Ubiquitin is synthesized as N-terminal ribosomal protein fusions, which undergo cleavage resulting in the liberation of the mature ubiquitin molecule (Ozkaynak, Finley et al. 1987, Finley, Bartel et al. 1989). In yeast, it was observed that ubiquitin specific proteases mediated the cleavage of non-precursor ubiquitin fusions and polyubiquitin *in vitro* (Baker, Tobias et al. 1992) and thus such proteases have been conjectured to process precursor ubiquitin fusion *in vivo* as well (Lacombe, Garcia-Gomez et al. 2009). A recent study in mammals identified numerous DUBs that were responsible for ubiquitin synthesis from precursors (Grou, Pinto et al. 2015). However in yeast, it remains unclear as to which proteases or DUBs are involved in *de novo* ubiquitin synthesis (Finley, Ulrich et al. 2012).

Our observations show that the absence of Yca1 or its activity led to reduced levels of monomeric ubiquitin (Figure 20), which suggests that Yca1 may be involved in regulating ubiquitin levels *in vivo*. Thus, to examine if Yca1 can directly act on precursor ubiquitin fusions to generate free ubiquitin, we setup cleavage assays *in vitro* using the Rps31 ubiquitin precursor protein as a substrate (Figure 21A). These proteins were incubated either together or alone and also either in the presence or absence of calcium, which has been suggested to be an activator of metacaspases (McLuskey, Rudolf et al. 2012, Wong, Yan et al. 2012, Machado, Marcondes et al. 2013). The reaction was resolved via SDS-PAGE and silver nitrate staining. We observed that in the replicate samples where Yca1 and Rps31 were incubated together and in the presence of calcium (Figure 20B; Lanes 5-7), the band corresponding to the size of Rps31 was completely absent. Instead, we observed three protein fragments (marked with a bracket) that were shorter in length than Rps31 and Yca1 present in these lanes. Interestingly, these fragments were only present in the lanes where the two proteins were incubated together and absent in the other lanes where either protein was incubated alone, which suggested that these fragments could be a result of Rps31 cleavage by Yca1. To further verify the identification of these fragments we excised the individual bands (Figure 21B; highlighted with bracket) and conducted LC-MS analysis to identify the constituents within these bands. The protein coverage from the LC-MS/MS analysis revealed that these shorter protein fragments contained the protein tag (6XHIS-SUMO) and the N-terminal ubiquitin domain of Rps31 but not the C-terminal S31 region (Figure 21C; highlighted in yellow). Taken together, these results suggest that the ubiquitin precursor protein Rps31 is amenable to cleavage by Yca1 leading to the separation of the ubiquitin moiety from the precursor.

CHAPTER 5

5. General Discussion

5.1. The role of Yca1 in proteostasis. Yca1 regulates the composition of the insoluble proteome

In this study, we identified the constituents of the insoluble protein fraction in wildtype and Yca1 null backgrounds during normal growth and heat stress. Surprisingly, the 2D LC-MS analysis led to the identification of over 2000 proteins within the insoluble fraction (Table S1). Although these proteins are not exclusive components of protein aggregates, this dataset suggests that the physical prelude to aggregate formation i.e. deposition to an insoluble protein compartment, is far more complex than has been previously suggested. A cohort of these proteins within our dataset could result from being confined within larger structures in the cell that resist solubilization but do not represent true insoluble protein species, a feature that has been reported previously (Bates 2006). Nonetheless, our approach implicates a wide array of proteins that may be targeted for aggregation, under normal conditions and stress. As such the dataset generated from this study will serve as a useful tool for subsequent investigations in this field.

To further validate the role of Yca1 in regulating cellular aggregate levels, we assessed the expression of Yca1-interacting proteins that had been previously and independently confirmed as components of protein aggregate remodeling platforms. The reduced levels of Cdc48 in the insoluble fraction and the concomitant retention within the soluble fraction of the Yca1 null strain during stressed conditions suggests a dependency on Yca1 to relocate Cdc48 to the insoluble protein fraction (Figure 7). Cdc48 is an AAA+ ATPase and has been well characterized in its role in ERAD factories as well as in the formation and clearing of protein aggregates (Jentsch and Rumpf 2007, Kobayashi, Manno et al. 2007). Therefore, it may be reasonable to conjecture that the presence of Cdc48 in the insoluble fraction may be to perform a similar role, i.e. re-solubilization or targeting aggregates for degradation. Interestingly, the other chaperone proteins known to interact with Yca1 did not display a similar co-localization to the insoluble fraction. This observation may indicate that the Yca1 and Hsp40/70 interactions are transient and do not persist within the insoluble protein compartment.

Additionally, the reduction in [NU+] levels observed (Figure 9), suggest that during stress conditions in Yca1 null cells as well as wildtype cells, may reflect a disparity between prion biology and proteostasis. Furthermore, of the numerous prions known in yeast (Halfmann, Alberti et al. 2010), we were only able to detect two in our analyses; [NU+] and [PIN+]. As such, this limited data set does not present us with sufficient information to conclude that Yca1 modifies prion forming susceptible proteins.

Our observation regarding alterations in ribosomal protein content as a result of heat stress induction was unexpected (Figure 8). Our analyses suggested that the ribosomal proteins listed in Table S2 are indeed affected by the stressed condition leading to their localization within the insoluble protein fraction, and that a proportion of these proteins may depend on Yca1 for this movement to occur. Most likely, the presence of these proteins within the insoluble protein fraction could result from the misfolding and aggregation of these proteins during heat stress (Sanchez and Lindquist 1990). However, the observed localization of these proteins may serve as a strategy to limit protein synthesis and thus prevent further misfolding and aggregation, which allows the cells to survive under heat stress. Indeed, reports in yeast suggest that cells favor re-solubilization of the aggregates which is dependent on the bi-chaperone system comprising of the disaggregase Hsp104 and the Hsp70 system, over the degradation of aggregates which is important for “thermotolerance” and survival under various stresses (Sanchez and Lindquist 1990, Sanchez, Taulien et al. 1992, Tyedmers, Mogk et al. 2010). Thus, it is a reasonable conjecture that Yca1 function may also have implications for ribosome biogenesis and protein synthesis under such conditions (Shrestha, Puente et al. 2013).

Furthermore, subsequent studies have shown similar sequestration for mRNA and translational machinery with misfolded aggregates in yeast and *Drosophila* under heat stress and inhibition of translation. Specifically, translational re-initiation was observed to be permitted only after significant re-solubilization of aggregates in the cytosol (Cherkasov, Hofmann et al. 2013). In addition to heat stress, similar effects of translational repression have been reported using other stressors. For example, during arsenite-induced stress conditions in yeast, ribosomal and translation-related proteins were observed to constitute a major proportion (59%) of the insoluble proteome as shown by GO analysis. Furthermore, the small size, high abundance and increased level of expression of these proteins were suggested to be features that increased their susceptibility to form aggregates (Ibstedt, Sideri et al. 2014). Furthermore, under severe heat conditions (46°C), protein synthesis and ribosome biogenesis were observed to be downregulated by sequestering proteins involved in these processes into heat stress granules (HSG), which are also present in the insoluble proteome (Cherkasov, Grousl et al. 2015). of note, Yca1 has also been observed to be a present in the insoluble pellet in such severe heat stress conditions (Wallace, Kear-Scott et al. 2015). Thus, together with these recent findings, our data suggests that Yca1 may be involved in global translational control, by mediating the incorporation of translational machinery into HSG during stress conditions.

5.2 Ubiquitin-mediated regulation of Yca1 during proteostasis

In our subsequent investigation, we concentrated our efforts on identifying regulatory protein interactions that directly modify Yca1 function/activity. Using a protein interaction screen coupled to proteomics we identified numerous protein interactions, in addition to those identified previously (Table S5). Within this Yca1 interactome, we observed that the key master signal for proteome regulation, ubiquitin, was present at high abundance (Figure 11). The presence of ubiquitin suggested an association of Yca1 to the UPS-mediated regulation of the proteome. Further investigation led to the identification of five sites on Yca1 that were post translationally modified by ubiquitin, including those that were previously reported but not characterized (Swaney, Beltrao et al. 2013). The presence of these ubiquitination sites, suggested a post-translational modification of Yca1, which could act as a switch to differentiate between Yca1 functions, presumably between death and non-death functions. Additionally, although not directly tested, the MS data also suggested the presence of K48 and K63 ubiquitin linkages (Table S6), which in turn suggests that Yca1 may have a role in protein degradation, as indicated by the presence of K48 chains, as well as in protein signalling, during which K63 linked ubiquitin chains are utilized for complex assembly and downstream signalling (Perrett, Lin et al. 2011, Komander and Rape 2012). Further characterization of the ubiquitination sites on Yca1 using a mutational approach suggested that the K355 site was observed to be important for establishing interactions with other ubiquitinated proteins (Figure 13) compared to the additional four sites analyzed. However, this interaction with ubiquitin and ubiquitinated proteins was not completely lost in the K355A mutant, most likely due to the presence of the additional ubiquitin modification sites as only single mutants for each site were created.

Nonetheless, the observed reduction in the level of ubiquitin-conjugated material suggests that the K355 residue has a greater influence on the interaction between Yca1 and ubiquitinated cellular components.

Furthermore, the K355 residue was also observed to have an effect on the proteostasis function of Yca1. The alteration of this residue to an alanine, compromised the ability to limit cellular insoluble protein content in cells expressing this mutant, similar to that observed in Yca1 knockout cells (Figure 17). This observation suggested that ubiquitination of this residue alters Yca1 function which may either directly or indirectly influence the ability to regulate the proteome. Additionally, we also observed an increase in the proportion of multivacuolated cells in K355A transformed Δ*yca1* cells (Figure 18). Our previous work observed similar effects upon the loss of Yca1 which was also accompanied by elevated expression of vacuolar peptidases, as assessed by iTRAQ analysis, which was suggestive of an upregulation of the autophagy process (Lee, Brunette et al. 2010). Unfortunately, we did not assess for the expression level of vacuolar peptidases within the K355A mutant (as well as the S346A mutant) and further experimentation is required to determine if affecting the ubiquitination of Yca1, which comprises the ability to regulate insoluble protein, has any impact on autophagy. Nevertheless, these observations suggest that the K355 residue is required for the function(s) of Yca1 that contributes to cellular proteostasis maintenance.

The structural analysis of Yca1 suggested that the K355 residue along with the adjacent K352, and upstream R93 and K107 residues were possible processing sites in Yca1, although no biochemical testing of this hypothesis was undertaken (Wong, Yan et al. 2012). Thus, our findings raise questions as to the importance of these two events (i.e.

ubiquitination and processing) and whether they are connected to the role of Yca1 in proteostasis. Of note, caspases have also been reported to be post-translationally modified by ubiquitin, which correlates to their proteolytic activity. For example, Cullin3-mediated K63 ubiquitination of caspase 8 leads to p62-mediated caspase 8 activation (Jin, Li et al. 2009). Alternatively, HECTD3-mediated K63 ubiquitination of caspase 8 has been observed to be inhibitory as it limited its recruitment to the DISC (Li, Kong et al. 2013). Thus, the ubiquitination of metacaspases may also serve a similar purpose and further, the result of the modification may be dependent on factors such as the E3 ligase involved and possibly even the type of ubiquitin linkage. Additionally, the observation that K residues can be subjected to both ubiquitin modification as well as proteolytic cleavage suggests that these sites could be critical in regulating Yca1 function. Currently, it is unclear whether the ubiquitination of Yca1 occurs post-processing or whether this happens independent of the processing event. Moreover, Yca1 activity has yet to be positively correlated with the processing events. However, a recent study assessing the activity of the type I metacaspase TbMCA2, reported that mutating the processing sites at K55 and K268 to glycine residues, resulted in reduced proteolytic capability as measured by the ability to process the azocasein substrate (Gilio, Marcondes et al. 2017), thus, linking processing and proteolytic activity for metacaspases as well. Furthermore, our previous work has shown that inactivating Yca1 via the C297A mutation leads also results in increased insoluble material and induction of vacuolar processes, suggesting that proteolytic activity of Yca1 is important for its role in proteostasis (Lee, Brunette et al. 2010). Thus, ubiquitination of Yca1 at K355 may serve as a mechanism to regulate Yca1 activity such that autoprocessing, which is associated with increase in proteolytic activity, at this residue occurs only under proper signals and in specific scenarios.

Additionally, among the multitude of E3 ligases present in yeast, we only detected the HECT family E3 ligase Rsp5 within the Yca1 interactome, which suggests that Rsp5 involvement may be specific to Yca1. As mentioned earlier in 4.3, Rsp5 is a member of the NEDD4 family and these family members have been shown to interact with phosphoserines. Our analyses show that the S346 residue, which was observed to be phosphorylated in our MS data (Table 3), is required for the proper interaction between Yca1 and Rsp5 (Figure 14). As such, the interaction between phosphorylated S346 and the E3 ligase Rsp5, would precede the ubiquitination event at the K355 residue. Thus, S346A mutant may be key to understanding the interplay between ubiquitination and cleavage at the K352 and K355 residues. Nonetheless, mutating the phosphorylation competent residue (S346A mutant) showed similar defects in proteostasis maintenance, particularly the reduced interaction with ubiquitin and ubiquitin conjugates and the increased retention of insoluble material, as the K355A mutant and Δ*yca1* strains. Thus, such observations with the S346A mutant provide added evidence that ubiquitination of Yca1, most likely via interaction with Rsp5, is important and influences the role of Yca1 in proteostasis (Figure 22). However, whether phosphorylation of Yca1 at S346A has any effect on the processing events at the K352 and K355 residues remains unknown. Of note, the K352 and K355 residues in the S346A mutant were preserved and in theory the S346A mutant was capable of being processed.

Furthermore, post-translational modification of caspases by kinases has also been shown to modulate caspase activity. Similar to that observed with ubiquitination, the inhibition or activation of caspase 8 is dependent on the kinase mediating the modification; Src acts to inhibit caspase 8 activity and apoptosis whereas, Plk3 leads to Fas induced caspase 8 activation (Helmke, Raab et al. 2016, Powley, Hughes et al. 2016). Intriguingly, the Y380 residue, which is flanked by the D374 and D384 processing sites, is the target of the Src kinase and, the phosphorylation of this tyrosine residue has been linked to various nonapoptotic functions of caspase 8 (Powley, Hughes et al. 2016, Zamaraev, Kopeina et al. 2017). Furthermore, caspase 8 undergoes Cdk1-mediated phosphorylation at S387 which affects the processing event at the adjacent D384 residue, which is required for caspase 8 maturation (Matthess, Raab et al. 2010). Thus, in our scenario it may be reasonable to speculate that the phosphorylation of S346 in Yca1 may affect processing at the K352 and K355 sites, as a consequence of Rsp5 recruitment and subsequent ubiquitination of the K352 and K355 residues, which acts as a steric hindrance (Figure 22). Likewise, phosphorylation signals on caspases could serve to recruit factors that limit caspase 8 processing such as components of the ubiquitin system. Of note, IAPs such as X-linked IAP (XIAP) can directly bind the active site of caspases and obstruct substrate entry thus curbing their effects (Huang, Park et al. 2001, Suzuki, Nakabayashi et al. 2001). This conserved suppressive function of IAPs is dependent on the presence of the really interesting new gene (RING) domain within its C-terminal which is characteristic of the RING family of E3 ligases (Yang, Fang et al. 2000, Lee, Fan et al. 2011, Meier, Morris et al. 2015).

The ability of Yca1 to undergo ubiquitination also implicated this PTM as a possible mechanism for its recruitment to specific quality control sites. As note above, Yca1 has been observed to localize to the two quality control compartments, namely the

IPOD and the JUNQ compartments. The colocalization between Yca1 and the nucleolar marker Sik1 suggests that Yca1 localization is in fact intranuclear (Hill, Hao et al. 2014, Miller, Ho et al. 2015). The first study that reported the spatial segregation of misfolded proteins in yeast, suggested that the ubiquitination of the misfolded protein favoured its localization to the JUNQ compartment (Kaganovich, Kopito et al. 2008). However, this role for ubiquitin as a sorting signal has been met with considerable debate. For instance, misfolded DegAB-GFP fusion protein was required to undergo ubiquitination to allow for its incorporation in the CytoQ compartment (Shiber, Breuer et al. 2013). Furthermore, the permanently misfolded protein substrate tGnd1-GFP was observed to accumulate in both the INQ and the CytoQ in conditions where it was unable to undergo ubiquitination (Miller, Ho et al. 2015). Thus, to further investigate the role of ubiquitin as a sorting tag, we compared the localization of Yca1 and the K355A mutant (Figure 19). Our analyses agreed with the latter observations as mutation of the K355 ubiquitination site did not affect its localization in proximity to the nuclear quality control compartments. As such, these observations lend further support to the argument that ubiquitination is not a clear sorting signal but rather a general indicator of misfolded proteins. However, we identified four other sites on Yca1 that displayed evidence of ubiquitin modification (K158, K170, K352 and K384) and the nuclear localization for these remaining ubiquitin site mutants have not yet been assessed. Accordingly, these additional ubiquitination sites could be involved in transporting Yca1 to the quality control compartments as they were unmodified in the K355A mutant. Furthermore, our analyses did not include known markers of these quality control compartments and as such may not be definitive (Hill, Hao et al. 2014, Miller, Ho et al. 2015).

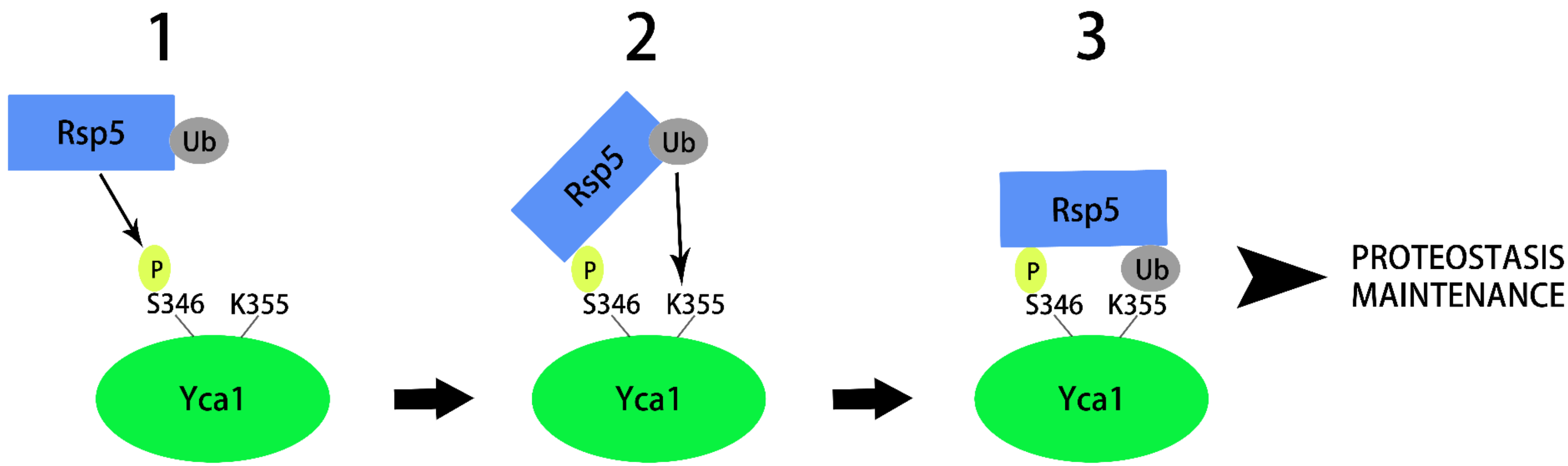


Figure 22. The proposed model for Yca1 ubiquitination. (1) The phosphorylation (yellow oval marked with 'P') of the S346 residue on Yca1 (green) is recognized by E3 ligases such as Rsp5 (blue) that are bound to ubiquitin (grey oval marked 'Ub'), which leads to its recruitment (2) and the ubiquitination of the adjacent K355 residue (3). These residues on Yca1 and the accompanying modifications are important for the function of Yca1 that contribute to cellular proteostasis maintenance.

A surprising observation from this study was that the ubiquitin precursor protein Rps31 could be processed by Yca1 to liberate the N-terminal ubiquitin moiety (Figure 21). This potential involvement of Yca1 in *de novo* ubiquitin synthesis could account for the reduced levels of monomeric ubiquitin observed upon the loss of Yca1 or its catalytic activity (Figure 20). However, further biochemical analysis is needed to understand if this Yca1-mediated cleavage yields a functional ubiquitin moiety. DUBs have been primarily associated with ubiquitin regulation as they actively recycle polyubiquitin chains at the proteasome. In yeast, the 19S RC lid component Rpn11 has been shown to catalyze the removal the polyubiquitin chain from the substrate (Yao and Cohen 2002). It is conjectured that other unidentified DUBs/proteases process the chains into shorter fragments. However, the yeast DUB Ubp14 has been implicated in the final cleavage step of these unanchored chains to produce ubiquitin monomers (Amerik, Swaminathan et al. 1997). As previously mentioned, in addition to polyubiquitin chains on substrates, DUBs have also been shown to process ubiquitin precursors in mammals, however, proteases that process ubiquitin precursor proteins have yet to be identified in yeast. Based on the R/K substrate specificity, we chose the Rps31 precursor as a candidate as it contains a series of K residues downstream of the C-terminal G76 residue of the ubiquitin domain (Figure 21A), which are residues preferred by metacaspases for cleavage (Lacombe, Garcia-Gomez et al. 2009, Tsiatsiani, Timmerman et al. 2013). However, whether Yca1 can cleave other ubiquitin precursors and polyubiquitin chains remains to be examined. Furthermore, during post-stress recovery conditions, when ubiquitin synthesis, specifically the level of the polyubiquitin fusion protein, is upregulated (Finley, Ozkaynak et al. 1987), we observed that all three strains contained similar levels of monomeric ubiquitin (Figure 20). This observation suggests that other proteases or DUBs are also most likely involved in synthesizing ubiquitin from the precursor ribosomal fusions in post-stress conditions.

Furthermore, metacaspases have been observed to undergo autoprocessing as well as recognize and cleave substrates at R and K residues (Vercammen, van de Cotte et al. 2004, Watanabe and Lam 2005, Tsiatsiani, Timmerman et al. 2013), As ubiquitin is anchored on to K residues on substrate proteins (Hershko and Ciechanover 1998), Yca1 could also be involved in the deubiquitination process where it would recognize the ubiquitin anchored K residue on the substrate and act to either release or modify the ubiquitin chain. A setting where Yca1 could perform this function would be at the JUNQ compartment where the ERAD pathway targets misfolded proteins for proteasomal degradation (Kaganovich, Kopito et al. 2008). Furthermore, in addition to Cdc48, which is involved in sorting of ubiquitinated proteins in the ER and targeting them for degradation (Stolz, Hilt et al. 2011), our analyses also identified the 19S RC ATPase Rpt5 as a protein interacting with Yca1. Rpt5, along with Rpt2, is involved in regulating the opening to the channel gate within the 20S CC upon proteasome assembly. This AAA+ ATPase has also been shown to be a receptor for ubiquitin and binds polyubiquitin chains (Lam, Lawson et al. 2002, Verma, Oania et al. 2004, Sorokin, Kim et al. 2009). Thus, it is tempting to speculate that Yca1 could coordinate its function with such candidates and fulfill this role although further insights into Yca1 cleavage site requirement on substrates is needed to determine if polyubiquitin chains are amenable to cleavage by Yca1.

In addition to the identification of ubiquitin, the Yca1 interactome provides a dataset to explore other Yca1 functions, either apoptotic or nonapoptotic processes. For example, a recent study directed at understanding the aggregation propensity of proteins under severe heat stress (46°C) led to the identification of 177 proteins, including Yca1, that were present in the pellet fraction (Wallace, Kear-Scott et al. 2015). This number is far less compared to our earlier findings, a fact that may originate from the differences in the fractionation process used to obtain the insoluble protein pellet. Of note, 22 of these aggregation prone proteins were also identified to interact with Yca1. Thus, these 22 proteins could represent substrates that are remodelled or regulated by Yca1 during heat stress (Table S7), however additional experimentation will be required to address this hypothesis. Of note, Yca1 and Rsp5 were identified within this group of aggregation prone proteins (Wallace, Kear-Scott et al. 2015), which provides further evidence to the notion that Yca1 and Rsp5 functions may be inherently linked and function together.

5.3. Future Directions

As discussed previously, ubiquitination of substrates can occur via multiple linkages with each linkage having a specific consequence (Swatek and Komander 2016). Our analyses did not provide insight into the nature of the ubiquitin modifications on Yca1, such as whether Yca1 was mono or polyubiquitinated. However, the ubiquitin molecules that were in interaction with Yca1 were observed to be conjugated via K48 and K63 linkages (Table S6). Such linkages are characteristically distinct and have different effects on Yca1 fate and function (Komander and Rape 2012). Thus, further in-depth investigation to understand the nature of Yca1 ubiquitination may be imperative as it determines the fate of the metacaspase. Of note, the E3 ligase Rsp5 which was detected to interact with Yca1, has been observed to favourably ubiquitinate its substrates via K63 linkage (Kee, Munoz et al. 2006, Saeki, Kudo et al. 2009), and this claim is further supported by our MS data which shows the presence of K63 linked polyubiquitin within the Yca1 interactome. Additionally, conducting ubiquitination assays with multiple other E3 ligases may provide further verification as to whether Yca1 is exclusively targeted by Rsp5 as suggested by our interaction studies. Furthermore, assessing and comparing the type of ubiquitin linkage between Yca1 and Yca1 mutants using such assays, may be insightful and influential delineating the functional effect of ubiquitination on Yca1. Particularly, the product of ubiquitination assays, i.e. ubiquitinated Yca1, could be treated with calcium to see if the ubiquitinated version of Yca1 is able to undergo processing.

Furthermore, the observation that processing sites on Yca1 can also undergo ubiquitination suggests that ubiquitination may in turn affect Yca1 activity. The catalytic activity of Yca1 has been previously observed to be required for its role in limiting insoluble protein content and inhibiting autophagy (Lee, Brunette et al. 2010). Here, we have shown that C297A cells possessed reduced levels of monomeric ubiquitin which may be a result of the inability to process ubiquitin precursors due to the lack of metacaspase activity by Yca1. Thus, as conducted with TbMCA2, generating a series of recombinant Yca1 mutants (single, double, triple and quadruple mutants), for the various reported processing sites as well as the modification sites reported in this study, and then assessing their ability to cleave metacaspase substrates, such as Rps31 utilized here or the fluorescent peptide Boc-GRR-AMC, will help elucidate whether processing of Yca1 correlates with its proteolytic activity.

Additionally, we observed that the K355A and the S346A mutants showed reduced interaction with ubiquitin compared to FL and the other mutants. These interactions may be critical to identifying additional events associated with the post-translational modifications, such as identifying additional players that physically coordinate or direct Yca1 activity. Furthermore, within our LC-MS data we observed that ubiquitin molecules were linked via the K63 residue (Table S6). K63-linked ubiquitin conjugates have been implicated in signalling events by acting as scaffolds for complex assembly and signal relay (Perrett, Lin et al. 2011, Swatek and Komander 2016), which leads to the intriguing speculation that Yca1 may be part of such complexes that are assembled on K63 linked ubiquitin scaffolds. Furthermore, the loss of interaction with ubiquitin observed for the K355A and S346A mutants would in turn affect complex assembly and overall signal transduction. Thus, comparing the interactome of the FL to the K355A and S346A mutants may be beneficial in identifying components of such complexes that either function together with Yca1 or act on Yca1 to regulate/direct its activity.

The hypothesized role for Yca1 as a DUB would require that Yca1 directly associates with the proteasome where ubiquitin chains are removed from substrates before being further processed to smaller chains. Thus, assessing Yca1 localization with the proteasome and further, assessing proteasome activity in wildtype and Yca1 knockout cells may provide evidence to support this conjecture. Of note, in addition to Rpt5, Yca1 was also observed to interact with Ecm29 which is a scaffold protein that is involved in stabilizing the interaction between the 19S RC and 20S CC component of the proteasome and acts as an adapter to relocate the proteasomes to specific cellular locations (Gorbea, Goellner et al. 2004). In addition, the non-ATPase regulatory component of the lid of the 19S RC, Rpn5 was also present within our dataset (Sorokin, Kim et al. 2009). Thus, these proteins constitute suitable candidates to further explore a role for Yca1 in directly affecting proteasome activity/function. Furthermore, conducting *in vitro* cleavage assays using recombinant Yca1 and additional ubiquitin precursors and polyubiquitin chains of various linkages will provide further information on the limits to the DUB-like activity exhibited by Yca1. Although the observation that Yca1 can process the ubiquitin precursor protein Rps31 to separate the N-terminal ubiquitin domain and the C-terminal S31 domain implicates this protease in *de novo* ubiquitin synthesis, questions remains as to whether the yielded ubiquitin domain is functional. Thus, further experimentation directed towards identifying cleavage sites on the Rps31 and other proposed ubiquitin substrates would further support or refute the concept that cleavage yields functional ubiquitin moieties or whether the event is non-specific. Additionally, such analyses may also shed light on cleavage site specificity for Yca1, which will be beneficial in identifying additional substrates.

Regarding the phosphorylation event observed at S346, our interaction studies identified the kinases Cdc19, Pfk1/2, Pgk1 and the Ser/Thr kinase Ypk1 as potential interaction partners of Yca1. Additionally, using the PhosphoMotif finder (www.hprd.org), we identified the S346 residue in the 'SLGS' sequence (residues 346-349) as a substrate recognition motif for the mammalian casein kinase CK1. CK1 phosphorylation is associated with limiting caspase cleavage, whereby CK1 mediated the phosphorylation of Bid at sites adjacent to the cleavage site, was observed to protect Bid from caspase 8 cleavage (Desagher, Osen-Sand et al. 2001). Thus, the homologous kinases in yeast constitute excellent candidates to further characterize the phosphorylation event at S346 on Yca1.

To further investigate how Yca1 is relocated to quality control sites, the remaining four ubiquitination sites should be directly tested with the methods we have employed for

K355A. Alternatively, as the role of ubiquitin as a sorting signal is debatable, characterizing interactions between Yca1 and other sorting/transport proteins that were identified through the interactions studies, may be of interest to elucidating the mechanism by which Yca1 is recruited to specific cellular compartments. Indeed, our Yca1 interaction data suggests that Yca1 may utilize additional mechanisms for managing proteostasis. For example, as noted previously, Hsp42 is a CytoQ compartment specific ‘aggregase’ that forms associations with Yca1 (Miller, Ho et al. 2015). We also identified the Hsp40 family member, Sis1 within the Yca1 interactome. This protein has been observed to be a toxicity-limiting component of the nuclear compartment INQ and is involved in nuclear transport of proteins marked for proteasomal degradation (Park, Kukushkin et al. 2013, Miller, Ho et al. 2015). Sis1 has been also observed to synergize with Hsp70 and deliver substrates to Hsp104 for disaggregation, particularly during the propagation of prions, which are structurally similar to aggregates (Higurashi, Hines et al. 2008, Tipton, Verges et al. 2008). Thus, characterization of the Yca1-Sis1 interaction may be of considerable interest.

In addition, various proteins identified as aggregation prone under arsenite-induced stress were found to have mammalian orthologs that are implicated in disorders related to protein misfolding. Of note a subset of these disease implicated proteins, such as Cdc48, Eno1/2, Vma2 and Chc1 were also identified in our MS analyses as interactors of Yca1 (Liao, Cheng et al. 2004, Wang, Woltjer et al. 2005, Basso, Samengo et al. 2009, Ibstedt, Sideri et al. 2014). Thus, further characterization of these interaction may be helpful to understand whether Yca1 (and by extension caspases) may have a role in modifying protein aggregation in various disease pathologies.

Finally, acquiring a complete understanding of Yca1 proteostasis function may require additional structural studies. For example, the regulatory role identified for the N-terminal prodomain in TbMCA2, whereby it is spans across the active site, has been suggested to also occur in Yca1. The sequence conservation in the prodomain between Yca1 and TbMCA2 is strong, specifically residues that are involved in the substrate access mechanism (Y31, C92, D95, S156 and D211) are conserved between these two type I metacaspases (McLuskey, Rudolf et al. 2012). However, the crystal structure analysis of Yca1 failed to include the prodomain and thus it remains unknown if the equivalent region in Yca1 is positioned and functions similarly to TbMCA2 (Wong, Yan et al. 2012). Further mutational analyses of these conserved residues in Yca1 will allow us to determine if the prodomain of Yca1 has a comparable role. Our previous work identified that the prodomain of Yca1 is required for targeting to protein aggregates as an N-terminal deletion of Yca1 redirected the metacaspase to the soluble proteome (Lee, Brunette et al. 2010). As such, the prodomain of Yca1 may act as an interaction platform for recruitment to aggregated proteins, where the metacaspase then undergoes a conformational change or is subjected to the proteolytic removal of the N-terminal region, which exposes the active site of the enzyme and initiates its aggregate management activity.

5.4. Conclusions

To further characterize the role of Yca1 in proteostasis we first conducted a 2D LC-MS analysis of the insoluble protein fraction in wildtype and Yca1 knockout cells. The resulting analysis determined that the composition of the insoluble protein fraction was non-specific and comprised a wide array of proteins. Furthermore, Cdc48 levels within this fraction were observed to be dependent on the presence of Yca1. Despite previous reports, our observations do not support the hypothesis that Yca1 has a direct role in prion biology. However, our results suggest that loss of Yca1 affects ribosomal protein function (Shrestha, Puente et al. 2013).

Additionally, to understand mechanisms that govern and/or mediate Yca1 functions we conducted protein interaction assays and identified a ubiquitin-mediated regulation mechanism for Yca1. Post-translational modifications on Yca1; specifically, the ubiquitination of the K355 residue and the phosphorylation of S346 residue are important features that allow for Yca1 to ensure proteostasis. Abrogation of these modifications by site directed mutagenesis led to a phenotype synonymous with Δ*yca1*, which was reflected by increased insoluble protein content and increased vacuolar structures. Furthermore, the ubiquitination of Yca1 did not serve as a sorting signal for nuclear quality control sites but rather was needed for interaction with ubiquitin and other proteins conjugated with ubiquitin. Surprisingly, the loss of Yca1 also affected ubiquitin homeostasis *in vivo* which suggested an intriguing role for Yca1 in proteostasis involving modification of the UPS pathway. This manipulation of the UPS pathway may involve *de novo* ubiquitin synthesis as evidenced by the ability of Yca1 to cleave Rps31 to liberate the N-terminal ubiquitin domain.

References

Alberti, S., R. Halfmann, O. King, A. Kapila and S. Lindquist (2009). "A systematic survey identifies prions and illuminates sequence features of prionogenic proteins." Cell **137**(1): 146-158.

Amerik, A., S. Swaminathan, B. A. Krantz, K. D. Wilkinson and M. Hochstrasser (1997). "In vivo disassembly of free polyubiquitin chains by yeast Ubp14 modulates rates of protein degradation by the proteasome." EMBO J **16**(16): 4826-4838.

Aravind, L. and E. V. Koonin (2002). "Classification of the caspase-hemoglobinase fold: detection of new families and implications for the origin of the eukaryotic separins." Proteins **46**(4): 355-367.

Arias, E. and A. M. Cuervo (2011). "Chaperone-mediated autophagy in protein quality control." Curr Opin Cell Biol **23**(2): 184-189.

Arndt, V., N. Dick, R. Tawo, M. Dreiseidler, D. Wenzel, M. Hesse, D. O. Furst, P. Saftig, R. Saint, B. K. Fleischmann, M. Hoch and J. Hohfeld (2010). "Chaperone-assisted selective autophagy is essential for muscle maintenance." Curr Biol **20**(2): 143-148.

Arrasate, M., S. Mitra, E. S. Schweitzer, M. R. Segal and S. Finkbeiner (2004). "Inclusion body formation reduces levels of mutant huntingtin and the risk of neuronal death." Nature **431**(7010): 805-810.

Bach, S. V. and A. N. Hegde (2016). "The proteasome and epigenetics: zooming in on histone modifications." Biomol Concepts **7**(4): 215-227.

Baker, R. T., J. W. Tobias and A. Varshavsky (1992). "Ubiquitin-specific proteases of Saccharomyces cerevisiae. Cloning of UBP2 and UBP3, and functional analysis of the UBP gene family." J Biol Chem **267**(32): 23364-23375.

Balch, W. E., R. I. Morimoto, A. Dillin and J. W. Kelly (2008). "Adapting proteostasis for disease intervention." Science **319**(5865): 916-919.

Basso, M., G. Samengo, G. Nardo, T. Massignan, G. D'Alessandro, S. Tartari, L. Cantoni, M. Marino, C. Cheroni, S. De Biasi, M. T. Giordana, M. J. Strong, A. G. Estevez, M. Salmona, C. Bendotti and V. Bonetto (2009). "Characterization of detergent-insoluble proteins in ALS indicates a causal link between nitrative stress and aggregation in pathogenesis." PLoS One **4**(12): e8130.

Bates, G. P. (2006). "BIOMEDICINE: One Misfolded Protein Allows Others to Sneak By." Science **311**(5766): 1385-1386.

Belenghi, B., M. C. Romero-Puertas, D. Vercammen, A. Brackenier, D. Inze, M. Delledonne and F. Van Breusegem (2007). "Metacaspase activity of Arabidopsis thaliana is regulated by S-nitrosylation of a critical cysteine residue." J Biol Chem **282**(2): 1352-1358.

Bell, R. A. and L. A. Megeney (2017). "Evolution of caspase-mediated cell death and differentiation: twins separated at birth." Cell Death Differ.

Bence, N. F., R. M. Sampat and R. R. Kopito (2001). "Impairment of the ubiquitin-proteasome system by protein aggregation." Science **292**(5521): 1552-1555.

Bett, J. S. (2016). "Proteostasis regulation by the ubiquitin system." Essays Biochem **60**(2): 143-151.

Bjorkoy, G., T. Lamark, A. Brech, H. Outzen, M. Perander, A. Overvatn, H. Stenmark and T. Johansen (2005). "p62/SQSTM1 forms protein aggregates degraded by autophagy and has a protective effect on huntingtin-induced cell death." J Cell Biol **171**(4): 603-614.
Boatright, K. M., M. Renatus, F. L. Scott, S. Sperandio, H. Shin, I. M. Pedersen, J. E. Ricci, W. A. Edris, D. P. Sutherlin, D. R. Green and G. S. Salvesen (2003). "A unified model for apical caspase activation." Mol Cell **11**(2): 529-541.
Boatright, K. M. and G. S. Salvesen (2003). "Caspase activation." Biochem Soc Symp(70): 233-242.
Boulares, A. H., A. G. Yakovlev, V. Ivanova, B. A. Stoica, G. Wang, S. Iyer and M. Smulson (1999). "Role of poly(ADP-ribose) polymerase (PARP) cleavage in apoptosis. Caspase 3-resistant PARP mutant increases rates of apoptosis in transfected cells." J Biol Chem **274**(33): 22932-22940.
Boya, P., R. A. Gonzalez-Polo, N. Casares, J. L. Perfettini, P. Dessen, N. Larochette, D. Metivier, D. Meley, S. Souquere, T. Yoshimori, G. Pierron, P. Codogno and G. Kroemer (2005). "Inhibition of macroautophagy triggers apoptosis." Mol Cell Biol **25**(3): 1025-1040.
Bukau, B. and A. L. Horwich (1998). "The Hsp70 and Hsp60 chaperone machines." Cell **92**(3): 351-366.
Carmona-Gutierrez, D., T. Eisenberg, S. Buttner, C. Meisinger, G. Kroemer and F. Madeo (2010). "Apoptosis in yeast: triggers, pathways, subroutines." Cell Death Differ **17**(5): 763-773.
Carra, S., S. J. Seguin, H. Lambert and J. Landry (2008). "HspB8 chaperone activity toward poly(Q)-containing proteins depends on its association with Bag3, a stimulator of macroautophagy." J Biol Chem **283**(3): 1437-1444.
Cashikar, A. G., M. Duennwald and S. L. Lindquist (2005). "A chaperone pathway in protein disaggregation. Hsp26 alters the nature of protein aggregates to facilitate reactivation by Hsp104." J Biol Chem **280**(25): 23869-23875.
Cerretti, D. P., C. J. Kozlosky, B. Mosley, N. Nelson, K. Van Ness, T. A. Greenstreet, C. J. March, S. R. Kronheim, T. Druck, L. A. Cannizzaro and et al. (1992). "Molecular cloning of the interleukin-1 beta converting enzyme." Science **256**(5053): 97-100.
Chastagner, P., A. Israel and C. Brou (2006). "Itch/AIP4 mediates Deltex degradation through the formation of K29-linked polyubiquitin chains." EMBO Rep **7**(11): 1147-1153.
Cherkasov, V., T. Grousl, P. Theer, Y. Vainshtein, C. Glasser, C. Mongis, G. Kramer, G. Stoecklin, M. Knop, A. Mogk and B. Bukau (2015). "Systemic control of protein synthesis through sequestration of translation and ribosome biogenesis factors during severe heat stress." FEBS Lett **589**(23): 3654-3664.
Cherkasov, V., S. Hofmann, S. Druffel-Augustin, A. Mogk, J. Tyedmers, G. Stoecklin and B. Bukau (2013). "Coordination of translational control and protein homeostasis during severe heat stress." Curr Biol **23**(24): 2452-2462.
Chiti, F. and C. M. Dobson (2006). "Protein misfolding, functional amyloid, and human disease." Annu Rev Biochem **75**: 333-366.
Choi, C. J. and J. A. Berges (2013). "New types of metacaspases in phytoplankton reveal diverse origins of cell death proteases." Cell Death Dis **4**: e490.
Coll, N. S., A. Smidler, M. Puigvert, C. Popa, M. Valls and J. L. Dangl (2014). "The plant metacaspase AtMC1 in pathogen-triggered programmed cell death and aging: functional linkage with autophagy." Cell Death Differ **21**(9): 1399-1408.

Coll, N. S., D. Vercammen, A. Smidler, C. Clover, F. Van Breusegem, J. L. Dangl and P. Epple (2010). "Arabidopsis type I metacaspases control cell death." Science **330**(6009): 1393-1397.

Cuervo, A. M. (2004). "Autophagy: in sickness and in health." Trends Cell Biol **14**(2): 70-77.

Degterev, A., M. Boyce and J. Yuan (2003). "A decade of caspases." Oncogene **22**(53): 8543-8567.

Denis, N. J., J. Vasilescu, J. P. Lambert, J. C. Smith and D. Figeys (2007). "Tryptic digestion of ubiquitin standards reveals an improved strategy for identifying ubiquitinated proteins by mass spectrometry." Proteomics **7**(6): 868-874.

Dennis, G., Jr., B. T. Sherman, D. A. Hosack, J. Yang, W. Gao, H. C. Lane and R. A. Lempicki (2003). "DAVID: Database for Annotation, Visualization, and Integrated Discovery." Genome Biol **4**(5): P3.

Desagher, S., A. Osen-Sand, S. Montessuit, E. Magnenat, F. Vilbois, A. Hochmann, L. Journot, B. Antonsson and J. C. Martinou (2001). "Phosphorylation of bid by casein kinases I and II regulates its cleavage by caspase 8." Mol Cell **8**(3): 601-611.

Ding, W. X., H. M. Ni, W. Gao, T. Yoshimori, D. B. Stolz, D. Ron and X. M. Yin (2007). "Linking of autophagy to ubiquitin-proteasome system is important for the regulation of endoplasmic reticulum stress and cell viability." Am J Pathol **171**(2): 513-524.

Dobson, C. M. (2003). "Protein folding and misfolding." Nature **426**(6968): 884-890.

Dobson, C. M. and R. J. Ellis (1998). "Protein folding and misfolding inside and outside the cell." EMBO J **17**(18): 5251-5254.

Du, L., Y. Su, D. Sun, W. Zhu, J. Wang, X. Zhuang, S. Zhou and Y. Lu (2008). "Formic acid induces Yca1p-independent apoptosis-like cell death in the yeast Saccharomyces cerevisiae." FEMS Yeast Res **8**(4): 531-539.

Dunker, A. K., I. Silman, V. N. Uversky and J. L. Sussman (2008). "Function and structure of inherently disordered proteins." Curr Opin Struct Biol **18**(6): 756-764.

Ellis, R. J. and A. P. Minton (2006). "Protein aggregation in crowded environments." Biol Chem **387**(5): 485-497.

Fernando, P. and L. A. Megeney (2007). "Is caspase-dependent apoptosis only cell differentiation taken to the extreme?" FASEB J **21**(1): 8-17.

Finley, D., B. Bartel and A. Varshavsky (1989). "The tails of ubiquitin precursors are ribosomal proteins whose fusion to ubiquitin facilitates ribosome biogenesis." Nature **338**(6214): 394-401.

Finley, D., E. Ozkaynak and A. Varshavsky (1987). "The yeast polyubiquitin gene is essential for resistance to high temperatures, starvation, and other stresses." Cell **48**(6): 1035-1046.

Finley, D., H. D. Ulrich, T. Sommer and P. Kaiser (2012). "The ubiquitin-proteasome system of Saccharomyces cerevisiae." Genetics **192**(2): 319-360.

Fleischer, T. C., C. M. Weaver, K. J. McAfee, J. L. Jennings and A. J. Link (2006). "Systematic identification and functional screens of uncharacterized proteins associated with eukaryotic ribosomal complexes." Genes Dev **20**(10): 1294-1307.

Fuchs, G., D. Hollander, Y. Voichek, G. Ast and M. Oren (2014). "Cotranscriptional histone H2B monoubiquitylation is tightly coupled with RNA polymerase II elongation rate." Genome Res **24**(10): 1572-1583.

Fuchs, G. and M. Oren (2014). "Writing and reading H2B monoubiquitylation." Biochim Biophys Acta **1839**(8): 694-701.
Fuchs, Y. and H. Steller (2011). "Programmed cell death in animal development and disease." Cell **147**(4): 742-758.
Fuentes-Prior, P. and G. S. Salvesen (2004). "The protein structures that shape caspase activity, specificity, activation and inhibition." Biochem J **384**(Pt 2): 201-232.
Fujiwara, K., Y. Ishihama, K. Nakahigashi, T. Soga and H. Taguchi (2010). "A systematic survey of in vivo obligate chaperonin-dependent substrates." EMBO J **29**(9): 1552-1564.
Gilio, J. M., M. F. Marcondes, D. Ferrari, M. A. Juliano, L. Juliano, V. Oliveira and M. F. Machado (2017). "Processing of metacaspase 2 from Trypanosoma brucei (TbMCA2) broadens its substrate specificity." Biochim Biophys Acta **1865**(4): 388-394.
Gilot, D., A. L. Serandour, G. P. Ilyin, D. Lagadic-Gossmann, P. Loyer, A. Corlu, A. Coutant, G. Baffet, M. E. Peter, O. Fardel and C. Guguen-Guillouzo (2005). "A role for caspase-8 and c-FLIPL in proliferation and cell-cycle progression of primary hepatocytes." Carcinogenesis **26**(12): 2086-2094.
Glover, J. R. and S. Lindquist (1998). "Hsp104, Hsp70, and Hsp40: a novel chaperone system that rescues previously aggregated proteins." Cell **94**(1): 73-82.
Goldberg, A. L. (2003). "Protein degradation and protection against misfolded or damaged proteins." Nature **426**(6968): 895-899.
Gong, Y., Y. Kakihara, N. Krogan, J. Greenblatt, A. Emili, Z. Zhang and W. A. Houry (2009). "An atlas of chaperone-protein interactions in Saccharomyces cerevisiae: implications to protein folding pathways in the cell." Mol Syst Biol **5**: 275.
Gorbea, C., G. M. Goellner, K. Teter, R. K. Holmes and M. Rechsteiner (2004). "Characterization of mammalian Ecm29, a 26 S proteasome-associated protein that localizes to the nucleus and membrane vesicles." J Biol Chem **279**(52): 54849-54861.
Grou, C. P., M. P. Pinto, A. V. Mendes, P. Domingues and J. E. Azevedo (2015). "The de novo synthesis of ubiquitin: identification of deubiquitinases acting on ubiquitin precursors." Sci Rep **5**: 12836.
Guscetti, F., N. Nath and N. Denko (2005). "Functional characterization of human proapoptotic molecules in yeast S. cerevisiae." FASEB J **19**(3): 464-466.
Gyrd-Hansen, M. and P. Meier (2010). "IAPs: from caspase inhibitors to modulators of NF-kappaB, inflammation and cancer." Nat Rev Cancer **10**(8): 561-574.
Haglund, K., S. Sigismund, S. Polo, I. Szymkiewicz, P. P. Di Fiore and I. Dikic (2003). "Multiple monoubiquitination of RTKs is sufficient for their endocytosis and degradation." Nat Cell Biol **5**(5): 461-466.
Hahne, H., F. Pachl, B. Ruprecht, S. K. Maier, S. Klaeger, D. Helm, G. Medard, M. Wilm, S. Lemeer and B. Kuster (2013). "DMSO enhances electrospray response, boosting sensitivity of proteomic experiments." Nat Methods **10**(10): 989-991.
Halfmann, R., S. Alberti and S. Lindquist (2010). "Prions, protein homeostasis, and phenotypic diversity." Trends Cell Biol **20**(3): 125-133.
Hartl, F. U. (1996). "Molecular chaperones in cellular protein folding." Nature **381**(6583): 571-579.
Hartl, F. U. and M. Hayer-Hartl (2009). "Converging concepts of protein folding in vitro and in vivo." Nat Struct Mol Biol **16**(6): 574-581.
Hegde, A. N. (2010). "The ubiquitin-proteasome pathway and synaptic plasticity." Learn Mem **17**(7): 314-327.

Hegde, A. N. and A. DiAntonio (2002). "Ubiquitin and the synapse." Nat Rev Neurosci **3**(11): 854-861.
Helmke, C., M. Raab, F. Rodel, Y. Matthess, T. Oellerich, R. Mandal, M. Sanhaji, H. Urlaub, C. Rodel, S. Becker and K. Strebhardt (2016). "Ligand stimulation of CD95 induces activation of Plk3 followed by phosphorylation of caspase-8." Cell Res **26**(8): 914-934.
Hershko, A. and A. Ciechanover (1998). "The ubiquitin system." Annu Rev Biochem **67**: 425-479.
Higurashi, T., J. K. Hines, C. Sahi, R. Aron and E. A. Craig (2008). "Specificity of the J-protein Sis1 in the propagation of 3 yeast prions." Proc Natl Acad Sci U S A **105**(43): 16596-16601.
Hill, S. M., X. Hao, B. Liu and T. Nystrom (2014). "Life-span extension by a metacaspase in the yeast Saccharomyces cerevisiae." Science **344**(6190): 1389-1392.
Hishiya, A. and S. Takayama (2008). "Molecular chaperones as regulators of cell death." Oncogene **27**(50): 6489-6506.
Holmberg, C. I., K. E. Staniszewski, K. N. Mensah, A. Matouschek and R. I. Morimoto (2004). "Inefficient degradation of truncated polyglutamine proteins by the proteasome." EMBO J **23**(21): 4307-4318.
Hsu, S. L., C. T. Yu, S. C. Yin, M. J. Tang, A. C. Tien, Y. M. Wu and C. Y. Huang (2006). "Caspase 3, periodically expressed and activated at G2/M transition, is required for nocodazole-induced mitotic checkpoint." Apoptosis **11**(5): 765-771.
Huang da, W., B. T. Sherman and R. A. Lempicki (2009). "Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources." Nat Protoc **4**(1): 44-57.
Huang, Y., Y. C. Park, R. L. Rich, D. Segal, D. G. Myszka and H. Wu (2001). "Structural basis of caspase inhibition by XIAP: differential roles of the linker versus the BIR domain." Cell **104**(5): 781-790.
Huibregtse, J. M., M. Scheffner, S. Beaudenon and P. M. Howley (1995). "A family of proteins structurally and functionally related to the E6-AP ubiquitin-protein ligase." Proc Natl Acad Sci U S A **92**(11): 5249.
Ibstedt, S., T. C. Sideri, C. M. Grant and M. J. Tamas (2014). "Global analysis of protein aggregation in yeast during physiological conditions and arsenite stress." Biol Open **3**(10): 913-923.
Im, E. and K. C. Chung (2016). "Precise assembly and regulation of 26S proteasome and correlation between proteasome dysfunction and neurodegenerative diseases." BMB Rep **49**(9): 459-473.
Izeradjene, K., L. Douglas, D. M. Tillman, A. B. Delaney and J. A. Houghton (2005). "Reactive oxygen species regulate caspase activation in tumor necrosis factor-related apoptosis-inducing ligand-resistant human colon carcinoma cell lines." Cancer Res **65**(16): 7436-7445.
Jackson, M. P. and E. W. Hewitt (2016). "Cellular proteostasis: degradation of misfolded proteins by lysosomes." Essays Biochem **60**(2): 173-180.
Jana, N. R., E. A. Zemskov, G. Wang and N. Nukina (2001). "Altered proteasomal function due to the expression of polyglutamine-expanded truncated N-terminal huntingtin induces apoptosis by caspase activation through mitochondrial cytochrome c release." Hum Mol Genet **10**(10): 1049-1059.

Jentsch, S. and S. Rumpf (2007). "Cdc48 (p97): a "molecular gearbox" in the ubiquitin pathway?" Trends Biochem Sci **32**(1): 6-11.
Jeong, J. H., S. E. Lee and J. Kim (2016). "Mutational analysis of metacaspase CaMca1 and decapping activator Edc3 in the pathogenicity of Candida albicans." Fungal Genet Biol **97**: 18-23.
Jin, Z., Y. Li, R. Pitti, D. Lawrence, V. C. Pham, J. R. Lill and A. Ashkenazi (2009). "Cullin3-based polyubiquitination and p62-dependent aggregation of caspase-8 mediate extrinsic apoptosis signaling." Cell **137**(4): 721-735.
Jung, J. H. and J. Kim (2014). "Roles of Edc3 in the oxidative stress response and CaMCA1-encoded metacaspase expression in Candida albicans." FEBS J **281**(21): 4841-4851.
Kaganovich, D., R. Kopito and J. Frydman (2008). "Misfolded proteins partition between two distinct quality control compartments." Nature **454**(7208): 1088-1095.
Kampinga, H. H. and E. A. Craig (2010). "The HSP70 chaperone machinery: J proteins as drivers of functional specificity." Nat Rev Mol Cell Biol **11**(8): 579-592.
Kaushik, S. and A. M. Cuervo (2012). "Chaperones in autophagy." Pharmacol Res **66**(6): 484-493.
Kawaguchi, Y., J. J. Kovacs, A. McLaurin, J. M. Vance, A. Ito and T. P. Yao (2003). "The deacetylase HDAC6 regulates aggresome formation and cell viability in response to misfolded protein stress." Cell **115**(6): 727-738.
Kee, Y., W. Munoz, N. Lyon and J. M. Huibregtse (2006). "The deubiquitinating enzyme Ubp2 modulates Rsp5-dependent Lys63-linked polyubiquitin conjugates in Saccharomyces cerevisiae." J Biol Chem **281**(48): 36724-36731.
Keilhauer, E. C., M. Y. Hein and M. Mann (2015). "Accurate protein complex retrieval by affinity enrichment mass spectrometry (AE-MS) rather than affinity purification mass spectrometry (AP-MS)." Mol Cell Proteomics **14**(1): 120-135.
Kerr, J. F., A. H. Wyllie and A. R. Currie (1972). "Apoptosis: a basic biological phenomenon with wide-ranging implications in tissue kinetics." Br J Cancer **26**(4): 239-257.
Khan, M. A., P. B. Chock and E. R. Stadtman (2005). "Knockout of caspase-like gene, YCA1, abrogates apoptosis and elevates oxidized proteins in Saccharomyces cerevisiae." Proc Natl Acad Sci U S A **102**(48): 17326-17331.
Kim, Y. E., M. S. Hipp, A. Bracher, M. Hayer-Hartl and F. U. Hartl (2013). "Molecular chaperone functions in protein folding and proteostasis." Annu Rev Biochem **82**: 323-355.
Kischkel, F. C., S. Hellbardt, I. Behrmann, M. Germer, M. Pawlita, P. H. Krammer and M. E. Peter (1995). "Cytotoxicity-dependent APO-1 (Fas/CD95)-associated proteins form a death-inducing signaling complex (DISC) with the receptor." EMBO J **14**(22): 5579-5588.
Kobayashi, T., A. Manno and A. Kakizuka (2007). "Involvement of valosin-containing protein (VCP)/p97 in the formation and clearance of abnormal protein aggregates." Genes Cells **12**(7): 889-901.
Komander, D. and M. Rape (2012). "The ubiquitin code." Annu Rev Biochem **81**: 203-229.
Kopito, R. R. and D. Ron (2000). "Conformational disease." Nat Cell Biol **2**(11): E207-209.
Lacombe, T., J. J. Garcia-Gomez, J. de la Cruz, D. Roser, E. Hurt, P. Linder and D. Kressler (2009). "Linear ubiquitin fusion to Rps31 and its subsequent cleavage are required for the

efficient production and functional integrity of 40S ribosomal subunits." Mol Microbiol **72**(1): 69-84.
Lam, Y. A., T. G. Lawson, M. Velayutham, J. L. Zweier and C. M. Pickart (2002). "A proteasomal ATPase subunit recognizes the polyubiquitin degradation signal." Nature **416**(6882): 763-767.
Lamkanfi, M., W. Declercq, M. Kalai, X. Saelens and P. Vandenabeele (2002). "Alice in caspase land. A phylogenetic analysis of caspases from worm to man." Cell Death Differ **9**(4): 358-361.
Laverriere, M., J. J. Cazzulo and V. E. Alvarez (2012). "Antagonic activities of Trypanosoma cruzi metacaspases affect the balance between cell proliferation, death and differentiation." Cell Death Differ **19**(8): 1358-1369.
Lee, J. Y., H. Koga, Y. Kawaguchi, W. Tang, E. Wong, Y. S. Gao, U. B. Pandey, S. Kaushik, E. Tresse, J. Lu, J. P. Taylor, A. M. Cuervo and T. P. Yao (2010). "HDAC6 controls autophagosome maturation essential for ubiquitin-selective quality-control autophagy." EMBO J **29**(5): 969-980.
Lee, R. E., S. Brunette, L. G. Puente and L. A. Megeney (2010). "Metacaspase Yca1 is required for clearance of insoluble protein aggregates." Proc Natl Acad Sci U S A **107**(30): 13348-13353.
Lee, R. E., L. G. Puente, M. Kaern and L. A. Megeney (2008). "A non-death role of the yeast metacaspase: Yca1p alters cell cycle dynamics." PLoS One **3**(8): e2956.
Lee, T. V., Y. Fan, S. Wang, M. Srivastava, M. Broemer, P. Meier and A. Bergmann (2011). "Drosophila IAP1-mediated ubiquitylation controls activation of the initiator caspase DRONC independent of protein degradation." PLoS Genet **7**(9): e1002261.
Leist, M. and M. Jaattela (2001). "Four deaths and a funeral: from caspases to alternative mechanisms." Nat Rev Mol Cell Biol **2**(8): 589-598.
Li, Y., Y. Kong, Z. Zhou, H. Chen, Z. Wang, Y. C. Hsieh, D. Zhao, X. Zhi, J. Huang, J. Zhang, H. Li and C. Chen (2013). "The HECTD3 E3 ubiquitin ligase facilitates cancer cell survival by promoting K63-linked polyubiquitination of caspase-8." Cell Death Dis **4**: e935.
Liang, Q. and B. Zhou (2007). "Copper and manganese induce yeast apoptosis via different pathways." Mol Biol Cell **18**(12): 4741-4749.
Liao, L., D. Cheng, J. Wang, D. M. Duong, T. G. Losik, M. Gearing, H. D. Rees, J. J. Lah, A. I. Levey and J. Peng (2004). "Proteomic characterization of postmortem amyloid plaques isolated by laser capture microdissection." J Biol Chem **279**(35): 37061-37068.
Ligr, M., F. Madeo, E. Frohlich, W. Hilt, K. U. Frohlich and D. H. Wolf (1998). "Mammalian Bax triggers apoptotic changes in yeast." FEBS Lett **438**(1-2): 61-65.
Lim, J., M. L. Lachenmayer, S. Wu, W. Liu, M. Kundu, R. Wang, M. Komatsu, Y. J. Oh, Y. Zhao and Z. Yue (2015). "Proteotoxic stress induces phosphorylation of p62/SQSTM1 by ULK1 to regulate selective autophagic clearance of protein aggregates." PLoS Genet **11**(2): e1004987.
Lindquist, S. and E. A. Craig (1988). "The heat-shock proteins." Annu Rev Genet **22**: 631-677.
Liu, B., L. Larsson, A. Caballero, X. Hao, D. Oling, J. Grantham and T. Nystrom (2010). "The polarisome is required for segregation and retrograde transport of protein aggregates." Cell **140**(2): 257-267.

Liu, I. C., S. W. Chiu, H. Y. Lee and J. Y. Leu (2012). "The histone deacetylase Hos2 forms an Hsp42-dependent cytoplasmic granule in quiescent yeast cells." Mol Biol Cell **23**(7): 1231-1242.
Lu, K., I. Psakhye and S. Jentsch (2014). "Autophagic clearance of polyQ proteins mediated by ubiquitin-Atg8 adaptors of the conserved CUET protein family." Cell **158**(3): 549-563.
Lu, P. J., X. Z. Zhou, M. Shen and K. P. Lu (1999). "Function of WW domains as phosphoserine- or phosphothreonine-binding modules." Science **283**(5406): 1325-1328.
Lynch-Day, M. A. and D. J. Klionsky (2010). "The Cvt pathway as a model for selective autophagy." FEBS Lett **584**(7): 1359-1366.
Machado, M. F., M. F. Marcondes, M. A. Juliano, K. McLuskey, J. C. Mottram, C. X. Moss, L. Juliano and V. Oliveira (2013). "Substrate specificity and the effect of calcium on Trypanosoma brucei metacaspase 2." FEBS J **280**(11): 2608-2621.
MacKenzie, S. H. and A. C. Clark (2012). "Death by caspase dimerization." Adv Exp Med Biol **747**: 55-73.
Madeo, F., D. Carmona-Gutierrez, J. Ring, S. Buttner, T. Eisenberg and G. Kroemer (2009). "Caspase-dependent and caspase-independent cell death pathways in yeast." Biochem Biophys Res Commun **382**(2): 227-231.
Madeo, F., T. Eisenberg and G. Kroemer (2009). "Autophagy for the avoidance of neurodegeneration." Genes Dev **23**(19): 2253-2259.
Madeo, F., E. Frohlich and K. U. Frohlich (1997). "A yeast mutant showing diagnostic markers of early and late apoptosis." J Cell Biol **139**(3): 729-734.
Madeo, F., E. Herker, C. Maldener, S. Wissing, S. Lachelt, M. Herlan, M. Fehr, K. Lauber, S. J. Sigrist, S. Wesselborg and K. U. Frohlich (2002). "A caspase-related protease regulates apoptosis in yeast." Mol Cell **9**(4): 911-917.
Matsumoto, G., K. Wada, M. Okuno, M. Kurosawa and N. Nukina (2011). "Serine 403 phosphorylation of p62/SQSTM1 regulates selective autophagic clearance of ubiquitinated proteins." Mol Cell **44**(2): 279-289.
Matthess, Y., M. Raab, M. Sanhaji, I. N. Lavrik and K. Strebhardt (2010). "Cdk1/cyclin B1 controls Fas-mediated apoptosis by regulating caspase-8 activity." Mol Cell Biol **30**(24): 5726-5740.
Mazzoni, C. and C. Falcone (2008). "Caspase-dependent apoptosis in yeast." Biochim Biophys Acta **1783**(7): 1320-1327.
McClellan, A. J., Y. Xia, A. M. Deutschbauer, R. W. Davis, M. Gerstein and J. Frydman (2007). "Diverse cellular functions of the Hsp90 molecular chaperone uncovered using systems approaches." Cell **131**(1): 121-135.
McLuskey, K. and J. C. Mottram (2015). "Comparative structural analysis of the caspase family with other clan CD cysteine peptidases." Biochem J **466**(2): 219-232.
McLuskey, K., J. Rudolf, W. R. Proto, N. W. Isaacs, G. H. Coombs, C. X. Moss and J. C. Mottram (2012). "Crystal structure of a Trypanosoma brucei metacaspase." Proc Natl Acad Sci U S A **109**(19): 7469-7474.
Meier, P., O. Morris and M. Broemer (2015). "Ubiquitin-Mediated Regulation of Cell Death, Inflammation, and Defense of Homeostasis." Curr Top Dev Biol **114**: 209-239.
Miller, S. B., C. T. Ho, J. Winkler, M. Khokhrina, A. Neuner, M. Y. Mohamed, D. L. Guilbride, K. Richter, M. Lisby, E. Schiebel, A. Mogk and B. Bukau (2015).

"Compartment-specific aggregases direct distinct nuclear and cytoplasmic aggregate deposition." EMBO J **34**(6): 778-797.
Miller, S. B., A. Mogk and B. Bukau (2015). "Spatially organized aggregation of misfolded proteins as cellular stress defense strategy." J Mol Biol **427**(7): 1564-1574.
Minina, E. A., N. S. Coll, H. Tuominen and P. V. Bozhkov (2017). "Metacaspases versus caspases in development and cell fate regulation." Cell Death Differ.
Mogk, A. and B. Bukau (2017). "Role of sHsps in organizing cytosolic protein aggregation and disaggregation." Cell Stress Chaperones.
Mottram, J. C., M. J. Helms, G. H. Coombs and M. Sajid (2003). "Clan CD cysteine peptidases of parasitic protozoa." Trends in Parasitology **19**(4): 182-187.
Nakagawa, T. and K. Nakayama (2015). "Protein monoubiquitylation: targets and diverse functions." Genes Cells **20**(7): 543-562.
Nhan, T. Q., W. C. Liles and S. M. Schwartz (2006). "Physiological functions of caspases beyond cell death." Am J Pathol **169**(3): 729-737.
Ozkaynak, E., D. Finley, M. J. Solomon and A. Varshavsky (1987). "The yeast ubiquitin genes: a family of natural gene fusions." EMBO J **6**(5): 1429-1439.
Park, S. H., Y. Kukushkin, R. Gupta, T. Chen, A. Konagai, M. S. Hipp, M. Hayer-Hartl and F. U. Hartl (2013). "PolyQ proteins interfere with nuclear degradation of cytosolic proteins by sequestering the Sis1p chaperone." Cell **154**(1): 134-145.
Parrish, A. B., C. D. Freel and S. Kornbluth (2013). "Cellular mechanisms controlling caspase activation and function." Cold Spring Harb Perspect Biol **5**(6).
Pereira, C., N. Camougrand, S. Manon, M. J. Sousa and M. Corte-Real (2007). "ADP/ATP carrier is required for mitochondrial outer membrane permeabilization and cytochrome c release in yeast apoptosis." Mol Microbiol **66**(3): 571-582.
Perrett, C. A., D. Y. Lin and D. Zhou (2011). "Interactions of bacterial proteins with host eukaryotic ubiquitin pathways." Front Microbiol **2**: 143.
Pestov, D. G., M. G. Stockelman, Z. Strezoska and L. F. Lau (2001). "ERB1, the yeast homolog of mammalian Bop1, is an essential gene required for maturation of the 25S and 5.8S ribosomal RNAs." Nucleic Acids Res **29**(17): 3621-3630.
Powers, E. T., R. I. Morimoto, A. Dillin, J. W. Kelly and W. E. Balch (2009). "Biological and chemical approaches to diseases of proteostasis deficiency." Annu Rev Biochem **78**: 959-991.
Powley, I. R., M. A. Hughes, K. Cain and M. MacFarlane (2016). "Caspase-8 tyrosine-380 phosphorylation inhibits CD95 DISC function by preventing procaspase-8 maturation and cycling within the complex." Oncogene **35**(43): 5629-5640.
Preissler, S. and E. Deuerling (2012). "Ribosome-associated chaperones as key players in proteostasis." Trends Biochem Sci **37**(7): 274-283.
Rajan, R. S., M. E. Illing, N. F. Bence and R. R. Kopito (2001). "Specificity in intracellular protein aggregation and inclusion body formation." Proc Natl Acad Sci U S A **98**(23): 13060-13065.
Ritossa, F. (1996). "Discovery of the heat shock response." Cell Stress Chaperones **1**(2): 97-98.
Ritossa, F. M. (1964). "Experimental Activation of Specific Loci in Polytene Chromosomes of Drosophila." Exp Cell Res **35**: 601-607.
Ross, C. A. and M. A. Poirier (2004). "Protein aggregation and neurodegenerative disease." Nat Med **10 Suppl**: S10-17.

Rubinsztein, D. C. (2006). "The roles of intracellular protein-degradation pathways in neurodegeneration." Nature **443**(7113): 780-786.
Rubinsztein, D. C., P. Codogno and B. Levine (2012). "Autophagy modulation as a potential therapeutic target for diverse diseases." Nat Rev Drug Discov **11**(9): 709-730.
Saeki, Y., T. Kudo, T. Sone, Y. Kikuchi, H. Yokosawa, A. Toh-e and K. Tanaka (2009). "Lysine 63-linked polyubiquitin chain may serve as a targeting signal for the 26S proteasome." EMBO J **28**(4): 359-371.
Sanchez, Y. and S. L. Lindquist (1990). "HSP104 required for induced thermotolerance." Science **248**(4959): 1112-1115.
Sanchez, Y., J. Taulien, K. A. Borkovich and S. Lindquist (1992). "Hsp104 is required for tolerance to many forms of stress." EMBO J **11**(6): 2357-2364.
Sarkar, S. (2013). "Regulation of autophagy by mTOR-dependent and mTOR-independent pathways: autophagy dysfunction in neurodegenerative diseases and therapeutic application of autophagy enhancers." Biochem Soc Trans **41**(5): 1103-1130.
Serio, T. R. and S. L. Lindquist (2000). "Protein-only inheritance in yeast: something to get [PSI+]-ched about." Trends Cell Biol **10**(3): 98-105.
Shao, W., G. Yeretssian, K. Doiron, S. N. Hussain and M. Saleh (2007). "The caspase-1 digestome identifies the glycolysis pathway as a target during infection and septic shock." J Biol Chem **282**(50): 36321-36329.
Shevchenko, A., M. Wilm, O. Vorm and M. Mann (1996). "Mass spectrometric sequencing of proteins silver-stained polyacrylamide gels." Anal Chem **68**(5): 850-858.
Shiber, A., W. Breuer, M. Brandeis and T. Ravid (2013). "Ubiquitin conjugation triggers misfolded protein sequestration into quality control foci when Hsp70 chaperone levels are limiting." Mol Biol Cell **24**(13): 2076-2087.
Shrestha, A. and L. A. Megeney (2012). "The non-death role of metacaspase proteases." Front Oncol **2**: 78.
Shrestha, A., L. G. Puente, S. Brunette and L. A. Megeney (2013). "The role of Yca1 in proteostasis. Yca1 regulates the composition of the insoluble proteome." J Proteomics **81**: 24-30.
Silva, A., B. Almeida, B. Sampaio-Marques, M. I. Reis, S. Ohlmeier, F. Rodrigues, A. Vale and P. Ludovico (2011). "Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) is a specific substrate of yeast metacaspase." Biochim Biophys Acta **1813**(12): 2044-2049.
Sorokin, A. V., E. R. Kim and L. P. Ovchinnikov (2009). "Proteasome system of protein degradation and processing." Biochemistry (Mosc) **74**(13): 1411-1442.
Spokoini, R., O. Moldavski, Y. Nahmias, J. L. England, M. Schuldiner and D. Kaganovich (2012). "Confinement to organelle-associated inclusion structures mediates asymmetric inheritance of aggregated protein in budding yeast." Cell Rep **2**(4): 738-747.
Stolz, A., W. Hilt, A. Buchberger and D. H. Wolf (2011). "Cdc48: a power machine in protein degradation." Trends Biochem Sci **36**(10): 515-523.
Strobel, I. and H. D. Osiewacz (2013). "Poly(ADP-ribose) polymerase is a substrate recognized by two metacaspases of Podospora anserina." Eukaryot Cell **12**(6): 900-912.
Sundstrom, J. F., A. Vaculova, A. P. Smertenko, E. I. Savenkov, A. Golovko, E. Minina, B. S. Tiwari, S. Rodriguez-Nieto, A. A. Zamyatnin, Jr., T. Valineva, J. Saarikettu, M. J. Frilander, M. F. Suarez, A. Zavialov, U. Stahl, P. J. Hussey, O. Silvennoinen, E. Sundberg, B. Zhivotovsky and P. V. Bozhkov (2009). "Tudor staphylococcal nuclease is an

evolutionarily conserved component of the programmed cell death degradome." Nat Cell Biol **11**(11): 1347-1354.
Suzuki, H., K. Lee and M. Matsuoka (2011). "TDP-43-induced death is associated with altered regulation of BIM and Bcl-xL and attenuated by caspase-mediated TDP-43 cleavage." J Biol Chem **286**(15): 13171-13183.
Suzuki, Y., Y. Nakabayashi, K. Nakata, J. C. Reed and R. Takahashi (2001). "X-linked inhibitor of apoptosis protein (XIAP) inhibits caspase-3 and -7 in distinct modes." J Biol Chem **276**(29): 27058-27063.
Swaney, D. L., P. Beltrao, L. Starita, A. Guo, J. Rush, S. Fields, N. J. Krogan and J. Villen (2013). "Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation." Nat Methods **10**(7): 676-682.
Swatek, K. N. and D. Komander (2016). "Ubiquitin modifications." Cell Res **26**(4): 399-422.
Szallies, A., B. K. Kubata and M. Duszenko (2002). "A metacaspase of Trypanosoma brucei causes loss of respiration competence and clonal death in the yeast Saccharomyces cerevisiae." FEBS Lett **517**(1-3): 144-150.
Taipale, M., D. F. Jarosz and S. Lindquist (2010). "HSP90 at the hub of protein homeostasis: emerging mechanistic insights." Nat Rev Mol Cell Biol **11**(7): 515-528.
Tanaka, M., Y. M. Kim, G. Lee, E. Junn, T. Iwatsubo and M. M. Mouradian (2004). "Aggresomes formed by alpha-synuclein and synphilin-1 are cytoprotective." J Biol Chem **279**(6): 4625-4631.
Tatusov, R. L., M. Y. Galperin, D. A. Natale and E. V. Koonin (2000). "The COG database: a tool for genome-scale analysis of protein functions and evolution." Nucleic Acids Res **28**(1): 33-36.
Thornberry, N. A. (1998). "Caspases: key mediators of apoptosis." Chem Biol **5**(5): R97-103.
Tipton, K. A., K. J. Verges and J. S. Weissman (2008). "In vivo monitoring of the prion replication cycle reveals a critical role for Sis1 in delivering substrates to Hsp104." Mol Cell **32**(4): 584-591.
Tsiatsiani, L., E. Timmerman, P. J. De Bock, D. Vercammen, S. Stael, B. van de Cotte, A. Staes, M. Goethals, T. Beunens, P. Van Damme, K. Gevaert and F. Van Breusegem (2013). "The Arabidopsis metacaspase9 degradome." Plant Cell **25**(8): 2831-2847.
Tsiatsiani, L., F. Van Breusegem, P. Gallois, A. Zavialov, E. Lam and P. V. Bozhkov (2011). "Metacaspases." Cell Death Differ **18**(8): 1279-1288.
Tuttle, D. L. and W. A. Dunn, Jr. (1995). "Divergent modes of autophagy in the methylotrophic yeast Pichia pastoris." J Cell Sci **108 (Pt 1)**: 25-35.
Tyedmers, J., A. Mogk and B. Bukau (2010). "Cellular strategies for controlling protein aggregation." Nat Rev Mol Cell Biol **11**(11): 777-788.
Uren, A. G., K. O'Rourke, L. A. Aravind, M. T. Pisabarro, S. Seshagiri, E. V. Koonin and V. M. Dixit (2000). "Identification of paracaspases and metacaspases: two ancient families of caspase-like proteins, one of which plays a key role in MALT lymphoma." Mol Cell **6**(4): 961-967.
Vercammen, D., B. van de Cotte, G. De Jaeger, D. Eeckhout, P. Casteels, K. Vandepoele, I. Vandenberghe, J. Van Beeumen, D. Inze and F. Van Breusegem (2004). "Type II metacaspases Atmc4 and Atmc9 of Arabidopsis thaliana cleave substrates after arginine and lysine." J Biol Chem **279**(44): 45329-45336.

Verma, R., R. Oania, J. Graumann and R. J. Deshaies (2004). "Multiubiquitin chain receptors define a layer of substrate selectivity in the ubiquitin-proteasome system." Cell **118**(1): 99-110.
Walker, N. P., R. V. Talanian, K. D. Brady, L. C. Dang, N. J. Bump, C. R. Ferenz, S. Franklin, T. Ghayur, M. C. Hackett, L. D. Hammill and et al. (1994). "Crystal structure of the cysteine protease interleukin-1 beta-converting enzyme: a (p20/p10)2 homodimer." Cell **78**(2): 343-352.
Wallace, E. W., J. L. Kear-Scott, E. V. Pilipenko, M. H. Schwartz, P. R. Laskowski, A. E. Rojek, C. D. Katanski, J. A. Riback, M. F. Dion, A. M. Franks, E. M. Airoldi, T. Pan, B. A. Budnik and D. A. Drummond (2015). "Reversible, Specific, Active Aggregates of Endogenous Proteins Assemble upon Heat Stress." Cell **162**(6): 1286-1298.
Wang, D. and R. J. Cotter (2005). "Approach for determining protein ubiquitination sites by MALDI-TOF mass spectrometry." Anal Chem **77**(5): 1458-1466.
Wang, G., J. Yang and J. M. Huibregtse (1999). "Functional domains of the Rsp5 ubiquitin-protein ligase." Mol Cell Biol **19**(1): 342-352.
Wang, Q., R. L. Woltjer, P. J. Cimino, C. Pan, K. S. Montine, J. Zhang and T. J. Montine (2005). "Proteomic analysis of neurofibrillary tangles in Alzheimer disease identifies GAPDH as a detergent-insoluble paired helical filament tau binding protein." FASEB J **19**(7): 869-871.
Watanabe, N. and E. Lam (2005). "Two Arabidopsis metacaspases AtMCP1b and AtMCP2b are arginine/lysine-specific cysteine proteases and activate apoptosis-like cell death in yeast." J Biol Chem **280**(15): 14691-14699.
Wilson, C. H., S. Shalini, A. Filipovska, T. R. Richman, S. Davies, S. D. Martin, S. L. McGee, J. Puccini, A. Nikolic, L. Dorstyn and S. Kumar (2015). "Age-related proteostasis and metabolic alterations in Caspase-2-deficient mice." Cell Death Dis **6**: e1615.
Wilson, K. P., J. A. Black, J. A. Thomson, E. E. Kim, J. P. Griffith, M. A. Navia, M. A. Murcko, S. P. Chambers, R. A. Aldape, S. A. Raybuck and et al. (1994). "Structure and mechanism of interleukin-1 beta converting enzyme." Nature **370**(6487): 270-275.
Winkler, J., J. Tyedmers, B. Bukau and A. Mogk (2012). "Chaperone networks in protein disaggregation and prion propagation." J Struct Biol **179**(2): 152-160.
Winkler, J., J. Tyedmers, B. Bukau and A. Mogk (2012). "Hsp70 targets Hsp100 chaperones to substrates for protein disaggregation and prion fragmentation." J Cell Biol **198**(3): 387-404.
Wojcik, S. (2013). "Crosstalk between autophagy and proteasome protein degradation systems: possible implications for cancer therapy." Folia Histochem Cytobiol **51**(4): 249-264.
Wong, A. H., C. Yan and Y. Shi (2012). "Crystal structure of the yeast metacaspase Yca1." J Biol Chem **287**(35): 29251-29259.
Woo, M., R. Hakem, C. Furlonger, A. Hakem, G. S. Duncan, T. Sasaki, D. Bouchard, L. Lu, G. E. Wu, C. J. Paige and T. W. Mak (2003). "Caspase-3 regulates cell cycle in B cells: a consequence of substrate specificity." Nat Immunol **4**(10): 1016-1022.
Wu, K., P. Wu and J. P. Aris (2001). "Nucleolar protein Nop12p participates in synthesis of 25S rRNA in Saccharomyces cerevisiae." Nucleic Acids Res **29**(14): 2938-2949.
Xu, P., D. M. Duong, N. T. Seyfried, D. Cheng, Y. Xie, J. Robert, J. Rush, M. Hochstrasser, D. Finley and J. Peng (2009). "Quantitative proteomics reveals the function of unconventional ubiquitin chains in proteasomal degradation." Cell **137**(1): 133-145.

Yam, A. Y., Y. Xia, H. T. Lin, A. Burlingame, M. Gerstein and J. Frydman (2008). "Defining the TRiC/CCT interactome links chaperonin function to stabilization of newly made proteins with complex topologies." Nat Struct Mol Biol **15**(12): 1255-1262.

Yan, J., M. L. Seibenhener, L. Calderilla-Barbosa, M. T. Diaz-Meco, J. Moscat, J. Jiang, M. W. Wooten and M. C. Wooten (2013). "SQSTM1/p62 interacts with HDAC6 and regulates deacetylase activity." PLoS One **8**(9): e76016.

Yang, Y., S. Fang, J. P. Jensen, A. M. Weissman and J. D. Ashwell (2000). "Ubiquitin protein ligase activity of IAPs and their degradation in proteasomes in response to apoptotic stimuli." Science **288**(5467): 874-877.

Yao, T. and R. E. Cohen (2002). "A cryptic protease couples deubiquitination and degradation by the proteasome." Nature **419**(6905): 403-407.

Yeung, Y. G., E. Nieves, R. H. Angeletti and E. R. Stanley (2008). "Removal of detergents from protein digests for mass spectrometry analysis." Anal Biochem **382**(2): 135-137.

Yoon, H. J. and J. Carbon (1999). "Participation of Bir1p, a member of the inhibitor of apoptosis family, in yeast chromosome segregation events." Proc Natl Acad Sci U S A **96**(23): 13208-13213.

Yuan, J., S. Shaham, S. Ledoux, H. M. Ellis and H. R. Horvitz (1993). "The C. elegans cell death gene ced-3 encodes a protein similar to mammalian interleukin-1 beta-converting enzyme." Cell **75**(4): 641-652.

Yuan, J. Y. and H. R. Horvitz (1990). "The Caenorhabditis elegans genes ced-3 and ced-4 act cell autonomously to cause programmed cell death." Dev Biol **138**(1): 33-41.

Zamaraev, A. V., G. S. Kopeina, E. A. Prokhorova, B. Zhivotovsky and I. N. Lavrik (2017). "Post-translational Modification of Caspases: The Other Side of Apoptosis Regulation." Trends Cell Biol.

Zattas, D. and M. Hochstrasser (2015). "Ubiquitin-dependent protein degradation at the yeast endoplasmic reticulum and nuclear envelope." Crit Rev Biochem Mol Biol **50**(1): 1-17.

Zhang, Q., H. K. Chieu, C. P. Low, S. Zhang, C. K. Heng and H. Yang (2003). "Schizosaccharomyces pombe cells deficient in triacylglycerols synthesis undergo apoptosis upon entry into the stationary phase." J Biol Chem **278**(47): 47145-47155.

Appendix I

Supplementary Information

Table S1. **Main data table containing the list of all proteins identified from the 2D LC-MS/MS analysis.** The emPAI scores reflect the relative abundance of each protein detected within the insoluble fraction. These scores were used to calculate the fold change in protein levels within normal and stress condition. *n*=2.

All Observed Proteins

All Observed Proteins	
Protein Name	**SwissProt**
(DL)-glycerol-3-phosphatase 1 OS=Saccharomyces cerevisiae GN=GPP1 PE=1 SV=3	GPP1_YEAST
(DL)-glycerol-3-phosphatase 2 OS=Saccharomyces cerevisiae GN=GPP2 PE=1 SV=1	GPP2_YEAST
(R,R)-butanediol dehydrogenase OS=Saccharomyces cerevisiae GN=BDH1 PE=1 SV=1	BDH1_YEAST
[NU+] prion formation protein 1 OS=Saccharomyces cerevisiae GN=NEW1 PE=1 SV=1	NEW1_YEAST
[PIN+] prion protein RNQ1 OS=Saccharomyces cerevisiae GN=RNQ1 PE=1 SV=2	RNQ1_YEAST
1,3-beta-glucan synthase component FKS1 OS=Saccharomyces cerevisiae GN=FKS1 PE=1	FKS1_YEAST
1,3-beta-glucan synthase component GSC2 OS=Saccharomyces cerevisiae GN=GSC2 PE=1	FKS2_YEAST
1,3-beta-glucanosyltransferase GAS1 OS=Saccharomyces cerevisiae GN=GAS1 PE=1 SV=2	GAS1_YEAST
1,3-beta-glucanosyltransferase GAS5 OS=Saccharomyces cerevisiae GN=GAS5 PE=1 SV=1	GAS5_YEAST
1,4-alpha-glucan-branching enzyme OS=Saccharomyces cerevisiae GN=GLC3 PE=1 SV=2	GLGB_YEAST
10 kDa heat shock protein, mitochondrial OS=Saccharomyces cerevisiae GN=HSP10 PE=1 S	CH10_YEAST
12 kDa heat shock protein OS=Saccharomyces cerevisiae GN=HSP12 PE=1 SV=1	HSP12_YEAST
13 kDa ribonucleoprotein-associated protein OS=Saccharomyces cerevisiae GN=SNU13 PE	SNU13_YEAST
20S-pre-rRNA D-site endonuclease NOB1 OS=Saccharomyces cerevisiae GN=NOB1 PE=1 S	NOB1_YEAST
26S protease regulatory subunit 4 homolog OS=Saccharomyces cerevisiae GN=RPT2 PE=1	PRS4_YEAST
26S protease regulatory subunit 6A OS=Saccharomyces cerevisiae GN=RPT5 PE=1 SV=3	PRS6A_YEAST
26S protease regulatory subunit 6B homolog OS=Saccharomyces cerevisiae GN=RPT3 PE=	PRS6B_YEAST
26S protease regulatory subunit 7 homolog OS=Saccharomyces cerevisiae GN=RPT1 PE=1	PRS7_YEAST
26S protease regulatory subunit 8 homolog OS=Saccharomyces cerevisiae GN=RPT6 PE=1	PRS8_YEAST
26S protease subunit RPT4 OS=Saccharomyces cerevisiae GN=RPT4 PE=1 SV=4	PRS10_YEAST
26S proteasome regulatory subunit RPN1 OS=Saccharomyces cerevisiae GN=RPN1 PE=1 S	RPN1_YEAST
26S proteasome regulatory subunit RPN11 OS=Saccharomyces cerevisiae GN=RPN11 PE=1	RPN11_YEAST
26S proteasome regulatory subunit RPN13 OS=Saccharomyces cerevisiae GN=RPN13 PE=1	RPN13_YEAST
26S proteasome regulatory subunit RPN2 OS=Saccharomyces cerevisiae GN=RPN2 PE=1 S	RPN2_YEAST
26S proteasome regulatory subunit RPN7 OS=Saccharomyces cerevisiae GN=RPN7 PE=1 S	RPN7_YEAST
26S proteasome regulatory subunit RPN8 OS=Saccharomyces cerevisiae GN=RPN8 PE=1 S	RPN8_YEAST
2-dehydropantoate 2-reductase OS=Saccharomyces cerevisiae GN=PAN5 PE=1 SV=1	PANE_YEAST
2-deoxyglucose-6-phosphate phosphatase 2 OS=Saccharomyces cerevisiae GN=DOG2 PE=	DOG2_YEAST
2-isopropylmalate synthase 2, mitochondrial OS=Saccharomyces cerevisiae GN=LEU9 PE=1	LEU9_YEAST
2-isopropylmalate synthase OS=Saccharomyces cerevisiae GN=LEU4 PE=1 SV=1	LEU1_YEAST
2-oxoglutarate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae GN=KGD1 PE=	ODO1_YEAST
3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Saccharomyces cerevisiae GN=RIB3 P	RIB3_YEAST
3',5'-cyclic-nucleotide phosphodiesterase 1 OS=Saccharomyces cerevisiae GN=PDE1 PE=1	PDE1_YEAST
30 kDa heat shock protein OS=Saccharomyces cerevisiae GN=HSP30 PE=1 SV=1	HSP30_YEAST
37S ribosomal protein MRP1, mitochondrial OS=Saccharomyces cerevisiae GN=MRP1 PE=1	RT01_YEAST
37S ribosomal protein MRP13, mitochondrial OS=Saccharomyces cerevisiae GN=MRP13 PE	RT13_YEAST
37S ribosomal protein MRP17, mitochondrial OS=Saccharomyces cerevisiae GN=MRP17 PE	RT06_YEAST
37S ribosomal protein MRP2, mitochondrial OS=Saccharomyces cerevisiae GN=MRP2 PE=1	RT02_YEAST
37S ribosomal protein MRP4, mitochondrial OS=Saccharomyces cerevisiae GN=MRP4 PE=1	RT04_YEAST
37S ribosomal protein MRP51, mitochondrial OS=Saccharomyces cerevisiae GN=MRP51 PE	RT51_YEAST
37S ribosomal protein NAM9, mitochondrial OS=Saccharomyces cerevisiae GN=NAM9 PE=1	NAM9_YEAST
37S ribosomal protein PET123, mitochondrial OS=Saccharomyces cerevisiae GN=PET123 P	RTPT_YEAST
37S ribosomal protein RSM28, mitochondrial OS=Saccharomyces cerevisiae GN=RSM28 PE	RSM28_YEAST

37S ribosomal protein S10, mitochondrial OS=Saccharomyces cerevisiae GN=RSM10 PE=1	RT10_YEAST
37S ribosomal protein S12, mitochondrial OS=Saccharomyces cerevisiae GN=MRPS12 PE=:	RT12_YEAST
37S ribosomal protein S17, mitochondrial OS=Saccharomyces cerevisiae GN=MRPS17 PE=:	RT17_YEAST
37S ribosomal protein S18, mitochondrial OS=Saccharomyces cerevisiae GN=MRPS18 PE=:	RT18_YEAST
37S ribosomal protein S19, mitochondrial OS=Saccharomyces cerevisiae GN=RSM19 PE=1	RT19_YEAST
37S ribosomal protein S23, mitochondrial OS=Saccharomyces cerevisiae GN=RSM23 PE=1	RT23_YEAST
37S ribosomal protein S24, mitochondrial OS=Saccharomyces cerevisiae GN=RSM24 PE=1	RT24_YEAST
37S ribosomal protein S25, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) GI	RT25_YEAS7
37S ribosomal protein S26, mitochondrial OS=Saccharomyces cerevisiae GN=RSM26 PE=1	RT26_YEAST
37S ribosomal protein S28, mitochondrial OS=Saccharomyces cerevisiae GN=MRPS28 PE=:	RT28_YEAST
37S ribosomal protein S35, mitochondrial OS=Saccharomyces cerevisiae GN=MRPS35 PE=:	RT35_YEAST
37S ribosomal protein S5, mitochondrial OS=Saccharomyces cerevisiae GN=MRPS5 PE=1 S	RT05_YEAST
37S ribosomal protein S7, mitochondrial OS=Saccharomyces cerevisiae GN=RSM7 PE=1 SV	RT07_YEAST
37S ribosomal protein S8, mitochondrial OS=Saccharomyces cerevisiae GN=MRPS8 PE=1 S	RT08_YEAST
37S ribosomal protein S9, mitochondrial OS=Saccharomyces cerevisiae GN=MRPS9 PE=1 S	RT09_YEAST
37S ribosomal protein SWS2, mitochondrial OS=Saccharomyces cerevisiae GN=SWS2 PE=:	SWS2_YEAST
3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 OS=Saccharomyces cerevisiae GN=HM	HMDH1_YEAST
3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 OS=Saccharomyces cerevisiae GN=HM	HMDH2_YEAST
3-hydroxyanthranilate 3,4-dioxygenase OS=Saccharomyces cerevisiae GN=BNA1 PE=1 SV=	3HAO_YEAST
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Saccharomyces cerevisiae GN=EHD3	HIBCH_YEAST
3-isopropylmalate dehydratase OS=Saccharomyces cerevisiae GN=LEU1 PE=1 SV=3	LEUC_YEAST
3-isopropylmalate dehydrogenase OS=Saccharomyces cerevisiae GN=LEU2 PE=1 SV=4	LEU3_YEAST
3-ketoacyl-CoA reductase OS=Saccharomyces cerevisiae GN=IFA38 PE=1 SV=1	MKAR_YEAST
3-keto-steroid reductase OS=Saccharomyces cerevisiae GN=ERG27 PE=1 SV=1	ERG27_YEAST
40S ribosomal protein S0-A OS=Saccharomyces cerevisiae (strain RM11-1a) GN=RPS0A PE	RSSA1_YEAS1
40S ribosomal protein S0-B OS=Saccharomyces cerevisiae (strain RM11-1a) GN=RPS0B PE	RSSA2_YEAS1
40S ribosomal protein S10-A OS=Saccharomyces cerevisiae GN=RPS10A PE=1 SV=1	RS10A_YEAST
40S ribosomal protein S11 OS=Saccharomyces cerevisiae GN=RPS11A PE=1 SV=3	RS11_YEAST
40S ribosomal protein S12 OS=Saccharomyces cerevisiae GN=RPS12 PE=1 SV=1	RS12_YEAST
40S ribosomal protein S13 OS=Saccharomyces cerevisiae GN=RPS13 PE=1 SV=3	RS13_YEAST
40S ribosomal protein S14-A OS=Saccharomyces cerevisiae GN=RPS14A PE=1 SV=5	RS14A_YEAST
40S ribosomal protein S14-B OS=Saccharomyces cerevisiae GN=RPS14B PE=1 SV=2	RS14B_YEAST
40S ribosomal protein S15 OS=Saccharomyces cerevisiae GN=RPS15 PE=1 SV=1	RS15_YEAST
40S ribosomal protein S16 OS=Saccharomyces cerevisiae GN=RPS16A PE=1 SV=2	RS16_YEAST
40S ribosomal protein S17-A OS=Saccharomyces cerevisiae GN=RPS17A PE=1 SV=1	RS17A_YEAST
40S ribosomal protein S18 OS=Saccharomyces cerevisiae GN=RPS18A PE=1 SV=4	RS18_YEAST
40S ribosomal protein S19-A OS=Saccharomyces cerevisiae GN=RPS19A PE=1 SV=2	RS19A_YEAST
40S ribosomal protein S1-A OS=Saccharomyces cerevisiae (strain RM11-1a) GN=RPS1A PE	RS3A1_YEAS1
40S ribosomal protein S1-B OS=Saccharomyces cerevisiae (strain RM11-1a) GN=RPS1B PE	RS3A2_YEAS1
40S ribosomal protein S2 OS=Saccharomyces cerevisiae GN=RPS2 PE=1 SV=3	RS2_YEAST
40S ribosomal protein S20 OS=Saccharomyces cerevisiae GN=RPS20 PE=1 SV=3	RS20_YEAST
40S ribosomal protein S21-A OS=Saccharomyces cerevisiae GN=RPS21A PE=1 SV=1	RS21A_YEAST
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40S ribosomal protein S22-A OS=Saccharomyces cerevisiae GN=RPS22A PE=1 SV=2	RS22A_YEAST
40S ribosomal protein S23 OS=Saccharomyces cerevisiae GN=RPS23A PE=1 SV=1	RS23_YEAST
40S ribosomal protein S24 OS=Saccharomyces cerevisiae GN=RPS24A PE=1 SV=3	RS24_YEAST
40S ribosomal protein S25-A OS=Saccharomyces cerevisiae GN=RPS25A PE=1 SV=1	RS25A_YEAST

40S ribosomal protein S26-A OS=Saccharomyces cerevisiae GN=RPS26A PE=1 SV=1	RS26A_YEAST
40S ribosomal protein S26-B OS=Saccharomyces cerevisiae GN=RPS26B PE=1 SV=1	RS26B_YEAST
40S ribosomal protein S27-A OS=Saccharomyces cerevisiae GN=RPS27A PE=1 SV=1	RS27A_YEAST
40S ribosomal protein S28-A OS=Saccharomyces cerevisiae GN=RPS28A PE=1 SV=1	RS28A_YEAST
40S ribosomal protein S28-B OS=Saccharomyces cerevisiae GN=RPS28B PE=1 SV=1	RS28B_YEAST
40S ribosomal protein S29-A OS=Saccharomyces cerevisiae GN=RPS29A PE=1 SV=3	RS29A_YEAST
40S ribosomal protein S29-B OS=Saccharomyces cerevisiae GN=RPS29B PE=1 SV=3	RS29B_YEAST
40S ribosomal protein S3 OS=Saccharomyces cerevisiae GN=RPS3 PE=1 SV=5	RS3_YEAST
40S ribosomal protein S30 OS=Saccharomyces cerevisiae GN=RPS30A PE=1 SV=2	RS30_YEAST
40S ribosomal protein S31 OS=Saccharomyces cerevisiae GN=UBI3 PE=1 SV=2	RS37_YEAST
40S ribosomal protein S4 OS=Saccharomyces cerevisiae GN=RPS4A PE=1 SV=3	RS4_YEAST
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40S ribosomal protein S6 OS=Saccharomyces cerevisiae GN=RPS6A PE=1 SV=1	RS6_YEAST
40S ribosomal protein S7-A OS=Saccharomyces cerevisiae GN=RPS7A PE=1 SV=4	RS7A_YEAST
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40S ribosomal protein S8 OS=Saccharomyces cerevisiae GN=RPS8A PE=1 SV=3	RS8_YEAST
40S ribosomal protein S9-A OS=Saccharomyces cerevisiae GN=RPS9A PE=1 SV=3	RS9A_YEAST
40S ribosomal protein S9-B OS=Saccharomyces cerevisiae GN=RPS9B PE=1 SV=4	RS9B_YEAST
4-aminobutyrate aminotransferase OS=Saccharomyces cerevisiae GN=UGA1 PE=1 SV=2	GATA_YEAST
4-nitrophenylphosphatase OS=Saccharomyces cerevisiae GN=PHO13 PE=1 SV=2	PNPP_YEAST
5'-3' exoribonuclease 1 OS=Saccharomyces cerevisiae GN=KEM1 PE=1 SV=1	XRN1_YEAST
5'-3' exoribonuclease 2 OS=Saccharomyces cerevisiae GN=RAT1 PE=1 SV=3	XRN2_YEAST
54S ribosomal protein IMG1, mitochondrial OS=Saccharomyces cerevisiae GN=IMG1 PE=1 S	IMG1_YEAST
54S ribosomal protein L1, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL1 PE=1 S	RM01_YEAST
54S ribosomal protein L11, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL11 PE=1	RM11_YEAST
54S ribosomal protein L12, mitochondrial OS=Saccharomyces cerevisiae GN=MNP1 PE=1 S	MNP1_YEAST
54S ribosomal protein L13, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL13 PE=1	RM13_YEAST
54S ribosomal protein L15, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL15 PE=1	RM15_YEAST
54S ribosomal protein L17, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL17 PE=1	RM17_YEAST
54S ribosomal protein L19, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL19 PE=1	RM19_YEAST
54S ribosomal protein L2, mitochondrial OS=Saccharomyces cerevisiae GN=MRP7 PE=1 SV	RM02_YEAST
54S ribosomal protein L23, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL23 PE=1	RM23_YEAST
54S ribosomal protein L24, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL24 PE=1	RM24_YEAST
54S ribosomal protein L28, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL28 PE=1	RM28_YEAST
54S ribosomal protein L3, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL3 PE=1 S	RM03_YEAST
54S ribosomal protein L33, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL33 PE=1	RM33_YEAST
54S ribosomal protein L34, mitochondrial OS=Saccharomyces cerevisiae GN=YDR115W PE	RM34_YEAST
54S ribosomal protein L35, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL35 PE=1	RM35_YEAST
54S ribosomal protein L36, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL36 PE=1	RM36_YEAST
54S ribosomal protein L38, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL38 PE=1	RM38_YEAST
54S ribosomal protein L4, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) GN	RM04_YEAS7
54S ribosomal protein L40, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL40 PE=1	RM40_YEAST
54S ribosomal protein L44, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL44 PE=1	RM44_YEAST
54S ribosomal protein L49, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL49 PE=1	RN49_YEAST
54S ribosomal protein L51, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL51 PE=1	RM51_YEAST
54S ribosomal protein L6, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL6 PE=1 S	RM06_YEAST
54S ribosomal protein L8, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL8 PE=1 S	RM08_YEAST

54S ribosomal protein L9, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL9 PE=1 S	RM09_YEAST
54S ribosomal protein YmL6, mitochondrial OS=Saccharomyces cerevisiae GN=YML6 PE=1	RL4P_YEAST
5-formyltetrahydrofolate cyclo-ligase OS=Saccharomyces cerevisiae GN=FAU1 PE=1 SV=1	FTHC_YEAST
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Saccharomyces	METE_YEAST
6,7-dimethyl-8-ribityllumazine synthase OS=Saccharomyces cerevisiae GN=RIB4 PE=1 SV=:	RIB4_YEAST
60S acidic ribosomal protein P0 OS=Saccharomyces cerevisiae GN=RPP0 PE=1 SV=1	RLA0_YEAST
60S acidic ribosomal protein P1-beta OS=Saccharomyces cerevisiae GN=RPP1B PE=1 SV=	RLA3_YEAST
60S acidic ribosomal protein P2-alpha OS=Saccharomyces cerevisiae GN=RPP2A PE=1 SV	RLA2_YEAST
60S acidic ribosomal protein P2-beta OS=Saccharomyces cerevisiae GN=RPP2B PE=1 SV=	RLA4_YEAST
60S ribosomal export protein NMD3 OS=Saccharomyces cerevisiae GN=NMD3 PE=1 SV=2	NMD3_YEAST
60S ribosomal protein L1 OS=Saccharomyces cerevisiae GN=RPL1A PE=1 SV=1	RL1_YEAST
60S ribosomal protein L10 OS=Saccharomyces cerevisiae GN=RPL10 PE=1 SV=1	RL10_YEAST
60S ribosomal protein L11-A OS=Saccharomyces cerevisiae GN=RPL11A PE=1 SV=2	RL11A_YEAST
60S ribosomal protein L11-B OS=Saccharomyces cerevisiae GN=RPL11B PE=1 SV=3	RL11B_YEAST
60S ribosomal protein L12 OS=Saccharomyces cerevisiae GN=RPL12A PE=1 SV=1	RL12_YEAST
60S ribosomal protein L13-A OS=Saccharomyces cerevisiae GN=RPL13A PE=1 SV=1	RL13A_YEAST
60S ribosomal protein L13-B OS=Saccharomyces cerevisiae GN=RPL13B PE=1 SV=1	RL13B_YEAST
60S ribosomal protein L14-A OS=Saccharomyces cerevisiae GN=RPL14A PE=1 SV=1	RL14A_YEAST
60S ribosomal protein L14-B OS=Saccharomyces cerevisiae GN=RPL14B PE=1 SV=1	RL14B_YEAST
60S ribosomal protein L15-A OS=Saccharomyces cerevisiae GN=RPL15A PE=1 SV=3	RL15A_YEAST
60S ribosomal protein L16-A OS=Saccharomyces cerevisiae GN=RPL16A PE=1 SV=3	RL16A_YEAST
60S ribosomal protein L16-B OS=Saccharomyces cerevisiae GN=RPL16B PE=1 SV=3	RL16B_YEAST
60S ribosomal protein L17-A OS=Saccharomyces cerevisiae GN=RPL17A PE=1 SV=4	RL17A_YEAST
60S ribosomal protein L17-B OS=Saccharomyces cerevisiae GN=RPL17B PE=1 SV=2	RL17B_YEAST
60S ribosomal protein L18 OS=Saccharomyces cerevisiae GN=RPL18A PE=1 SV=1	RL18_YEAST
60S ribosomal protein L19 OS=Saccharomyces cerevisiae GN=RPL19A PE=1 SV=5	RL19_YEAST
60S ribosomal protein L2 OS=Saccharomyces cerevisiae GN=RPL2A PE=1 SV=3	RL2_YEAST
60S ribosomal protein L20 OS=Saccharomyces cerevisiae GN=RPL20A PE=1 SV=2	RL20_YEAST
60S ribosomal protein L21-A OS=Saccharomyces cerevisiae GN=RPL21A PE=1 SV=1	RL21A_YEAST
60S ribosomal protein L21-B OS=Saccharomyces cerevisiae GN=RPL21B PE=1 SV=1	RL21B_YEAST
60S ribosomal protein L22-A OS=Saccharomyces cerevisiae GN=RPL22A PE=1 SV=3	RL22A_YEAST
60S ribosomal protein L23 OS=Saccharomyces cerevisiae GN=RPL23A PE=1 SV=3	RL23_YEAST
60S ribosomal protein L24-A OS=Saccharomyces cerevisiae GN=RPL24A PE=1 SV=1	RL24A_YEAST
60S ribosomal protein L24-B OS=Saccharomyces cerevisiae GN=RPL24B PE=1 SV=1	RL24B_YEAST
60S ribosomal protein L25 OS=Saccharomyces cerevisiae GN=RPL25 PE=1 SV=4	RL25_YEAST
60S ribosomal protein L26-A OS=Saccharomyces cerevisiae GN=RPL26A PE=1 SV=3	RL26A_YEAST
60S ribosomal protein L27-A OS=Saccharomyces cerevisiae GN=RPL27A PE=1 SV=1	RL27A_YEAST
60S ribosomal protein L27-B OS=Saccharomyces cerevisiae GN=RPL27B PE=1 SV=1	RL27B_YEAST
60S ribosomal protein L28 OS=Saccharomyces cerevisiae GN=RPL28 PE=1 SV=2	RL28_YEAST
60S ribosomal protein L3 OS=Saccharomyces cerevisiae GN=RPL3 PE=1 SV=4	RL3_YEAST
60S ribosomal protein L30 OS=Saccharomyces cerevisiae GN=RPL30 PE=1 SV=3	RL30_YEAST
60S ribosomal protein L31-A OS=Saccharomyces cerevisiae GN=RPL31A PE=1 SV=1	RL31A_YEAST
60S ribosomal protein L32 OS=Saccharomyces cerevisiae GN=RPL32 PE=1 SV=1	RL32_YEAST
60S ribosomal protein L33-A OS=Saccharomyces cerevisiae GN=RPL33A PE=1 SV=3	RL33A_YEAST
60S ribosomal protein L33-B OS=Saccharomyces cerevisiae GN=RPL33B PE=1 SV=2	RL33B_YEAST
60S ribosomal protein L34-A OS=Saccharomyces cerevisiae GN=RPL34A PE=1 SV=1	RL34A_YEAST
60S ribosomal protein L34-B OS=Saccharomyces cerevisiae GN=RPL34B PE=1 SV=1	RL34B_YEAST

60S ribosomal protein L35 OS=Saccharomyces cerevisiae GN=RPL35A PE=1 SV=1	RL35_YEAST
60S ribosomal protein L36-A OS=Saccharomyces cerevisiae GN=RPL36A PE=1 SV=3	RL36A_YEAST
60S ribosomal protein L36-B OS=Saccharomyces cerevisiae GN=RPL36B PE=1 SV=3	RL36B_YEAST
60S ribosomal protein L38 OS=Saccharomyces cerevisiae GN=RPL38 PE=1 SV=1	RL38_YEAST
60S ribosomal protein L39 OS=Saccharomyces cerevisiae GN=RPL39 PE=1 SV=3	RL39_YEAST
60S ribosomal protein L40 OS=Saccharomyces cerevisiae GN=UBI1 PE=1 SV=1	RL40_YEAST
60S ribosomal protein L42 OS=Saccharomyces cerevisiae GN=RPL42A PE=1 SV=3	RL44_YEAST
60S ribosomal protein L43 OS=Saccharomyces cerevisiae GN=RPL43A PE=1 SV=2	RL43_YEAST
60S ribosomal protein L4-B OS=Saccharomyces cerevisiae GN=RPL4B PE=1 SV=2	RL4B_YEAST
60S ribosomal protein L5 OS=Saccharomyces cerevisiae GN=RPL5 PE=1 SV=3	RL5_YEAST
60S ribosomal protein L6-A OS=Saccharomyces cerevisiae GN=RPL6A PE=1 SV=2	RL6A_YEAST
60S ribosomal protein L6-B OS=Saccharomyces cerevisiae GN=RPL6B PE=1 SV=4	RL6B_YEAST
60S ribosomal protein L7-A OS=Saccharomyces cerevisiae GN=RPL7A PE=1 SV=3	RL7A_YEAST
60S ribosomal protein L7-B OS=Saccharomyces cerevisiae GN=RPL7B PE=1 SV=3	RL7B_YEAST
60S ribosomal protein L8-A OS=Saccharomyces cerevisiae GN=RPL8A PE=1 SV=4	RL8A_YEAST
60S ribosomal protein L8-B OS=Saccharomyces cerevisiae GN=RPL8B PE=1 SV=3	RL8B_YEAST
60S ribosomal protein L9-A OS=Saccharomyces cerevisiae GN=RPL9A PE=1 SV=2	RL9A_YEAST
60S ribosomal protein L9-B OS=Saccharomyces cerevisiae GN=RPL9B PE=1 SV=1	RL9B_YEAST
60S ribosomal subunit assembly/export protein LOC1 OS=Saccharomyces cerevisiae (strain	LOC1_YEAS7
60S ribosome subunit biogenesis protein NIP7 OS=Saccharomyces cerevisiae GN=NIP7 PE=	NIP7_YEAST
60S ribosome subunit biogenesis protein NOP8 OS=Saccharomyces cerevisiae GN=NOP8 P	NOP8_YEAST
6-phosphofructokinase subunit alpha OS=Saccharomyces cerevisiae GN=PFK1 PE=1 SV=1	K6PF1_YEAST
6-phosphofructokinase subunit beta OS=Saccharomyces cerevisiae GN=PFK2 PE=1 SV=4	K6PF2_YEAST
6-phosphogluconate dehydrogenase, decarboxylating 1 OS=Saccharomyces cerevisiae GN=	6PGD1_YEAST
6-phosphogluconate dehydrogenase, decarboxylating 2 OS=Saccharomyces cerevisiae GN=	6PGD2_YEAST
6-phosphogluconolactonase 4 OS=Saccharomyces cerevisiae GN=SOL4 PE=1 SV=1	SOL4_YEAST
6-phosphogluconolactonase-like protein 2 OS=Saccharomyces cerevisiae GN=SOL2 PE=1 S	SOL2_YEAST
78 kDa glucose-regulated protein homolog OS=Saccharomyces cerevisiae GN=KAR2 PE=1	GRP78_YEAST
ABC transporter ATP-binding protein ARB1 OS=Saccharomyces cerevisiae GN=ARB1 PE=1	ARB1_YEAST
Accumulates dyads protein 4 OS=Saccharomyces cerevisiae GN=ADY4 PE=1 SV=1	ADY4_YEAST
Acetolactate synthase catalytic subunit, mitochondrial OS=Saccharomyces cerevisiae GN=IL	ILVB_YEAST
Acetolactate synthase small subunit, mitochondrial OS=Saccharomyces cerevisiae GN=ILV6	ILV6_YEAST
Acetyl-CoA acetyltransferase OS=Saccharomyces cerevisiae GN=ERG10 PE=1 SV=3	THIL_YEAST
Acetyl-CoA carboxylase OS=Saccharomyces cerevisiae GN=FAS3 PE=1 SV=2	ACAC_YEAST
Acetyl-CoA hydrolase OS=Saccharomyces cerevisiae GN=ACH1 PE=1 SV=2	ACH1_YEAST
Acetyl-coenzyme A synthetase 2 OS=Saccharomyces cerevisiae GN=ACS2 PE=1 SV=1	ACS2_YEAST
Acetylornithine aminotransferase, mitochondrial OS=Saccharomyces cerevisiae GN=ARG8 F	ARGD_YEAST
Aconitate hydratase, mitochondrial OS=Saccharomyces cerevisiae GN=ACO1 PE=1 SV=2	ACON_YEAST
Actin cytoskeleton-regulatory complex protein END3 OS=Saccharomyces cerevisiae (strain Y	END3_YEAS7
Actin cytoskeleton-regulatory complex protein END3 OS=Saccharomyces cerevisiae GN=EN	END3_YEAST
Actin cytoskeleton-regulatory complex protein PAN1 OS=Saccharomyces cerevisiae (strain Y	PAN1_YEAS7
Actin cytoskeleton-regulatory complex protein PAN1 OS=Saccharomyces cerevisiae GN=PAI	PAN1_YEAST
Actin cytoskeleton-regulatory complex protein SLA1 OS=Saccharomyces cerevisiae (strain Y	SLA1_YEAS7
Actin OS=Saccharomyces cerevisiae GN=ACT1 PE=1 SV=1	ACT_YEAST
Actin patches distal protein 1 OS=Saccharomyces cerevisiae GN=APD1 PE=1 SV=1	APD1_YEAST
Actin-binding protein OS=Saccharomyces cerevisiae GN=ABP1 PE=1 SV=4	ABP1_YEAST
Actin-interacting protein 1 OS=Saccharomyces cerevisiae GN=AIP1 PE=1 SV=1	AIP1_YEAST

Actin-like protein ARP9 OS=Saccharomyces cerevisiae GN=ARP9 PE=1 SV=1	ARP9_YEAST
Actin-regulating kinase PRK1 OS=Saccharomyces cerevisiae GN=PRK1 PE=1 SV=1	PRK1_YEAST
Actin-related protein 2 OS=Saccharomyces cerevisiae GN=ARP2 PE=1 SV=1	ARP2_YEAST
Actin-related protein 2/3 complex subunit 1 OS=Saccharomyces cerevisiae GN=ARC40 PE=	ARPC1_YEAST
Actin-related protein 2/3 complex subunit 2 OS=Saccharomyces cerevisiae GN=ARC35 PE=	ARPC2_YEAST
Actin-related protein 2/3 complex subunit 3 OS=Saccharomyces cerevisiae GN=ARC18 PE=	ARPC3_YEAST
Actin-related protein 2/3 complex subunit 4 OS=Saccharomyces cerevisiae GN=ARC19 PE=	ARPC4_YEAST
Actin-related protein 2/3 complex subunit 5 OS=Saccharomyces cerevisiae GN=ARC15 PE=	ARPC5_YEAST
Actin-related protein 3 OS=Saccharomyces cerevisiae GN=ARP3 PE=1 SV=1	ARP3_YEAST
Actin-related protein 5 OS=Saccharomyces cerevisiae GN=ARP5 PE=1 SV=1	ARP5_YEAST
Activator of C kinase protein 1 OS=Saccharomyces cerevisiae GN=ACK1 PE=1 SV=1	ACK1_YEAST
Acyl carrier protein, mitochondrial OS=Saccharomyces cerevisiae GN=ACP1 PE=1 SV=1	ACPM_YEAST
Acyl-CoA desaturase 1 OS=Saccharomyces cerevisiae GN=OLE1 PE=1 SV=2	ACO1_YEAST
ADA histone acetyltransferase complex component 2 OS=Saccharomyces cerevisiae GN=A	AHC2_YEAST
Adenine phosphoribosyltransferase 1 OS=Saccharomyces cerevisiae GN=APT1 PE=1 SV=3	APT1_YEAST
Adenosine deaminase OS=Saccharomyces cerevisiae GN=AAH1 PE=1 SV=1	ADA_YEAST
Adenosine kinase OS=Saccharomyces cerevisiae GN=ADO1 PE=1 SV=1	ADK_YEAST
Adenosylhomocysteinase OS=Saccharomyces cerevisiae GN=SAH1 PE=1 SV=1	SAHH_YEAST
Adenylate kinase 1 OS=Saccharomyces cerevisiae (strain RM11-1a) GN=ADK1 PE=3 SV=1	KAD1_YEAS1
Adenylate kinase 2 OS=Saccharomyces cerevisiae GN=ADK2 PE=1 SV=1	KAD2_YEAST
Adenylosuccinate lyase OS=Saccharomyces cerevisiae GN=ADE13 PE=1 SV=1	PUR8_YEAST
Adenylosuccinate synthetase OS=Saccharomyces cerevisiae GN=ADE12 PE=1 SV=3	PURA_YEAST
Adenylyl cyclase-associated protein OS=Saccharomyces cerevisiae GN=SRV2 PE=1 SV=1	CAP_YEAST
Adenylyltransferase and sulfurtransferase UBA4 OS=Saccharomyces cerevisiae (strain RM1	UBA4_YEAS1
Adenylyltransferase and sulfurtransferase UBA4 OS=Saccharomyces cerevisiae (strain YJM	UBA4_YEAS7
AdoMet-dependent rRNA methyltransferase SPB1 OS=Saccharomyces cerevisiae GN=SPB1	SPB1_YEAST
ADP,ATP carrier protein 2 OS=Saccharomyces cerevisiae GN=AAC2 PE=1 SV=2	ADT2_YEAST
ADP-ribose pyrophosphatase OS=Saccharomyces cerevisiae GN=YSA1 PE=1 SV=2	ADPP_YEAST
ADP-ribosylation factor 1 OS=Saccharomyces cerevisiae GN=ARF1 PE=1 SV=3	ARF1_YEAST
ADP-ribosylation factor GTPase-activating protein effector protein 1 OS=Saccharomyces cer	AGE1_YEAST
ADP-ribosylation factor GTPase-activating protein effector protein 2 OS=Saccharomyces cer	AGE2_YEAST
ADP-ribosylation factor GTPase-activating protein GCS1 OS=Saccharomyces cerevisiae GN	GCS1_YEAST
ADP-ribosylation factor GTPase-activating protein GLO3 OS=Saccharomyces cerevisiae GN	GLO3_YEAST
ADP-ribosylation factor-binding protein GGA1 OS=Saccharomyces cerevisiae GN=GGA1 PE	GGA1_YEAST
ADP-ribosylation factor-binding protein GGA2 OS=Saccharomyces cerevisiae GN=GGA2 PE	GGA2_YEAST
Alanine/arginine aminopeptidase OS=Saccharomyces cerevisiae GN=AAP1 PE=1 SV=2	AAP1_YEAST
Alanyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=ALA1 PE=1 SV=2	SYAC_YEAST
Alcohol dehydrogenase 1 OS=Saccharomyces cerevisiae GN=ADH1 PE=1 SV=4	ADH1_YEAST
Alcohol dehydrogenase 3, mitochondrial OS=Saccharomyces cerevisiae GN=ADH3 PE=1 S	ADH3_YEAST
Alcohol dehydrogenase 4 OS=Saccharomyces cerevisiae (strain YJM789) GN=ADH4 PE=2	ADH4_YEAS7
Alcohol dehydrogenase 5 OS=Saccharomyces cerevisiae GN=ADH5 PE=1 SV=1	ADH5_YEAST
Alcohol O-acetyltransferase 2 OS=Saccharomyces cerevisiae GN=ATF2 PE=1 SV=1	ATF2_YEAST
Aldehyde dehydrogenase [NAD(P)+] 1 OS=Saccharomyces cerevisiae GN=ALD2 PE=1 SV=	ALDH2_YEAST
Aldehyde dehydrogenase [NAD(P)+] 2 OS=Saccharomyces cerevisiae GN=ALD3 PE=1 SV=	ALDH3_YEAST
Aldehyde dehydrogenase 5, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) G	ALDH5_YEAS7
Alkylphosphocholine resistance protein LEM3 OS=Saccharomyces cerevisiae GN=LEM3 PE	LEM3_YEAST
Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 56 kDa subunit OS=Saccharomyc	TPS1_YEAST

Alpha-1,2 mannosyltransferase KTR1 OS=Saccharomyces cerevisiae GN=KTR1 PE=1 SV=1	KTR1_YEAST
Alpha1-proteinase inhibitor-degradation deficient protein 37 OS=Saccharomyces cerevisiae (	ADD37_YEAST
Alpha-glucosides permease MPH3 OS=Saccharomyces cerevisiae (strain Lalvin EC1118 / Pr	MPH3_YEAS8
Alpha-mannosidase OS=Saccharomyces cerevisiae GN=AMS1 PE=1 SV=2	MAN1_YEAST
Altered inheritance rate of mitochondria protein 38 OS=Saccharomyces cerevisiae GN=AIM3	AIM38_YEAST
Aminomethyltransferase, mitochondrial OS=Saccharomyces cerevisiae GN=GCV1 PE=1 SV=	GCST_YEAST
Aminopeptidase 2, mitochondrial OS=Saccharomyces cerevisiae GN=APE2 PE=1 SV=3	APE2_YEAST
Ammonia transport outward protein 3 OS=Saccharomyces cerevisiae GN=ATO3 PE=1 SV=1	ATO3_YEAST
AMP deaminase OS=Saccharomyces cerevisiae GN=AMD1 PE=1 SV=2	AMPD_YEAST
AN1-type zinc finger protein YNL155W OS=Saccharomyces cerevisiae GN=YNL155W PE=1	YNP5_YEAST
AN1-type zinc finger protein YOR052C OS=Saccharomyces cerevisiae GN=YOR052C PE=1	YO052_YEAST
Anaphase-promoting complex subunit CDC23 OS=Saccharomyces cerevisiae GN=CDC23 P	CDC23_YEAST
Ankyrin repeat-containing protein YCR051W OS=Saccharomyces cerevisiae GN=YCR051W	YCU1_YEAST
Anthranilate phosphoribosyltransferase OS=Saccharomyces cerevisiae GN=TRP4 PE=1 SV=	TRPD_YEAST
Anthranilate synthase component 1 OS=Saccharomyces cerevisiae GN=TRP2 PE=1 SV=4	TRPE_YEAST
Anthranilate synthase component 2 OS=Saccharomyces cerevisiae GN=TRP3 PE=1 SV=2	TRPG_YEAST
Antiviral helicase SLH1 OS=Saccharomyces cerevisiae GN=SLH1 PE=1 SV=1	SLH1_YEAST
AP-1 complex subunit beta-1 OS=Saccharomyces cerevisiae GN=APL2 PE=1 SV=1	AP1B1_YEAST
AP-1 complex subunit mu-1-I OS=Saccharomyces cerevisiae GN=APM1 PE=1 SV=2	AP1M1_YEAST
AP-1 complex subunit sigma-1 OS=Saccharomyces cerevisiae GN=APS1 PE=1 SV=1	AP1S1_YEAST
AP-2 complex subunit alpha OS=Saccharomyces cerevisiae GN=APL3 PE=1 SV=1	AP2A_YEAST
AP-2 complex subunit mu OS=Saccharomyces cerevisiae GN=APM4 PE=1 SV=1	AP2M_YEAST
AP-2 complex subunit sigma OS=Saccharomyces cerevisiae GN=APS2 PE=1 SV=1	AP2S_YEAST
Apoptosis-inducing factor 1 OS=Saccharomyces cerevisiae GN=AIF1 PE=1 SV=1	AIF1_YEAST
Arf guanine nucleotide exchange factor SYT1 OS=Saccharomyces cerevisiae GN=SYT1 PE=	SYT1_YEAST
ARF guanine-nucleotide exchange factor 1 OS=Saccharomyces cerevisiae GN=GEA1 PE=1	GEA1_YEAST
ARF guanine-nucleotide exchange factor 2 OS=Saccharomyces cerevisiae GN=GEA2 PE=1	GEA2_YEAST
Arginase OS=Saccharomyces cerevisiae GN=CAR1 PE=1 SV=1	ARGI_YEAST
Arginine biosynthesis bifunctional protein ARG7, mitochondrial OS=Saccharomyces cerevisia	ARGJ_YEAST
Arginine N-methyltransferase 2 OS=Saccharomyces cerevisiae GN=RMT2 PE=1 SV=1	RMT2_YEAST
Argininosuccinate lyase OS=Saccharomyces cerevisiae GN=ARG4 PE=1 SV=2	ARLY_YEAST
Argininosuccinate synthase OS=Saccharomyces cerevisiae GN=ARG1 PE=1 SV=2	ASSY_YEAST
Arginyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=YDR341C PE=1 S	SYRC_YEAST
Arginyl-tRNA synthetase, mitochondrial OS=Saccharomyces cerevisiae GN=MSR1 PE=2 SV:	SYRM_YEAST
Aromatic amino acid aminotransferase 1 OS=Saccharomyces cerevisiae GN=ARO8 PE=1 SV	ARO8_YEAST
ARS-binding factor 2, mitochondrial OS=Saccharomyces cerevisiae GN=ABF2 PE=1 SV=1	ABF2_YEAST
Asparagine synthetase [glutamine-hydrolyzing] 2 OS=Saccharomyces cerevisiae GN=ASN2 I	ASNS2_YEAST
Asparaginyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=DED81 PE=1	SYNC_YEAST
Aspartate aminotransferase, cytoplasmic OS=Saccharomyces cerevisiae GN=AAT2 PE=1 SV	AATC_YEAST
Aspartate aminotransferase, mitochondrial OS=Saccharomyces cerevisiae GN=AAT1 PE=1 S	AATM_YEAST
Aspartate-semialdehyde dehydrogenase OS=Saccharomyces cerevisiae GN=HOM2 PE=1 S'	DHAS_YEAST
Aspartic proteinase MKC7 OS=Saccharomyces cerevisiae GN=MKC7 PE=1 SV=2	MKC7_YEAST
Aspartyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=DPS1 PE=1 SV=	SYDC_YEAST
Aspartyl-tRNA synthetase, mitochondrial OS=Saccharomyces cerevisiae GN=MSD1 PE=1 S\	SYDM_YEAST
ATP phosphoribosyltransferase OS=Saccharomyces cerevisiae GN=HIS1 PE=1 SV=1	HIS1_YEAST
ATP synthase subunit 4, mitochondrial OS=Saccharomyces cerevisiae GN=ATP4 PE=1 SV=:	ATPF_YEAST
ATP synthase subunit 5, mitochondrial OS=Saccharomyces cerevisiae GN=ATP5 PE=1 SV=:	ATPO_YEAST

ATP synthase subunit alpha, mitochondrial OS=Saccharomyces cerevisiae GN=ATP1 PE=1 S	ATPA_YEAST
ATP synthase subunit beta, mitochondrial OS=Saccharomyces cerevisiae GN=ATP2 PE=1 S	ATPB_YEAST
ATP synthase subunit d, mitochondrial OS=Saccharomyces cerevisiae GN=ATP7 PE=1 SV=	ATP7_YEAST
ATP synthase subunit delta, mitochondrial OS=Saccharomyces cerevisiae GN=ATP16 PE=1	ATPD_YEAST
ATP synthase subunit e, mitochondrial OS=Saccharomyces cerevisiae GN=ATP21 PE=1 SV	ATPJ_YEAST
ATP synthase subunit f, mitochondrial OS=Saccharomyces cerevisiae GN=ATP17 PE=1 SV=	ATPK_YEAST
ATP synthase subunit g, mitochondrial OS=Saccharomyces cerevisiae GN=ATP20 PE=1 SV	ATPN_YEAST
ATP synthase subunit gamma, mitochondrial OS=Saccharomyces cerevisiae GN=ATP3 PE=	ATPG_YEAST
ATP synthase subunit H, mitochondrial OS=Saccharomyces cerevisiae GN=ATP14 PE=1 SV	ATP14_YEAST
ATP synthase subunit J, mitochondrial OS=Saccharomyces cerevisiae GN=ATP18 PE=1 SV	ATP18_YEAST
ATPase-stabilizing factor 15 kDa protein OS=Saccharomyces cerevisiae GN=STF2 PE=1 SV	STF2_YEAST
ATP-dependent DNA helicase HMI1, mitochondrial OS=Saccharomyces cerevisiae GN=HMI1	HMI1_YEAST
ATP-dependent DNA helicase II subunit 1 OS=Saccharomyces cerevisiae GN=YKU70 PE=1	KU70_YEAST
ATP-dependent helicase NAM7 OS=Saccharomyces cerevisiae GN=NAM7 PE=1 SV=1	NAM7_YEAST
ATP-dependent helicase ULS1 OS=Saccharomyces cerevisiae GN=ULS1 PE=1 SV=1	ULS1_YEAST
ATP-dependent molecular chaperone HSC82 OS=Saccharomyces cerevisiae GN=HSC82 PE	HSC82_YEAST
ATP-dependent molecular chaperone HSP82 OS=Saccharomyces cerevisiae GN=HSP82 PE	HSP82_YEAST
ATP-dependent permease MDL1, mitochondrial OS=Saccharomyces cerevisiae GN=MDL1 P	MDL1_YEAST
ATP-dependent permease PDR12 OS=Saccharomyces cerevisiae GN=PDR12 PE=1 SV=1	PDR12_YEAST
ATP-dependent permease PDR15 OS=Saccharomyces cerevisiae GN=PDR15 PE=1 SV=1	PDR15_YEAST
ATP-dependent RNA helicase CHL1 OS=Saccharomyces cerevisiae (strain YJM789) GN=CH	CHL1_YEAS7
ATP-dependent RNA helicase DBP1 OS=Saccharomyces cerevisiae (strain YJM789) GN=DE	DBP1_YEAS7
ATP-dependent RNA helicase DBP10 OS=Saccharomyces cerevisiae (strain YJM789) GN=D	DBP10_YEAS7
ATP-dependent RNA helicase DBP10 OS=Saccharomyces cerevisiae GN=DBP10 PE=1 SV=	DBP10_YEAST
ATP-dependent RNA helicase DBP2 OS=Saccharomyces cerevisiae (strain YJM789) GN=DE	DBP2_YEAS7
ATP-dependent RNA helicase DBP3 OS=Saccharomyces cerevisiae (strain YJM789) GN=DE	DBP3_YEAS7
ATP-dependent RNA helicase DBP3 OS=Saccharomyces cerevisiae GN=DBP3 PE=1 SV=2	DBP3_YEAST
ATP-dependent RNA helicase DBP4 OS=Saccharomyces cerevisiae (strain YJM789) GN=DE	DBP4_YEAS7
ATP-dependent RNA helicase DBP5 OS=Saccharomyces cerevisiae (strain YJM789) GN=DE	DBP5_YEAS7
ATP-dependent RNA helicase DBP6 OS=Saccharomyces cerevisiae (strain YJM789) GN=DE	DBP6_YEAS7
ATP-dependent RNA helicase DBP6 OS=Saccharomyces cerevisiae GN=DBP6 PE=1 SV=1	DBP6_YEAST
ATP-dependent RNA helicase DBP8 OS=Saccharomyces cerevisiae (strain YJM789) GN=DE	DBP8_YEAS7
ATP-dependent RNA helicase DBP9 OS=Saccharomyces cerevisiae (strain YJM789) GN=DE	DBP9_YEAS7
ATP-dependent RNA helicase DED1 OS=Saccharomyces cerevisiae (strain YJM789) GN=DE	DED1_YEAS7
ATP-dependent RNA helicase DHH1 OS=Saccharomyces cerevisiae (strain YJM789) GN=DI	DHH1_YEAS7
ATP-dependent RNA helicase DOB1 OS=Saccharomyces cerevisiae GN=MTR4 PE=1 SV=1	MTR4_YEAST
ATP-dependent RNA helicase DRS1 OS=Saccharomyces cerevisiae (strain YJM789) GN=DI	DRS1_YEAS7
ATP-dependent RNA helicase eIF4A OS=Saccharomyces cerevisiae (strain YJM789) GN=TI	IF4A_YEAS7
ATP-dependent RNA helicase FAL1 OS=Saccharomyces cerevisiae (strain YJM789) GN=FA	FAL1_YEAS7
ATP-dependent RNA helicase HAS1 OS=Saccharomyces cerevisiae GN=HAS1 PE=1 SV=1	HAS1_YEAST
ATP-dependent RNA helicase MAK5 OS=Saccharomyces cerevisiae (strain YJM789) GN=M	MAK5_YEAS7
ATP-dependent RNA helicase MAK5 OS=Saccharomyces cerevisiae GN=MAK5 PE=1 SV=1	MAK5_YEAST
ATP-dependent RNA helicase MSS116, mitochondrial OS=Saccharomyces cerevisiae GN=M	MS116_YEAST
ATP-dependent RNA helicase ROK1 OS=Saccharomyces cerevisiae (strain YJM789) GN=R	ROK1_YEAS7
ATP-dependent RNA helicase SUB2 OS=Saccharomyces cerevisiae (strain YJM789) GN=SU	SUB2_YEAS7
ATP-dependent RNA helicase SUV3, mitochondrial OS=Saccharomyces cerevisiae GN=SUV	SUV3_YEAST
ATP-dependent rRNA helicase RRP3 OS=Saccharomyces cerevisiae (strain YJM789) GN=R	RRP3_YEAS7

ATP-dependent rRNA helicase RRP3 OS=Saccharomyces cerevisiae GN=RRP3 PE=1 SV=2	RRP3_YEAST
ATP-dependent rRNA helicase SPB4 OS=Saccharomyces cerevisiae (strain YJM789) GN=SI	SPB4_YEAS7
Autophagy-related protein 14 OS=Saccharomyces cerevisiae GN=ATG14 PE=1 SV=1	ATG14_YEAST
Autophagy-related protein 16 OS=Saccharomyces cerevisiae (strain YJM789) GN=ATG16 PI	ATG16_YEAS7
Autophagy-related protein 19 OS=Saccharomyces cerevisiae (strain YJM789) GN=ATG19 PI	ATG19_YEAS7
Autophagy-related protein 2 OS=Saccharomyces cerevisiae (strain YJM789) GN=ATG2 PE=:	ATG2_YEAS7
Autophagy-related protein 21 OS=Saccharomyces cerevisiae (strain YJM789) GN=ATG21 PI	ATG21_YEAS7
Autophagy-related protein 29 OS=Saccharomyces cerevisiae (strain YJM789) GN=ATG29 PI	ATG29_YEAS7
Autophagy-related protein 29 OS=Saccharomyces cerevisiae GN=ATG29 PE=1 SV=1	ATG29_YEAST
Autophagy-related protein 31 OS=Saccharomyces cerevisiae GN=CIS1 PE=1 SV=1	CIS1_YEAST
Barrierpepsin OS=Saccharomyces cerevisiae GN=BAR1 PE=1 SV=1	BAR1_YEAST
Bifunctional purine biosynthesis protein ADE16 OS=Saccharomyces cerevisiae GN=ADE16 F	PUR91_YEAST
Bifunctional purine biosynthesis protein ADE17 OS=Saccharomyces cerevisiae GN=ADE17 F	PUR92_YEAST
Bifunctional purine biosynthetic protein ADE5,7 OS=Saccharomyces cerevisiae GN=ADE5,7	PUR2_YEAST
Branched-chain-amino-acid aminotransferase, cytosolic OS=Saccharomyces cerevisiae GN=	BCA2_YEAST
Branched-chain-amino-acid aminotransferase, mitochondrial OS=Saccharomyces cerevisiae	BCA1_YEAST
Bromodomain-containing factor 2 OS=Saccharomyces cerevisiae GN=BDF2 PE=1 SV=1	BDF2_YEAST
Bud emergence protein 1 OS=Saccharomyces cerevisiae GN=BEM1 PE=1 SV=1	BEM1_YEAST
Bud emergence protein 4 OS=Saccharomyces cerevisiae GN=BEM4 PE=1 SV=1	BEM4_YEAST
Bud site selection protein 4 OS=Saccharomyces cerevisiae (strain YJM789) GN=BUD4 PE=2	BUD4_YEAS7
Bud site selection protein 6 OS=Saccharomyces cerevisiae GN=BUD6 PE=1 SV=1	BUD6_YEAST
Bud site selection protein RAX1 OS=Saccharomyces cerevisiae GN=RAX1 PE=1 SV=1	RAX1_YEAST
C-1-tetrahydrofolate synthase, cytoplasmic OS=Saccharomyces cerevisiae GN=ADE3 PE=1	C1TC_YEAST
C-1-tetrahydrofolate synthase, mitochondrial OS=Saccharomyces cerevisiae GN=MIS1 PE=1	C1TM_YEAST
C-8 sterol isomerase OS=Saccharomyces cerevisiae GN=ERG2 PE=1 SV=1	ERG2_YEAST
Calcineurin subunit B OS=Saccharomyces cerevisiae GN=CNB1 PE=1 SV=3	CANB_YEAST
Calcium/calmodulin-dependent protein kinase II OS=Saccharomyces cerevisiae GN=CMK2 F	KCC2_YEAST
Calcium-binding protein NCS-1 OS=Saccharomyces cerevisiae GN=FRQ1 PE=1 SV=2	NCS1_YEAST
Calmodulin OS=Saccharomyces cerevisiae GN=CMD1 PE=1 SV=1	CALM_YEAST
cAMP-dependent protein kinase regulatory subunit OS=Saccharomyces cerevisiae GN=BCY	KAPR_YEAST
cAMP-dependent protein kinase type 1 OS=Saccharomyces cerevisiae GN=TPK1 PE=1 SV=	KAPA_YEAST
cAMP-dependent protein kinase type 2 OS=Saccharomyces cerevisiae GN=TPK2 PE=1 SV=	KAPB_YEAST
cAMP-dependent protein kinase type 3 OS=Saccharomyces cerevisiae GN=TPK3 PE=1 SV=	KAPC_YEAST
Carbonic anhydrase OS=Saccharomyces cerevisiae GN=NCE103 PE=1 SV=1	CAN_YEAST
Carboxypeptidase S OS=Saccharomyces cerevisiae GN=CPS1 PE=1 SV=2	CBPS_YEAST
Carboxypeptidase Y inhibitor OS=Saccharomyces cerevisiae GN=DKA1 PE=1 SV=2	CPYI_YEAST
Cargo-transport protein YPP1 OS=Saccharomyces cerevisiae (strain YJM789) GN=YPP1 PE	YPP1_YEAS7
Cargo-transport protein YPP1 OS=Saccharomyces cerevisiae GN=YPP1 PE=1 SV=1	YPP1_YEAST
Carnitine O-acetyltransferase YAT2 OS=Saccharomyces cerevisiae GN=YAT2 PE=1 SV=1	YAT2_YEAST
Carrier protein YMC1, mitochondrial OS=Saccharomyces cerevisiae GN=YMC1 PE=1 SV=2	YMC1_YEAST
Casein kinase I homolog 1 OS=Saccharomyces cerevisiae GN=YCK1 PE=1 SV=1	KC11_YEAST
Casein kinase I homolog 2 OS=Saccharomyces cerevisiae GN=YCK2 PE=1 SV=1	KC12_YEAST
Casein kinase I homolog 3 OS=Saccharomyces cerevisiae GN=YCK3 PE=1 SV=2	KC13_YEAST
Casein kinase I homolog HRR25 OS=Saccharomyces cerevisiae GN=HRR25 PE=1 SV=1	HRR25_YEAST
Casein kinase II subunit beta OS=Saccharomyces cerevisiae GN=CKB1 PE=1 SV=1	CSK2B_YEAST
Casein kinase II subunit beta' OS=Saccharomyces cerevisiae GN=CKB2 PE=1 SV=1	CSK2C_YEAST
Catabolic L-serine/threonine dehydratase OS=Saccharomyces cerevisiae GN=CHA1 PE=1 S	STDH_YEAST

Catabolite repression protein CAT5 OS=Saccharomyces cerevisiae GN=CAT5 PE=1 SV=2	CAT5_YEAST
Catalase T OS=Saccharomyces cerevisiae GN=CTT1 PE=1 SV=3	CATT_YEAST
Cation transport regulator-like protein OS=Saccharomyces cerevisiae GN=YER163C PE=1 S	CHAC_YEAST
CBK1 kinase activator protein MOB2 OS=Saccharomyces cerevisiae GN=MOB2 PE=1 SV=2	MOB2_YEAST
Cell cycle protein kinase DBF2 OS=Saccharomyces cerevisiae GN=DBF2 PE=1 SV=3	DBF2_YEAST
Cell division control protein 10 OS=Saccharomyces cerevisiae GN=CDC10 PE=1 SV=1	CDC10_YEAST
Cell division control protein 11 OS=Saccharomyces cerevisiae GN=CDC11 PE=1 SV=1	CDC11_YEAST
Cell division control protein 12 OS=Saccharomyces cerevisiae GN=CDC12 PE=1 SV=1	CDC12_YEAST
Cell division control protein 24 OS=Saccharomyces cerevisiae GN=CDC24 PE=1 SV=2	CDC24_YEAST
Cell division control protein 28 OS=Saccharomyces cerevisiae GN=CDC28 PE=1 SV=1	CDC28_YEAST
Cell division control protein 3 OS=Saccharomyces cerevisiae GN=CDC3 PE=1 SV=2	CDC3_YEAST
Cell division control protein 42 OS=Saccharomyces cerevisiae GN=CDC42 PE=1 SV=2	CDC42_YEAST
Cell division control protein 48 OS=Saccharomyces cerevisiae GN=CDC48 PE=1 SV=3	CDC48_YEAST
Cell division control protein 53 OS=Saccharomyces cerevisiae GN=CDC53 PE=1 SV=1	CDC53_YEAST
Cell division control protein 54 OS=Saccharomyces cerevisiae GN=CDC54 PE=1 SV=2	CDC54_YEAST
Cell division control protein 7 OS=Saccharomyces cerevisiae GN=CDC7 PE=1 SV=2	CDC7_YEAST
Cell membrane protein YLR413W OS=Saccharomyces cerevisiae GN=YLR413W PE=1 SV=:	YL413_YEAST
Cell morphogenesis protein PAG1 OS=Saccharomyces cerevisiae GN=TAO3 PE=1 SV=1	TAO3_YEAST
Cell wall integrity and stress response component 2 OS=Saccharomyces cerevisiae GN=WS	WSC2_YEAST
Cell wall mannoprotein HSP150 OS=Saccharomyces cerevisiae (strain AWRI1631) GN=HSP	HS150_YEAS6
Cell wall mannoprotein PST1 OS=Saccharomyces cerevisiae (strain YJM789) GN=PST1 PE=	PST1_YEAS7
Cell wall protein CWP1 OS=Saccharomyces cerevisiae GN=CWP1 PE=1 SV=2	CWP1_YEAST
Cell wall protein ECM33 OS=Saccharomyces cerevisiae (strain JAY291) GN=ECM33 PE=3 S	ECM33_YEAS2
Central kinetochore subunit CHL4 OS=Saccharomyces cerevisiae GN=CHL4 PE=1 SV=1	CHL4_YEAST
Centromere DNA-binding protein complex CBF3 subunit A OS=Saccharomyces cerevisiae G	CBF3A_YEAST
Cerevisin OS=Saccharomyces cerevisiae GN=PRB1 PE=1 SV=1	PRTB_YEAST
Chaotic nuclear migration protein 67 OS=Saccharomyces cerevisiae GN=CNM67 PE=1 SV=:	CNM67_YEAST
Chitin biosynthesis protein CHS5 OS=Saccharomyces cerevisiae GN=CHS5 PE=1 SV=1	CHS5_YEAST
Chitin synthase 3 OS=Saccharomyces cerevisiae GN=CHS3 PE=1 SV=3	CHS3_YEAST
Chorismate synthase OS=Saccharomyces cerevisiae GN=ARO2 PE=1 SV=1	AROC_YEAST
Chromatin assembly factor 1 subunit p90 OS=Saccharomyces cerevisiae GN=RLF2 PE=1 S\	RLF2_YEAST
Chromatin modification-related protein EAF3 OS=Saccharomyces cerevisiae GN=EAF3 PE=:	EAF3_YEAST
Chromatin modification-related protein EAF7 OS=Saccharomyces cerevisiae GN=EAF7 PE=:	EAF7_YEAST
Chromatin structure-remodeling complex protein RSC30 OS=Saccharomyces cerevisiae GN=	RSC30_YEAST
Chromatin structure-remodeling complex protein RSC58 OS=Saccharomyces cerevisiae GN=	RSC58_YEAST
Chromatin structure-remodeling complex protein RSC8 OS=Saccharomyces cerevisiae GN=F	RSC8_YEAST
Chromatin structure-remodeling complex subunit RSC4 OS=Saccharomyces cerevisiae GN=I	RSC4_YEAST
Chromatin structure-remodeling complex subunit RSC7 OS=Saccharomyces cerevisiae GN=I	RSC7_YEAST
Chromatin structure-remodeling complex subunit RSC9 OS=Saccharomyces cerevisiae GN=I	RSC9_YEAST
Chromatin structure-remodeling complex subunit SFH1 OS=Saccharomyces cerevisiae GN=S	SFH1_YEAST
Chromo domain-containing protein 1 OS=Saccharomyces cerevisiae GN=CHD1 PE=1 SV=1	CHD1_YEAST
Chromosome segregation in meiosis protein 3 OS=Saccharomyces cerevisiae GN=CSM3 PE	CSM3_YEAST
Chromosome stability protein 9 OS=Saccharomyces cerevisiae GN=CST9 PE=1 SV=1	CST9_YEAST
Chromosome transmission fidelity protein 8 OS=Saccharomyces cerevisiae GN=CTF8 PE=1	CTF8_YEAST
Citrate synthase, mitochondrial OS=Saccharomyces cerevisiae GN=CIT1 PE=1 SV=2	CISY1_YEAST
Clathrin coat assembly protein AP180B OS=Saccharomyces cerevisiae GN=YAP1802 PE=1	AP18B_YEAST
Clathrin heavy chain OS=Saccharomyces cerevisiae GN=CHC1 PE=1 SV=1	CLH_YEAST

Clathrin light chain OS=Saccharomyces cerevisiae GN=CLC1 PE=1 SV=1	CLC1_YEAST
Coatomer subunit alpha OS=Saccharomyces cerevisiae GN=RET1 PE=1 SV=2	COPA_YEAST
Coatomer subunit beta OS=Saccharomyces cerevisiae GN=SEC26 PE=1 SV=2	COPB_YEAST
Coatomer subunit beta' OS=Saccharomyces cerevisiae GN=SEC27 PE=1 SV=1	COPB2_YEAST
Coatomer subunit delta OS=Saccharomyces cerevisiae GN=RET2 PE=1 SV=3	COPD_YEAST
Coatomer subunit epsilon OS=Saccharomyces cerevisiae GN=SEC28 PE=1 SV=2	COPE_YEAST
Coatomer subunit gamma OS=Saccharomyces cerevisiae GN=SEC21 PE=1 SV=2	COPG_YEAST
Coatomer subunit zeta OS=Saccharomyces cerevisiae GN=RET3 PE=1 SV=1	COPZ_YEAST
Cofilin OS=Saccharomyces cerevisiae GN=COF1 PE=1 SV=1	COFI_YEAST
COMPASS component SWD2 OS=Saccharomyces cerevisiae GN=SWD2 PE=1 SV=1	SWD2_YEAST
Conserved oligomeric Golgi complex subunit 4 OS=Saccharomyces cerevisiae GN=COG4 PI	COG4_YEAST
Conserved oligomeric Golgi complex subunit 5 OS=Saccharomyces cerevisiae GN=COG5 PI	COG5_YEAST
Conserved oligomeric Golgi complex subunit 7 OS=Saccharomyces cerevisiae GN=COG7 PI	COG7_YEAST
COP9 signalosome complex subunit 10 OS=Saccharomyces cerevisiae GN=RRI2 PE=1 SV=	CSN10_YEAST
COP9 signalosome complex subunit 9 OS=Saccharomyces cerevisiae GN=CSN9 PE=1 SV=:	CSN9_YEAST
COPII coat assembly protein SEC16 OS=Saccharomyces cerevisiae GN=SEC16 PE=1 SV=2	SEC16_YEAST
Copper transport protein CTR1 OS=Saccharomyces cerevisiae GN=CTR1 PE=1 SV=1	CTR1_YEAST
Coronin-like protein OS=Saccharomyces cerevisiae GN=CRN1 PE=1 SV=1	CORO_YEAST
Covalently-linked cell wall protein 12 OS=Saccharomyces cerevisiae GN=CCW12 PE=1 SV=	CCW12_YEAST
CRAL-TRIO domain-containing protein YKL091C OS=Saccharomyces cerevisiae GN=YKL09	YKJ1_YEAST
CTD kinase subunit alpha OS=Saccharomyces cerevisiae GN=CTK1 PE=1 SV=1	CTK1_YEAST
CTD kinase subunit gamma OS=Saccharomyces cerevisiae GN=CTK3 PE=1 SV=2	CTK3_YEAST
CTP synthase 1 OS=Saccharomyces cerevisiae GN=URA7 PE=1 SV=2	URA7_YEAST
CTP synthase 2 OS=Saccharomyces cerevisiae (strain YJM789) GN=URA8 PE=3 SV=1	URA8_YEAS7
Cyclin-dependent protein kinase PHO85 OS=Saccharomyces cerevisiae GN=PHO85 PE=1 S	PHO85_YEAST
Cys-Gly metallodipeptidase DUG1 OS=Saccharomyces cerevisiae GN=DUG1 PE=1 SV=1	DUG1_YEAST
Cystathionine beta-lyase OS=Saccharomyces cerevisiae GN=STR3 PE=1 SV=1	STR3_YEAST
Cystathionine beta-synthase OS=Saccharomyces cerevisiae GN=CYS4 PE=1 SV=1	CBS_YEAST
Cystathionine gamma-lyase OS=Saccharomyces cerevisiae GN=CYS3 PE=1 SV=2	CYS3_YEAST
Cysteine desulfurase, mitochondrial OS=Saccharomyces cerevisiae GN=NFS1 PE=1 SV=2	NFS1_YEAST
Cysteine proteinase 1, mitochondrial OS=Saccharomyces cerevisiae GN=LAP3 PE=1 SV=3	BLH1_YEAST
Cysteinyl-tRNA synthetase OS=Saccharomyces cerevisiae GN=YNL247W PE=1 SV=1	SYC_YEAST
Cytidine deaminase OS=Saccharomyces cerevisiae GN=CDD1 PE=1 SV=1	CDD_YEAST
Cytochrome b mRNA maturase bI2 OS=Saccharomyces cerevisiae GN=bI2 PE=1 SV=2	MBI2_YEAST
Cytochrome B pre-mRNA-processing protein 2 OS=Saccharomyces cerevisiae GN=CBP2 PE	CBP2_YEAST
Cytochrome B pre-mRNA-processing protein 6 OS=Saccharomyces cerevisiae GN=CBP6 PE	CBP6_YEAST
Cytochrome b-c1 complex subunit 1, mitochondrial OS=Saccharomyces cerevisiae GN=COR	QCR1_YEAST
Cytochrome b-c1 complex subunit 2, mitochondrial OS=Saccharomyces cerevisiae GN=QCR	QCR2_YEAST
Cytochrome b-c1 complex subunit 6 OS=Saccharomyces cerevisiae GN=QCR6 PE=1 SV=2	QCR6_YEAST
Cytochrome b-c1 complex subunit 7 OS=Saccharomyces cerevisiae GN=QCR7 PE=1 SV=2	QCR7_YEAST
Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Saccharomyces cerevisiae GN=	UCRI_YEAST
Cytochrome c heme lyase OS=Saccharomyces cerevisiae GN=CYC3 PE=1 SV=1	CCHL_YEAST
Cytochrome c iso-1 OS=Saccharomyces cerevisiae GN=CYC1 PE=1 SV=2	CYC1_YEAST
Cytochrome c oxidase polypeptide 5A, mitochondrial OS=Saccharomyces cerevisiae GN=CC	COX5A_YEAST
Cytochrome c oxidase polypeptide VIII, mitochondrial OS=Saccharomyces cerevisiae GN=C(	COX8_YEAST
Cytochrome c oxidase subunit 4, mitochondrial OS=Saccharomyces cerevisiae GN=COX4 PI	COX4_YEAST
Cytochrome c oxidase subunit 6, mitochondrial OS=Saccharomyces cerevisiae GN=COX6 PI	COX6_YEAST

Cytochrome c oxidase subunit 7A OS=Saccharomyces cerevisiae GN=COX9 PE=1 SV=2	COX9_YEAST
Cytochrome c1, heme protein, mitochondrial OS=Saccharomyces cerevisiae GN=CTC1 PE=1	CY1_YEAST
Cytochrome P450 61 OS=Saccharomyces cerevisiae GN=ERG5 PE=1 SV=1	ERG5_YEAST
Cytokinesis protein 2 OS=Saccharomyces cerevisiae GN=CYK2 PE=1 SV=1	CYK2_YEAST
Cytokinesis protein 3 OS=Saccharomyces cerevisiae GN=CYK3 PE=1 SV=1	CYK3_YEAST
Cytoplasmic tRNA 2-thiolation protein 1 OS=Saccharomyces cerevisiae (strain RM11-1a) GN	CTU1_YEAS1
Cytosolic Fe-S cluster assembly factor NAR1 OS=Saccharomyces cerevisiae (strain YJM789	NAR1_YEAS7
Cytosolic Fe-S cluster assembly factor NBP35 OS=Saccharomyces cerevisiae GN=NBP35 P	NBP35_YEAST
D-3-phosphoglycerate dehydrogenase 2 OS=Saccharomyces cerevisiae GN=SER33 PE=1 S	SER33_YEAST
D-arabinose 1-dehydrogenase OS=Saccharomyces cerevisiae GN=ARA2 PE=1 SV=1	ARA2_YEAST
D-arabinose dehydrogenase [NAD(P)+] heavy chain OS=Saccharomyces cerevisiae GN=AR.	ARA1_YEAST
DASH complex subunit DAD3 OS=Saccharomyces cerevisiae GN=DAD3 PE=1 SV=1	DAD3_YEAST
DBF2 kinase activator protein MOB1 OS=Saccharomyces cerevisiae GN=MOB1 PE=1 SV=2	MOB1_YEAST
Delta(24(24(1)))-sterol reductase OS=Saccharomyces cerevisiae GN=ERG4 PE=1 SV=2	ERG4_YEAST
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Saccharomyces cerevisia	PUT2_YEAST
Delta-aminolevulinic acid dehydratase OS=Saccharomyces cerevisiae GN=HEM2 PE=1 SV=	HEM2_YEAST
Deoxycytidylate deaminase OS=Saccharomyces cerevisiae GN=DCD1 PE=1 SV=2	DCTD_YEAST
Deoxyhypusine hydroxylase OS=Saccharomyces cerevisiae GN=LIA1 PE=1 SV=1	DOHH_YEAST
Deoxyhypusine synthase OS=Saccharomyces cerevisiae GN=DYS1 PE=1 SV=1	DHYS_YEAST
DER1-like family member protein 1 OS=Saccharomyces cerevisiae GN=DFM1 PE=1 SV=1	DFM1_YEAST
Dicarboxylic amino acid permease OS=Saccharomyces cerevisiae GN=DIP5 PE=1 SV=1	DIP5_YEAST
Dihydrolipoyl dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae GN=LPD1 PE=1	DLDH_YEAST
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase comple:	ODP2_YEAST
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase	ODO2_YEAST
Dihydroorotate dehydrogenase OS=Saccharomyces cerevisiae GN=URA1 PE=1 SV=1	PYRD_YEAST
Dihydroxyacetone kinase 1 OS=Saccharomyces cerevisiae GN=DAK1 PE=1 SV=1	DAK1_YEAST
Dihydroxyacetone kinase 2 OS=Saccharomyces cerevisiae GN=DAK2 PE=1 SV=1	DAK2_YEAST
Dihydroxy-acid dehydratase, mitochondrial OS=Saccharomyces cerevisiae GN=ILV3 PE=1 S	ILV3_YEAST
Dimethyladenosine transferase OS=Saccharomyces cerevisiae GN=DIM1 PE=1 SV=1	DIM1_YEAST
Diphosphomevalonate decarboxylase OS=Saccharomyces cerevisiae GN=ERG19 PE=1 SV=	ERG19_YEAST
D-lactate dehydrogenase [cytochrome] 1, mitochondrial OS=Saccharomyces cerevisiae GN=	DLD1_YEAST
D-lactate dehydrogenase [cytochrome] 2, mitochondrial OS=Saccharomyces cerevisiae GN=	DLD2_YEAST
D-lactate dehydrogenase [cytochrome] 3 OS=Saccharomyces cerevisiae GN=DLD3 PE=1 S\	DLD3_YEAST
DNA damage checkpoint control protein RAD17 OS=Saccharomyces cerevisiae GN=RAD17	RAD17_YEAST
DNA damage checkpoint protein LCD1 OS=Saccharomyces cerevisiae GN=LCD1 PE=1 SV=	LCD1_YEAST
DNA damage response protein kinase DUN1 OS=Saccharomyces cerevisiae GN=DUN1 PE=	DUN1_YEAST
DNA damage-responsive transcriptional repressor RPH1 OS=Saccharomyces cerevisiae GN	RPH1_YEAST
DNA mismatch repair protein MSH1, mitochondrial OS=Saccharomyces cerevisiae GN=MSH	MSH1_YEAST
DNA polymerase alpha catalytic subunit A OS=Saccharomyces cerevisiae GN=POL1 PE=1 S	DPOA_YEAST
DNA polymerase alpha-associated DNA helicase A OS=Saccharomyces cerevisiae GN=HCS	HCS1_YEAST
DNA polymerase delta small subunit OS=Saccharomyces cerevisiae GN=HYS2 PE=1 SV=1	DPOD2_YEAST
DNA polymerase epsilon catalytic subunit A OS=Saccharomyces cerevisiae GN=POL2 PE=1	DPOE_YEAST
DNA polymerase V OS=Saccharomyces cerevisiae GN=POL5 PE=1 SV=1	DPO5_YEAST
DNA polymerase zeta catalytic subunit OS=Saccharomyces cerevisiae GN=REV3 PE=1 SV=	DPOZ_YEAST
DNA primase small subunit OS=Saccharomyces cerevisiae GN=PRI1 PE=1 SV=2	PRI1_YEAST
DNA repair and recombination protein RAD52 OS=Saccharomyces cerevisiae GN=RAD52 PI	RAD52_YEAST
DNA repair and recombination protein RDH54 OS=Saccharomyces cerevisiae GN=RDH54 P	RDH54_YEAST

DNA repair protein RAD16 OS=Saccharomyces cerevisiae GN=RAD16 PE=1 SV=1	RAD16_YEAST
DNA repair protein RAD2 OS=Saccharomyces cerevisiae GN=RAD2 PE=1 SV=2	RAD2_YEAST
DNA repair protein RAD50 OS=Saccharomyces cerevisiae GN=RAD50 PE=1 SV=1	RAD50_YEAST
DNA repair protein RAD51 OS=Saccharomyces cerevisiae GN=RAD51 PE=1 SV=1	RAD51_YEAST
DNA repair protein RAD9 OS=Saccharomyces cerevisiae GN=RAD9 PE=1 SV=1	RAD9_YEAST
DNA replication ATP-dependent helicase DNA2 OS=Saccharomyces cerevisiae GN=DNA2 F	DNA2_YEAST
DNA replication licensing factor CDC47 OS=Saccharomyces cerevisiae GN=CDC47 PE=1 S'	CDC47_YEAST
DNA replication licensing factor MCM2 OS=Saccharomyces cerevisiae GN=MCM2 PE=1 SV=	MCM2_YEAST
DNA replication licensing factor MCM6 OS=Saccharomyces cerevisiae GN=MCM6 PE=1 SV=	MCM6_YEAST
DNA topoisomerase 1 OS=Saccharomyces cerevisiae GN=TOP1 PE=1 SV=2	TOP1_YEAST
DNA topoisomerase 2 OS=Saccharomyces cerevisiae GN=TOP2 PE=1 SV=2	TOP2_YEAST
DNA topoisomerase 2-associated protein PAT1 OS=Saccharomyces cerevisiae GN=PAT1 PI	PAT1_YEAST
DNA-(apurinic or apyrimidinic site) lyase 1 OS=Saccharomyces cerevisiae GN=APN1 PE=1 S	APN1_YEAST
DNA-3-methyladenine glycosylase OS=Saccharomyces cerevisiae GN=MAG1 PE=1 SV=1	MAG_YEAST
DNA-binding protein RAP1 OS=Saccharomyces cerevisiae GN=RAP1 PE=1 SV=2	RAP1_YEAST
DNA-directed RNA polymerase I subunit RPA1 OS=Saccharomyces cerevisiae GN=RPA1 PE	RPA1_YEAST
DNA-directed RNA polymerase I subunit RPA12 OS=Saccharomyces cerevisiae GN=RPA12	RPA12_YEAST
DNA-directed RNA polymerase I subunit RPA2 OS=Saccharomyces cerevisiae GN=RPA2 PE	RPA2_YEAST
DNA-directed RNA polymerase I subunit RPA34 OS=Saccharomyces cerevisiae GN=RPA34	RPA34_YEAST
DNA-directed RNA polymerase I subunit RPA43 OS=Saccharomyces cerevisiae GN=RPA43	RPA43_YEAST
DNA-directed RNA polymerase I subunit RPA49 OS=Saccharomyces cerevisiae GN=RPA49	RPA49_YEAST
DNA-directed RNA polymerase II subunit RPB1 OS=Saccharomyces cerevisiae GN=RPB1 P	RPB1_YEAST
DNA-directed RNA polymerase II subunit RPB11 OS=Saccharomyces cerevisiae GN=RPB11	RPB11_YEAST
DNA-directed RNA polymerase II subunit RPB2 OS=Saccharomyces cerevisiae GN=RPB2 P	RPB2_YEAST
DNA-directed RNA polymerase II subunit RPB3 OS=Saccharomyces cerevisiae GN=RPB3 P	RPB3_YEAST
DNA-directed RNA polymerase II subunit RPB4 OS=Saccharomyces cerevisiae GN=RPB4 P	RPB4_YEAST
DNA-directed RNA polymerase III subunit RPC10 OS=Saccharomyces cerevisiae GN=RPC1	RPC10_YEAST
DNA-directed RNA polymerase III subunit RPC2 OS=Saccharomyces cerevisiae GN=RET1 F	RPC2_YEAST
DNA-directed RNA polymerase III subunit RPC6 OS=Saccharomyces cerevisiae GN=RPC34	RPC6_YEAST
DNA-directed RNA polymerase III subunit RPC9 OS=Saccharomyces cerevisiae GN=RPC17	RPC9_YEAST
DNA-directed RNA polymerases I and III subunit RPAC1 OS=Saccharomyces cerevisiae GN=	RPAC1_YEAST
DNA-directed RNA polymerases I and III subunit RPAC2 OS=Saccharomyces cerevisiae GN=	RPAC2_YEAST
DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Saccharomyces cerevisiae	RPAB1_YEAST
DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Saccharomyces cerevisiae	RPAB3_YEAST
DNA-directed RNA polymerases I, II, and III subunit RPABC4 OS=Saccharomyces cerevisiae	RPAB4_YEAST
DNA-directed RNA polymerases I, II, and III subunit RPABC5 OS=Saccharomyces cerevisiae	RPAB5_YEAST
DnaJ homolog 1, mitochondrial OS=Saccharomyces cerevisiae GN=MDJ1 PE=1 SV=1	MDJ1_YEAST
DnaJ protein homolog XDJ1 OS=Saccharomyces cerevisiae GN=XDJ1 PE=1 SV=2	XDJ1_YEAST
DnaJ-like chaperone JEM1 OS=Saccharomyces cerevisiae GN=JEM1 PE=1 SV=3	JEM1_YEAST
DnaJ-related protein SCJ1 OS=Saccharomyces cerevisiae GN=SCJ1 PE=1 SV=2	SCJ1_YEAST
DOA4-independent degradation protein 4 OS=Saccharomyces cerevisiae GN=DID4 PE=1 S\	DID4_YEAST
DOCK-like protein YLR422W OS=Saccharomyces cerevisiae GN=YLR422W PE=1 SV=1	YL422_YEAST
Dolichol-phosphate mannosyltransferase OS=Saccharomyces cerevisiae GN=DPM1 PE=1 S	DPM1_YEAST
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 3 OS=Saccharomyce	OST3_YEAST
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST2 OS=Saccharo	OST2_YEAST
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit WBP1 OS=Saccharo	OSTB_YEAST
Dolichyl-phosphate-mannose--protein mannosyltransferase 2 OS=Saccharomyces cerevisiae	PMT2_YEAST

Dolichyl-phosphate-mannose--protein mannosyltransferase 4 OS=Saccharomyces cerevisiae	PMT4_YEAST
Double-strand break repair protein MRE11 OS=Saccharomyces cerevisiae GN=MRE11 PE=1	MRE11_YEAST
Dynamin-like GTPase MGM1, mitochondrial OS=Saccharomyces cerevisiae GN=MGM1 PE=	MGM1_YEAST
E3 ubiquitin-protein ligase BRE1 OS=Saccharomyces cerevisiae GN=BRE1 PE=1 SV=1	BRE1_YEAST
E3 ubiquitin-protein ligase DMA1 OS=Saccharomyces cerevisiae GN=DMA1 PE=1 SV=1	DMA1_YEAST
E3 ubiquitin-protein ligase RSP5 OS=Saccharomyces cerevisiae GN=RSP5 PE=1 SV=1	RSP5_YEAST
Early meiotic induction protein 1 OS=Saccharomyces cerevisiae GN=EMI1 PE=1 SV=1	EMI1_YEAST
EH domain-containing and endocytosis protein 1 OS=Saccharomyces cerevisiae GN=EDE1 I	EDE1_YEAST
Elongation factor 1-alpha OS=Saccharomyces cerevisiae GN=TEF1 PE=1 SV=1	EF1A_YEAST
Elongation factor 1-beta OS=Saccharomyces cerevisiae GN=EFB1 PE=1 SV=4	EF1B_YEAST
Elongation factor 1-gamma 1 OS=Saccharomyces cerevisiae GN=CAM1 PE=1 SV=2	EF1G1_YEAST
Elongation factor 1-gamma 2 OS=Saccharomyces cerevisiae GN=TEF4 PE=1 SV=1	EF1G2_YEAST
Elongation factor 2 OS=Saccharomyces cerevisiae GN=EFT1 PE=1 SV=1	EF2_YEAST
Elongation factor 3A OS=Saccharomyces cerevisiae GN=YEF3 PE=1 SV=3	EF3A_YEAST
Elongation factor Tu, mitochondrial OS=Saccharomyces cerevisiae GN=TUF1 PE=1 SV=1	EFTU_YEAST
Elongation of fatty acids protein 2 OS=Saccharomyces cerevisiae GN=ELO2 PE=1 SV=1	ELO2_YEAST
Elongator complex protein 1 OS=Saccharomyces cerevisiae GN=IKI3 PE=1 SV=1	ELP1_YEAST
Elongator complex protein 3 OS=Saccharomyces cerevisiae GN=ELP3 PE=1 SV=1	ELP3_YEAST
Elongator complex protein 4 OS=Saccharomyces cerevisiae GN=ELP4 PE=1 SV=1	ELP4_YEAST
Elongator complex protein 5 OS=Saccharomyces cerevisiae GN=IKI1 PE=1 SV=1	ELP5_YEAST
Elongator complex protein 6 OS=Saccharomyces cerevisiae GN=ELP6 PE=1 SV=1	ELP6_YEAST
Endopolyphosphatase OS=Saccharomyces cerevisiae GN=PPN1 PE=1 SV=1	PPN1_YEAST
Enhancer of mRNA-decapping protein 3 OS=Saccharomyces cerevisiae GN=EDC3 PE=1 SV	EDC3_YEAST
Enolase 1 OS=Saccharomyces cerevisiae GN=ENO1 PE=1 SV=2	ENO1_YEAST
Enolase 2 OS=Saccharomyces cerevisiae GN=ENO2 PE=1 SV=2	ENO2_YEAST
Enolase-related protein 1/2 OS=Saccharomyces cerevisiae GN=ERR1 PE=1 SV=1	ERR1_YEAST
Enolase-related protein 3 OS=Saccharomyces cerevisiae GN=ERR3 PE=1 SV=2	ERR3_YEAST
Enoyl reductase TSC13 OS=Saccharomyces cerevisiae GN=TSC13 PE=1 SV=1	TSC13_YEAST
Enoyl-[acyl-carrier protein] reductase [NADPH, B-specific], mitochondrial OS=Saccharomyces	ETR1_YEAST
Epsin-1 OS=Saccharomyces cerevisiae GN=ENT1 PE=1 SV=1	ENT1_YEAST
Epsin-2 OS=Saccharomyces cerevisiae GN=ENT2 PE=1 SV=1	ENT2_YEAST
Epsin-3 OS=Saccharomyces cerevisiae GN=ENT3 PE=1 SV=1	ENT3_YEAST
Epsin-4 OS=Saccharomyces cerevisiae GN=ENT4 PE=1 SV=1	ENT4_YEAST
Epsin-5 OS=Saccharomyces cerevisiae GN=ENT5 PE=1 SV=1	ENT5_YEAST
ER-derived vesicles protein ERV29 OS=Saccharomyces cerevisiae GN=ERV29 PE=1 SV=1	ERV29_YEAST
ER-derived vesicles protein ERV46 OS=Saccharomyces cerevisiae GN=ERV46 PE=1 SV=2	ERV46_YEAST
Ergosterol biosynthetic protein 28 OS=Saccharomyces cerevisiae GN=ERG28 PE=1 SV=1	ERG28_YEAST
ER-localized J domain-containing protein 5 OS=Saccharomyces cerevisiae GN=ERJ5 PE=1	ERJ5_YEAST
Essential for mitotic growth 1 OS=Saccharomyces cerevisiae GN=EMG1 PE=1 SV=1	EMG1_YEAST
Essential nuclear protein 1 OS=Saccharomyces cerevisiae GN=ENP1 PE=1 SV=1	ENP1_YEAST
Eukaryotic initiation factor 4F subunit p130 OS=Saccharomyces cerevisiae GN=TIF4632 PE=	IF4F2_YEAST
Eukaryotic initiation factor 4F subunit p150 OS=Saccharomyces cerevisiae GN=TIF4631 PE=	IF4F1_YEAST
Eukaryotic peptide chain release factor GTP-binding subunit OS=Saccharomyces cerevisiae	ERF3_YEAST
Eukaryotic peptide chain release factor subunit 1 OS=Saccharomyces cerevisiae GN=SUP1	ERF1_YEAST
Eukaryotic translation initiation factor 1A OS=Saccharomyces cerevisiae GN=TIF11 PE=1 SV	IF1A_YEAST
Eukaryotic translation initiation factor 2 subunit alpha OS=Saccharomyces cerevisiae GN=SU	IF2A_YEAST
Eukaryotic translation initiation factor 2 subunit beta OS=Saccharomyces cerevisiae GN=SUI	IF2B_YEAST

Eukaryotic translation initiation factor 2 subunit gamma OS=Saccharomyces cerevisiae GN=(	IF2G_YEAST
Eukaryotic translation initiation factor 2A OS=Saccharomyces cerevisiae GN=YGR054W PE=	EIF2A_YEAST
Eukaryotic translation initiation factor 3 subunit A OS=Saccharomyces cerevisiae GN=TIF32	EIF3A_YEAST
Eukaryotic translation initiation factor 3 subunit B OS=Saccharomyces cerevisiae (strain YJM	EIF3B_YEAS7
Eukaryotic translation initiation factor 3 subunit C OS=Saccharomyces cerevisiae (strain YJM	EIF3C_YEAS7
Eukaryotic translation initiation factor 3 subunit C OS=Saccharomyces cerevisiae GN=NIP1 F	EIF3C_YEAST
Eukaryotic translation initiation factor 3 subunit G OS=Saccharomyces cerevisiae (strain YJM	EIF3G_YEAS7
Eukaryotic translation initiation factor 3 subunit G OS=Saccharomyces cerevisiae GN=TIF35	EIF3G_YEAST
Eukaryotic translation initiation factor 3 subunit I OS=Saccharomyces cerevisiae (strain YJM7	EIF3I_YEAS7
Eukaryotic translation initiation factor 3 subunit J OS=Saccharomyces cerevisiae GN=HCR1	EIF3J_YEAST
Eukaryotic translation initiation factor 4B OS=Saccharomyces cerevisiae GN=TIF3 PE=1 SV=	IF4B_YEAST
Eukaryotic translation initiation factor 4E OS=Saccharomyces cerevisiae GN=TIF45 PE=1 SV	IF4E_YEAST
Eukaryotic translation initiation factor 5 OS=Saccharomyces cerevisiae GN=TIF5 PE=1 SV=1	IF5_YEAST
Eukaryotic translation initiation factor 5A-2 OS=Saccharomyces cerevisiae GN=HYP2 PE=1 S	IF5A2_YEAST
Eukaryotic translation initiation factor 5B OS=Saccharomyces cerevisiae GN=FUN12 PE=1 S	IF2P_YEAST
Eukaryotic translation initiation factor 6 OS=Saccharomyces cerevisiae GN=TIF6 PE=1 SV=1	IF6_YEAST
Eukaryotic translation initiation factor eIF-1 OS=Saccharomyces cerevisiae GN=SUI1 PE=1 S	SUI1_YEAST
Exocyst complex component EXO70 OS=Saccharomyces cerevisiae GN=EXO70 PE=1 SV=1	EXO70_YEAST
Exocyst complex component SEC10 OS=Saccharomyces cerevisiae GN=SEC10 PE=1 SV=1	SEC10_YEAST
Exocyst complex component SEC15 OS=Saccharomyces cerevisiae GN=SEC15 PE=1 SV=2	SEC15_YEAST
Exocyst complex component SEC3 OS=Saccharomyces cerevisiae GN=SEC3 PE=1 SV=1	SEC3_YEAST
Exocyst complex component SEC5 OS=Saccharomyces cerevisiae GN=SEC5 PE=1 SV=1	SEC5_YEAST
Exocyst complex component SEC6 OS=Saccharomyces cerevisiae GN=SEC6 PE=1 SV=2	SEC6_YEAST
Exocyst complex component SEC8 OS=Saccharomyces cerevisiae GN=SEC8 PE=1 SV=1	SEC8_YEAST
Exodeoxyribonuclease 1 OS=Saccharomyces cerevisiae GN=EXO1 PE=1 SV=2	EXO1_YEAST
Exosome complex component CSL4 OS=Saccharomyces cerevisiae GN=CSL4 PE=1 SV=1	CSL4_YEAST
Exosome complex component RRP40 OS=Saccharomyces cerevisiae GN=RRP40 PE=1 SV=	RRP40_YEAST
Exosome complex component RRP43 OS=Saccharomyces cerevisiae GN=RRP43 PE=1 SV=	RRP43_YEAST
Exosome complex component RRP45 OS=Saccharomyces cerevisiae GN=RRP45 PE=1 SV=	RRP45_YEAST
Exosome complex component RRP46 OS=Saccharomyces cerevisiae GN=RRP46 PE=1 SV=	RRP46_YEAST
Exosome complex exonuclease DIS3 OS=Saccharomyces cerevisiae GN=DIS3 PE=1 SV=1	RRP44_YEAST
FACT complex subunit POB3 OS=Saccharomyces cerevisiae GN=POB3 PE=1 SV=1	POB3_YEAST
FACT complex subunit SPT16 OS=Saccharomyces cerevisiae GN=SPT16 PE=1 SV=1	SPT16_YEAST
F-actin-capping protein subunit beta OS=Saccharomyces cerevisiae GN=CAP2 PE=1 SV=3	CAPZB_YEAST
Family of serine hydrolases 1 OS=Saccharomyces cerevisiae GN=FSH1 PE=1 SV=1	FSH1_YEAST
Family of serine hydrolases 3 OS=Saccharomyces cerevisiae GN=FSH3 PE=1 SV=1	FSH3_YEAST
Farnesyl pyrophosphate synthase OS=Saccharomyces cerevisiae GN=FPP1 PE=1 SV=2	FPPS_YEAST
Fatty acid synthase subunit alpha OS=Saccharomyces cerevisiae GN=FAS2 PE=1 SV=2	FAS2_YEAST
Fatty acid synthase subunit beta OS=Saccharomyces cerevisiae GN=FAS1 PE=1 SV=2	FAS1_YEAST
F-box protein YLR352W OS=Saccharomyces cerevisiae GN=YLR352W PE=1 SV=1	YL352_YEAST
Ferric/cupric reductase transmembrane component 1 OS=Saccharomyces cerevisiae GN=FR	FRE1_YEAST
Ferrochelatase, mitochondrial OS=Saccharomyces cerevisiae GN=HEM15 PE=1 SV=1	HEMH_YEAST
Fimbrin OS=Saccharomyces cerevisiae GN=SAC6 PE=1 SV=1	FIMB_YEAST
FK506-binding nuclear protein OS=Saccharomyces cerevisiae GN=FPR3 PE=1 SV=2	FKBP3_YEAST
FK506-binding protein 1 OS=Saccharomyces cerevisiae GN=FPR1 PE=1 SV=2	FKBP_YEAST
FK506-binding protein 4 OS=Saccharomyces cerevisiae GN=FPR4 PE=1 SV=1	FKBP4_YEAST
Flavin carrier protein 1 OS=Saccharomyces cerevisiae GN=FLC1 PE=1 SV=1	FLC1_YEAST

Flavohemoprotein OS=Saccharomyces cerevisiae GN=YHB1 PE=1 SV=2	FHP_YEAST
Flavoprotein-like protein YCP4 OS=Saccharomyces cerevisiae GN=YCP4 PE=1 SV=1	YCP4_YEAST
Fructose-2,6-bisphosphatase OS=Saccharomyces cerevisiae GN=FBP26 PE=1 SV=2	F26_YEAST
Fructose-bisphosphate aldolase OS=Saccharomyces cerevisiae GN=FBA1 PE=1 SV=3	ALF_YEAST
Fumarate hydratase, mitochondrial OS=Saccharomyces cerevisiae GN=FUM1 PE=1 SV=2	FUMH_YEAST
Fumarate reductase OS=Saccharomyces cerevisiae GN=YEL047C PE=1 SV=1	FRDS_YEAST
General negative regulator of transcription subunit 1 OS=Saccharomyces cerevisiae GN=NO	NOT1_YEAST
General negative regulator of transcription subunit 2 OS=Saccharomyces cerevisiae GN=NO	NOT2_YEAST
General negative regulator of transcription subunit 4 OS=Saccharomyces cerevisiae GN=NO	NOT4_YEAST
General negative regulator of transcription subunit 5 OS=Saccharomyces cerevisiae GN=NO	NOT5_YEAST
GLC7-interacting protein 2 OS=Saccharomyces cerevisiae GN=GIP2 PE=1 SV=1	GIP2_YEAST
GLC7-interacting protein 4 OS=Saccharomyces cerevisiae GN=GIP4 PE=1 SV=2	GIP4_YEAST
Glucan 1,3-beta-glucosidase I/II OS=Saccharomyces cerevisiae GN=EXG1 PE=1 SV=1	EXG1_YEAST
Glucan 1,3-beta-glucosidase OS=Saccharomyces cerevisiae GN=BGL2 PE=1 SV=1	BGL2_YEAST
Glucokinase-1 OS=Saccharomyces cerevisiae GN=GLK1 PE=1 SV=1	HXKG_YEAST
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Saccharomyces cere	GFA1_YEAST
Glucose-6-phosphate 1-dehydrogenase OS=Saccharomyces cerevisiae GN=ZWF1 PE=1 SV	G6PD_YEAST
Glucose-6-phosphate 1-epimerase OS=Saccharomyces cerevisiae GN=YMR099C PE=1 SV=	YMY9_YEAST
Glucose-6-phosphate isomerase OS=Saccharomyces cerevisiae GN=PGI1 PE=1 SV=3	G6PI_YEAST
Glucose-induced degradation protein 8 OS=Saccharomyces cerevisiae GN=GID8 PE=1 SV=	GID8_YEAST
Glucose-repressible alcohol dehydrogenase transcriptional effector OS=Saccharomyces cere	CCR4_YEAST
Glutamate 5-kinase OS=Saccharomyces cerevisiae GN=PRO1 PE=1 SV=2	PROB_YEAST
Glutamate decarboxylase OS=Saccharomyces cerevisiae GN=GAD1 PE=1 SV=1	DCE_YEAST
Glutamate synthase [NADH] OS=Saccharomyces cerevisiae GN=GLT1 PE=1 SV=2	GLT1_YEAST
Glutamate--cysteine ligase OS=Saccharomyces cerevisiae GN=GSH1 PE=1 SV=1	GSH1_YEAST
Glutamine synthetase OS=Saccharomyces cerevisiae GN=GLN1 PE=1 SV=2	GLNA_YEAST
Glutamyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=GUS1 PE=1 SV	SYEC_YEAST
Glutaredoxin-2, mitochondrial OS=Saccharomyces cerevisiae GN=GRX2 PE=1 SV=3	GLRX2_YEAST
Glutathione peroxidase 2 OS=Saccharomyces cerevisiae GN=GPX2 PE=1 SV=1	GPX2_YEAST
Glutathione reductase OS=Saccharomyces cerevisiae GN=GLR1 PE=1 SV=2	GSHR_YEAST
Glutathione S-transferase 1 OS=Saccharomyces cerevisiae GN=GTT1 PE=1 SV=1	GST1_YEAST
Glutathione S-transferase 2 OS=Saccharomyces cerevisiae GN=GTT2 PE=1 SV=1	GST2_YEAST
Glutathione synthetase OS=Saccharomyces cerevisiae GN=GSH2 PE=1 SV=1	GSHB_YEAST
Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Saccharomyces cerevisiae GN=TDH1 PI	G3P1_YEAST
Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Saccharomyces cerevisiae GN=TDH2 PI	G3P2_YEAST
Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Saccharomyces cerevisiae GN=TDH3 PI	G3P3_YEAST
Glycerol-3-phosphate dehydrogenase [NAD+] 1 OS=Saccharomyces cerevisiae GN=GPD1 F	GPD1_YEAST
Glycerol-3-phosphate dehydrogenase [NAD+] 2, mitochondrial OS=Saccharomyces cerevisia	GPD2_YEAST
Glycerol-3-phosphate O-acyltransferase 1 OS=Saccharomyces cerevisiae GN=GPT1 PE=1 S	GPT1_YEAST
Glycerophosphodiester phosphodiesterase GDE1 OS=Saccharomyces cerevisiae GN=GDE1	GDE1_YEAST
Glycine cleavage system H protein, mitochondrial OS=Saccharomyces cerevisiae GN=GCV3	GCSH_YEAST
Glycine dehydrogenase [decarboxylating], mitochondrial OS=Saccharomyces cerevisiae GN=	GCSP_YEAST
Glycogen [starch] synthase isoform 1 OS=Saccharomyces cerevisiae GN=GSY1 PE=1 SV=3	GYS1_YEAST
Glycogen [starch] synthase isoform 2 OS=Saccharomyces cerevisiae GN=GSY2 PE=1 SV=3	GYS2_YEAST
Glycogen debranching enzyme OS=Saccharomyces cerevisiae GN=GDB1 PE=1 SV=1	GDE_YEAST
Glycogen phosphorylase OS=Saccharomyces cerevisiae GN=GPH1 PE=1 SV=3	PHSG_YEAST
Glycolipid 2-alpha-mannosyltransferase OS=Saccharomyces cerevisiae GN=KRE2 PE=1 SV	KRE2_YEAST

Glycyl-tRNA synthetase 1 OS=Saccharomyces cerevisiae GN=GRS1 PE=1 SV=1	SYG_YEAST
Glycyl-tRNA synthetase 2 OS=Saccharomyces cerevisiae GN=GRS2 PE=1 SV=1	SYG2_YEAST
GMP synthase [glutamine-hydrolyzing] OS=Saccharomyces cerevisiae GN=GUA1 PE=1 SV=	GUAA_YEAST
Golgin IMH1 OS=Saccharomyces cerevisiae GN=IMH1 PE=1 SV=1	IMH1_YEAST
GRAM domain-containing protein YSP2 OS=Saccharomyces cerevisiae GN=YSP2 PE=1 SV:	YSP2_YEAST
GRASP65 homolog protein 1 OS=Saccharomyces cerevisiae GN=GRH1 PE=1 SV=1	GRH1_YEAST
Growth regulation protein OS=Saccharomyces cerevisiae GN=WHI2 PE=1 SV=2	WHI2_YEAST
GTP cyclohydrolase 1 OS=Saccharomyces cerevisiae GN=FOL2 PE=1 SV=1	GCH1_YEAST
GTP cyclohydrolase-2 OS=Saccharomyces cerevisiae GN=RIB1 PE=1 SV=2	RIB1_YEAST
GTPase MTG2, mitochondrial OS=Saccharomyces cerevisiae GN=MTG2 PE=1 SV=2	MTG2_YEAST
GTPase-activating protein BEM2/IPL2 OS=Saccharomyces cerevisiae GN=BEM2 PE=1 SV=	BEM2_YEAST
GTPase-activating protein GYP1 OS=Saccharomyces cerevisiae GN=GYP1 PE=1 SV=1	GYP1_YEAST
GTPase-activating protein GYP3 OS=Saccharomyces cerevisiae GN=MSB3 PE=1 SV=1	GYP3_YEAST
GTPase-activating protein GYP8 OS=Saccharomyces cerevisiae GN=GYP8 PE=1 SV=1	GYP8_YEAST
GTPase-activating protein SAC7 OS=Saccharomyces cerevisiae GN=SAC7 PE=1 SV=2	SAC7_YEAST
GTP-binding nuclear protein GSP1/CNR1 OS=Saccharomyces cerevisiae GN=GSP1 PE=1 S	GSP1_YEAST
GTP-binding nuclear protein GSP2/CNR2 OS=Saccharomyces cerevisiae GN=GSP2 PE=1 S	GSP2_YEAST
GTP-binding protein GTR2 OS=Saccharomyces cerevisiae GN=GTR2 PE=1 SV=1	GTR2_YEAST
GTP-binding protein RBG1 OS=Saccharomyces cerevisiae GN=RBG1 PE=1 SV=1	RBG1_YEAST
GTP-binding protein RHO1 OS=Saccharomyces cerevisiae GN=RHO1 PE=1 SV=3	RHO1_YEAST
GTP-binding protein RHO3 OS=Saccharomyces cerevisiae GN=RHO3 PE=1 SV=2	RHO3_YEAST
GTP-binding protein RHO5 OS=Saccharomyces cerevisiae GN=RHO5 PE=1 SV=2	RHO5_YEAST
GTP-binding protein YPT1 OS=Saccharomyces cerevisiae GN=YPT1 PE=1 SV=2	YPT1_YEAST
GTP-binding protein YPT7 OS=Saccharomyces cerevisiae GN=YPT7 PE=1 SV=1	YPT7_YEAST
GU4 nucleic-binding protein 1 OS=Saccharomyces cerevisiae GN=ARC1 PE=1 SV=2	G4P1_YEAST
Guanine nucleotide exchange factor LTE1 OS=Saccharomyces cerevisiae GN=LTE1 PE=1 S	LTE1_YEAST
Guanine nucleotide-binding protein subunit beta 1 OS=Saccharomyces cerevisiae GN=GPB1	GPB1_YEAST
Guanine nucleotide-binding protein subunit beta-like protein OS=Saccharomyces cerevisiae	GBLP_YEAST
Guanine nucleotide-binding protein subunit gamma OS=Saccharomyces cerevisiae GN=STE	GBG_YEAST
Guanylate kinase OS=Saccharomyces cerevisiae GN=GUK1 PE=1 SV=2	KGUA_YEAST
H/ACA ribonucleoprotein complex subunit 1 OS=Saccharomyces cerevisiae GN=GAR1 PE=1	GAR1_YEAST
H/ACA ribonucleoprotein complex subunit 2 OS=Saccharomyces cerevisiae GN=NHP2 PE=1	NHP2_YEAST
H/ACA ribonucleoprotein complex subunit 3 OS=Saccharomyces cerevisiae GN=NOP10 PE=	NOP10_YEAST
H/ACA ribonucleoprotein complex subunit 4 OS=Saccharomyces cerevisiae GN=CBF5 PE=1	CBF5_YEAST
HD domain-containing protein YBR242W OS=Saccharomyces cerevisiae GN=YBR242W PE	YB92_YEAST
HD domain-containing protein YGL101W OS=Saccharomyces cerevisiae GN=YGL101W PE	YGK1_YEAST
Heat shock protein 104 OS=Saccharomyces cerevisiae GN=HSP104 PE=1 SV=2	HS104_YEAST
Heat shock protein 26 OS=Saccharomyces cerevisiae GN=HSP26 PE=1 SV=3	HSP26_YEAST
Heat shock protein 42 OS=Saccharomyces cerevisiae GN=HSP42 PE=1 SV=1	HSP42_YEAST
Heat shock protein 60, mitochondrial OS=Saccharomyces cerevisiae GN=HSP60 PE=1 SV=1	HSP60_YEAST
Heat shock protein 78, mitochondrial OS=Saccharomyces cerevisiae GN=HSP78 PE=1 SV=2	HSP78_YEAST
Heat shock protein homolog SSE1 OS=Saccharomyces cerevisiae GN=SSE1 PE=1 SV=4	HSP7F_YEAST
Heat shock protein homolog SSE2 OS=Saccharomyces cerevisiae GN=SSE2 PE=1 SV=3	HSP79_YEAST
Heat shock protein SSA1 OS=Saccharomyces cerevisiae GN=SSA1 PE=1 SV=4	HSP71_YEAST
Heat shock protein SSA2 OS=Saccharomyces cerevisiae GN=SSA2 PE=1 SV=3	HSP72_YEAST
Heat shock protein SSA3 OS=Saccharomyces cerevisiae GN=SSA3 PE=1 SV=3	HSP73_YEAST
Heat shock protein SSA4 OS=Saccharomyces cerevisiae GN=SSA4 PE=1 SV=3	HSP74_YEAST

Heat shock protein SSB1 OS=Saccharomyces cerevisiae GN=SSB1 PE=1 SV=3	HSP75_YEAST
Heat shock protein SSB2 OS=Saccharomyces cerevisiae GN=SSB2 PE=1 SV=2	HSP76_YEAST
Heat shock protein SSC1, mitochondrial OS=Saccharomyces cerevisiae GN=SSC1 PE=1 SV	HSP77_YEAST
Heat shock protein STI1 OS=Saccharomyces cerevisiae GN=STI1 PE=1 SV=1	STI1_YEAST
Helicase SEN1 OS=Saccharomyces cerevisiae GN=SEN1 PE=1 SV=2	SEN1_YEAST
Helper of Tim protein 13 OS=Saccharomyces cerevisiae GN=HOT13 PE=1 SV=1	HOT13_YEAST
Heme-responsive zinc finger transcription factor HAP1 OS=Saccharomyces cerevisiae GN=H	HAP1W_YEAST
Heterotrimeric G protein gamma subunit GPG1 OS=Saccharomyces cerevisiae GN=GPG1 P	GPG1_YEAST
Hexaprenyl pyrophosphate synthase, mitochondrial OS=Saccharomyces cerevisiae GN=CO(	COQ1_YEAST
Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial OS=Saccharomyces cerevisi	COQ3_YEAST
Hexokinase-1 OS=Saccharomyces cerevisiae GN=HXK1 PE=1 SV=2	HXKA_YEAST
Hexokinase-2 OS=Saccharomyces cerevisiae GN=HXK2 PE=1 SV=4	HXKB_YEAST
High mobility group protein 1 OS=Saccharomyces cerevisiae GN=HMO1 PE=1 SV=1	HMO1_YEAST
High-affinity glutamine permease OS=Saccharomyces cerevisiae GN=GNP1 PE=1 SV=2	GNP1_YEAST
High-affinity hexose transporter HXT6 OS=Saccharomyces cerevisiae GN=HXT7 PE=1 SV=1	HXT7_YEAST
High-affinity potassium transport protein OS=Saccharomyces cerevisiae GN=TRK1 PE=1 SV	TRK1_YEAST
High-osmolarity-induced transcription protein 1 OS=Saccharomyces cerevisiae GN=HOT1 PI	HOT1_YEAST
Histidine biosynthesis trifunctional protein OS=Saccharomyces cerevisiae GN=HIS4 PE=1 S\	HIS2_YEAST
Histidyl-tRNA synthetase, mitochondrial OS=Saccharomyces cerevisiae GN=HTS1 PE=1 SV:	SYH_YEAST
Histone acetyltransferase GCN5 OS=Saccharomyces cerevisiae GN=GCN5 PE=1 SV=1	GCN5_YEAST
Histone acetyltransferase SAS3 OS=Saccharomyces cerevisiae GN=SAS3 PE=1 SV=1	SAS3_YEAST
Histone chaperone ASF1 OS=Saccharomyces cerevisiae GN=ASF1 PE=1 SV=1	ASF1_YEAST
Histone deacetylase complex subunit CTI6 OS=Saccharomyces cerevisiae GN=CTI6 PE=1 S	CTI6_YEAST
Histone deacetylase HDA1 OS=Saccharomyces cerevisiae GN=HDA1 PE=1 SV=1	HDA1_YEAST
Histone deacetylase HOS3 OS=Saccharomyces cerevisiae GN=HOS3 PE=1 SV=1	HOS3_YEAST
Histone deacetylase RPD3 OS=Saccharomyces cerevisiae GN=RPD3 PE=1 SV=1	RPD3_YEAST
Histone H1 OS=Saccharomyces cerevisiae GN=HHO1 PE=1 SV=1	H1_YEAST
Histone H2A.1 OS=Saccharomyces cerevisiae GN=HTA1 PE=1 SV=2	H2A1_YEAST
Histone H2A.Z OS=Saccharomyces cerevisiae GN=HTZ1 PE=1 SV=3	H2AZ_YEAST
Histone H2B.1 OS=Saccharomyces cerevisiae GN=HTB1 PE=1 SV=2	H2B1_YEAST
Histone H2B.2 OS=Saccharomyces cerevisiae GN=HTB2 PE=1 SV=2	H2B2_YEAST
Histone H3 OS=Saccharomyces cerevisiae GN=HHT1 PE=1 SV=2	H3_YEAST
Histone H4 OS=Saccharomyces cerevisiae GN=HHF1 PE=1 SV=2	H4_YEAST
Histone-lysine N-methyltransferase, H3 lysine-4 specific OS=Saccharomyces cerevisiae GN=	SET1_YEAST
Hit family protein 1 OS=Saccharomyces cerevisiae GN=HNT1 PE=1 SV=2	HNT1_YEAST
HNRNP arginine N-methyltransferase OS=Saccharomyces cerevisiae GN=HMT1 PE=1 SV=1	HMT1_YEAST
Homoaconitase, mitochondrial OS=Saccharomyces cerevisiae GN=LYS4 PE=1 SV=1	LYS4_YEAST
Homocitrate synthase, cytosolic isozyme OS=Saccharomyces cerevisiae GN=LYS20 PE=1 S	HOSC_YEAST
Homoserine dehydrogenase OS=Saccharomyces cerevisiae GN=HOM6 PE=1 SV=1	DHOM_YEAST
Homoserine kinase OS=Saccharomyces cerevisiae GN=THR1 PE=1 SV=4	KHSE_YEAST
HSP70 co-chaperone SNL1 OS=Saccharomyces cerevisiae GN=SNL1 PE=1 SV=1	SNL1_YEAST
Hsp90 co-chaperone AHA1 OS=Saccharomyces cerevisiae GN=AHA1 PE=1 SV=1	AHA1_YEAST
Hydroxymethylglutaryl-CoA synthase OS=Saccharomyces cerevisiae GN=ERG13 PE=1 SV=	HMCS_YEAST
Hypoxanthine-guanine phosphoribosyltransferase OS=Saccharomyces cerevisiae GN=HPT1	HPRT_YEAST
Importin subunit alpha OS=Saccharomyces cerevisiae GN=SRP1 PE=1 SV=1	IMA1_YEAST
Importin subunit beta-1 OS=Saccharomyces cerevisiae GN=KAP95 PE=1 SV=1	IMB1_YEAST
Importin subunit beta-4 OS=Saccharomyces cerevisiae GN=KAP123 PE=1 SV=1	IMB4_YEAST

IMP-specific 5'-nucleotidase 1 OS=Saccharomyces cerevisiae GN=ISN1 PE=1 SV=1	ISN1_YEAST
Increased sodium tolerance protein 2 OS=Saccharomyces cerevisiae GN=IST2 PE=1 SV=1	IST2_YEAST
Indoleamine 2,3-dioxygenase family protein OS=Saccharomyces cerevisiae GN=BNA2 PE=1	I23O_YEAST
Inhibitory regulator protein BUD2/CLA2 OS=Saccharomyces cerevisiae GN=BUD2 PE=1 SV=	BUD2_YEAST
Inhibitory regulator protein IRA1 OS=Saccharomyces cerevisiae GN=IRA1 PE=1 SV=2	IRA1_YEAST
Inner centromere protein-related protein SLI15 OS=Saccharomyces cerevisiae GN=SLI15 PE	SLI15_YEAST
Ino eighty subunit 5 OS=Saccharomyces cerevisiae GN=IES5 PE=1 SV=1	IES5_YEAST
Inorganic phosphate transport protein PHO88 OS=Saccharomyces cerevisiae GN=PHO88 PI	PHO88_YEAST
Inorganic phosphate transporter PHO86 OS=Saccharomyces cerevisiae GN=PHO86 PE=1 S	PHO86_YEAST
Inorganic pyrophosphatase OS=Saccharomyces cerevisiae GN=IPP1 PE=1 SV=4	IPYR_YEAST
Inorganic pyrophosphatase, mitochondrial OS=Saccharomyces cerevisiae GN=IPP2 PE=1 S'	IPYR2_YEAST
Inosine-5'-monophosphate dehydrogenase IMD2 OS=Saccharomyces cerevisiae GN=IMD2 F	IMDH2_YEAST
Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase OS=Saccharomy	VIP1_YEAST
Inositol phosphosphingolipids phospholipase C OS=Saccharomyces cerevisiae GN=ISC1 PE	ISC1_YEAST
Inositol-1,4,5-trisphosphate 5-phosphatase 2 OS=Saccharomyces cerevisiae GN=INP52 PE=	INP52_YEAST
Inositol-1,4,5-trisphosphate 5-phosphatase 3 OS=Saccharomyces cerevisiae GN=INP53 PE=	INP53_YEAST
Invertase 1 OS=Saccharomyces cerevisiae GN=SUC1 PE=1 SV=1	INV1_YEAST
Iron sulfur cluster assembly protein 1, mitochondrial OS=Saccharomyces cerevisiae GN=ISU	ISU1_YEAST
Iron sulfur cluster assembly protein 2, mitochondrial OS=Saccharomyces cerevisiae GN=ISU	ISU2_YEAST
Iron-regulated transcriptional activator AFT1 OS=Saccharomyces cerevisiae GN=AFT1 PE=1	AFT1_YEAST
Isoamyl acetate-hydrolyzing esterase OS=Saccharomyces cerevisiae GN=IAH1 PE=1 SV=1	IAH1_YEAST
Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial OS=Saccharomyces cerevisiae GN=	IDH1_YEAST
Isocitrate dehydrogenase [NAD] subunit 2, mitochondrial OS=Saccharomyces cerevisiae GN=	IDH2_YEAST
Isocitrate dehydrogenase [NADP] OS=Saccharomyces cerevisiae GN=IDP3 PE=1 SV=1	IDHH_YEAST
Isocitrate dehydrogenase [NADP], mitochondrial OS=Saccharomyces cerevisiae GN=IDP1 P	IDHP_YEAST
Isoleucyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=ILS1 PE=1 SV=	SYIC_YEAST
Isopentenyl-diphosphate Delta-isomerase OS=Saccharomyces cerevisiae GN=IDI1 PE=1 SV	IDI1_YEAST
ISWI chromatin-remodeling complex ATPase ISW1 OS=Saccharomyces cerevisiae GN=ISW	ISW1_YEAST
ISWI chromatin-remodeling complex ATPase ISW2 OS=Saccharomyces cerevisiae GN=ISW	ISW2_YEAST
ISWI one complex protein 3 OS=Saccharomyces cerevisiae GN=IOC3 PE=1 SV=1	IOC3_YEAST
ISWI one complex protein 4 OS=Saccharomyces cerevisiae GN=IOC4 PE=1 SV=1	IOC4_YEAST
J domain-containing protein APJ1 OS=Saccharomyces cerevisiae GN=APJ1 PE=1 SV=1	APJ1_YEAST
Karyogamy protein KAR4 OS=Saccharomyces cerevisiae GN=KAR4 PE=1 SV=1	KAR4_YEAST
Kelch repeat-containing protein 1 OS=Saccharomyces cerevisiae GN=KEL1 PE=1 SV=1	KEL1_YEAST
Ketol-acid reductoisomerase, mitochondrial OS=Saccharomyces cerevisiae GN=ILV5 PE=1 S	ILV5_YEAST
KH domain-containing protein YBL032W OS=Saccharomyces cerevisiae GN=YBL032W PE=	YBD2_YEAST
KH domain-containing protein YLL032C OS=Saccharomyces cerevisiae GN=YLL032C PE=1	YL032_YEAST
Killer toxin-resistance protein 5 OS=Saccharomyces cerevisiae GN=KRE5 PE=1 SV=2	KRE5_YEAST
Kinesin-like protein CIN8 OS=Saccharomyces cerevisiae GN=CIN8 PE=1 SV=3	CIN8_YEAST
Kinesin-like protein KAR3 OS=Saccharomyces cerevisiae GN=KAR3 PE=1 SV=1	KAR3_YEAST
Kinesin-like protein KIP2 OS=Saccharomyces cerevisiae GN=KIP2 PE=1 SV=1	KIP2_YEAST
Kinesin-related protein SMY1 OS=Saccharomyces cerevisiae GN=SMY1 PE=1 SV=1	SMY1_YEAST
Kinetochore protein NUF2 OS=Saccharomyces cerevisiae GN=NUF2 PE=1 SV=1	NUF2_YEAST
Kynureninase OS=Saccharomyces cerevisiae GN=BNA5 PE=1 SV=1	KYNU_YEAST
La protein homolog OS=Saccharomyces cerevisiae GN=LAH1 PE=1 SV=2	LAH1_YEAST
Lactoylglutathione lyase OS=Saccharomyces cerevisiae GN=GLO1 PE=1 SV=1	LGUL_YEAST
Laminarase-resistance protein LRE1 OS=Saccharomyces cerevisiae GN=LRE1 PE=1 SV=2	LRE1_YEAST

L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase OS=Saccha	LYS5_YEAST
Lanosterol 14-alpha demethylase OS=Saccharomyces cerevisiae GN=ERG11 PE=1 SV=1	CP51_YEAST
Large subunit GTPase 1 OS=Saccharomyces cerevisiae GN=LSG1 PE=1 SV=1	LSG1_YEAST
LAS seventeen-binding protein 1 OS=Saccharomyces cerevisiae GN=LSB1 PE=1 SV=1	LSB1_YEAST
LAS seventeen-binding protein 3 OS=Saccharomyces cerevisiae (strain YJM789) GN=LSB3	LSB3_YEAS7
L-asparaginase 1 OS=Saccharomyces cerevisiae GN=ASP1 PE=1 SV=1	ASPG1_YEAST
Leucine carboxyl methyltransferase 2 OS=Saccharomyces cerevisiae GN=PPM2 PE=1 SV=1	LCMT2_YEAST
Leucine-rich repeat-containing protein SOG2 OS=Saccharomyces cerevisiae GN=SOG2 PE=	SOG2_YEAST
Leucyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=CDC60 PE=1 SV=	SYLC_YEAST
LIM domain and RING finger protein YDR266C OS=Saccharomyces cerevisiae GN=YDR266	YD266_YEAST
Lipase 3 OS=Saccharomyces cerevisiae GN=TGL3 PE=1 SV=2	TGL3_YEAST
Lipase 5 OS=Saccharomyces cerevisiae GN=TGL5 PE=1 SV=1	TGL5_YEAST
Lipoyl synthase, mitochondrial OS=Saccharomyces cerevisiae GN=LIP5 PE=1 SV=1	LIP5_YEAST
Long-chain-fatty-acid--CoA ligase 1 OS=Saccharomyces cerevisiae GN=FAA1 PE=1 SV=1	LCF1_YEAST
Long-chain-fatty-acid--CoA ligase 3 OS=Saccharomyces cerevisiae GN=FAA3 PE=1 SV=1	LCF3_YEAST
Long-chain-fatty-acid--CoA ligase 4 OS=Saccharomyces cerevisiae GN=FAA4 PE=1 SV=1	LCF4_YEAST
Low molecular weight phosphotyrosine protein phosphatase OS=Saccharomyces cerevisiae	PPAL_YEAST
Low specificity L-threonine aldolase OS=Saccharomyces cerevisiae GN=GLY1 PE=1 SV=1	GLY1_YEAST
Low-affinity glucose transporter HXT1 OS=Saccharomyces cerevisiae GN=HXT1 PE=1 SV=1	HXT1_YEAST
Low-affinity glucose transporter HXT3 OS=Saccharomyces cerevisiae GN=HXT3 PE=1 SV=1	HXT3_YEAST
Lysophospholipase 1 OS=Saccharomyces cerevisiae GN=PLB1 PE=1 SV=2	PLB1_YEAST
Lysophospholipase NTE1 OS=Saccharomyces cerevisiae GN=NTE1 PE=1 SV=1	NTE1_YEAST
Lysyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=KRS1 PE=1 SV=2	SYKC_YEAST
Lysyl-tRNA synthetase, mitochondrial OS=Saccharomyces cerevisiae GN=MSK1 PE=1 SV=3	SYKM_YEAST
Maf-like protein YOR111W OS=Saccharomyces cerevisiae GN=YOR111W PE=1 SV=1	YO111_YEAST
Magnesium transporter ALR1 OS=Saccharomyces cerevisiae GN=ALR1 PE=1 SV=1	ALR1_YEAST
Magnesium transporter ALR2 OS=Saccharomyces cerevisiae GN=ALR2 PE=1 SV=1	ALR2_YEAST
Magnesium-activated aldehyde dehydrogenase, cytosolic OS=Saccharomyces cerevisiae GN	ALDH6_YEAST
Malate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae GN=MDH1 PE=1 SV=2	MDHM_YEAST
Malate dehydrogenase, peroxisomal OS=Saccharomyces cerevisiae GN=MDH3 PE=1 SV=3	MDHP_YEAST
Malate synthase 1, glyoxysomal OS=Saccharomyces cerevisiae GN=MLS1 PE=1 SV=1	MASY_YEAST
Malonyl CoA-acyl carrier protein transacylase, mitochondrial OS=Saccharomyces cerevisiae	FABD_YEAST
Manganese resistance protein MNR2 OS=Saccharomyces cerevisiae GN=MNR2 PE=1 SV=1	MNR2_YEAST
Mannan endo-1,6-alpha-mannosidase DCW1 OS=Saccharomyces cerevisiae GN=DCW1 PE	DCW1_YEAST
Mannan polymerase complexes subunit MNN9 OS=Saccharomyces cerevisiae GN=MNN9 PE	MNN9_YEAST
Mannan polymerase I complex VAN1 subunit OS=Saccharomyces cerevisiae GN=VAN1 PE=	VAN1_YEAST
Mannose-1-phosphate guanyltransferase OS=Saccharomyces cerevisiae GN=MPG1 PE=1 S	MPG1_YEAST
Mannose-6-phosphate isomerase OS=Saccharomyces cerevisiae GN=PMI40 PE=1 SV=4	MPI_YEAST
MAP kinase kinase MKK2/SSP33 OS=Saccharomyces cerevisiae GN=MKK2 PE=1 SV=2	MKK2_YEAST
MAP kinase kinase PBS2 OS=Saccharomyces cerevisiae GN=PBS2 PE=1 SV=3	PBS2_YEAST
MAP-homologous protein 1 OS=Saccharomyces cerevisiae GN=MHP1 PE=1 SV=1	MHP1_YEAST
Mating-type protein A1 OS=Saccharomyces cerevisiae GN=MATA1 PE=1 SV=1	MATA1_YEAST
Mediator of replication checkpoint protein 1 OS=Saccharomyces cerevisiae GN=MRC1 PE=1	MRC1_YEAST
Mediator of RNA polymerase II transcription subunit 11 OS=Saccharomyces cerevisiae GN=	MED11_YEAST
Mediator of RNA polymerase II transcription subunit 15 OS=Saccharomyces cerevisiae GN=	MED15_YEAST
Mediator of RNA polymerase II transcription subunit 20 OS=Saccharomyces cerevisiae GN=	MED20_YEAST
Mediator of RNA polymerase II transcription subunit 22 OS=Saccharomyces cerevisiae GN=	MED22_YEAST

Mediator of RNA polymerase II transcription subunit 5 OS=Saccharomyces cerevisiae GN=N	MED5_YEAST
Mediator of RNA polymerase II transcription subunit 8 OS=Saccharomyces cerevisiae GN=M	MED8_YEAST
Meiotic activator RIM4 OS=Saccharomyces cerevisiae GN=RIM4 PE=1 SV=1	RIM4_YEAST
Meiotic sister-chromatid recombination protein 3 OS=Saccharomyces cerevisiae GN=MSC3 I	MSC3_YEAST
Meiotic sister-chromatid recombination protein 6, mitochondrial OS=Saccharomyces cerevisi	MSC6_YEAST
Metacaspase-1 OS=Saccharomyces cerevisiae (strain YJM789) GN=MCA1 PE=3 SV=2	MCA1_YEAS7
Methionine aminopeptidase 1 OS=Saccharomyces cerevisiae GN=MAP1 PE=1 SV=2	AMPM1_YEAST
Methionine aminopeptidase 2 OS=Saccharomyces cerevisiae GN=MAP2 PE=1 SV=3	AMPM2_YEAST
Methionyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=MES1 PE=1 S\	SYMC_YEAST
Methyl methanesulfonate-sensitivity protein 1 OS=Saccharomyces cerevisiae GN=MMS1 PE	MMS1_YEAST
Methyltransferase-like protein YBR261C OS=Saccharomyces cerevisiae GN=YBR261C PE=	YB9H_YEAST
Midasin OS=Saccharomyces cerevisiae GN=MDN1 PE=1 SV=1	MDN1_YEAST
Minichromosome maintenance protein 10 OS=Saccharomyces cerevisiae GN=MCM10 PE=1	MCM10_YEAST
Minichromosome maintenance protein 5 OS=Saccharomyces cerevisiae GN=MCM5 PE=1 S\	MCM5_YEAST
Mitochondria fission 1 protein OS=Saccharomyces cerevisiae GN=FIS1 PE=1 SV=1	FIS1_YEAST
Mitochondrial 2-methylisocitrate lyase OS=Saccharomyces cerevisiae GN=ICL2 PE=1 SV=1	ACEB_YEAST
Mitochondrial 2-oxodicarboxylate carrier 2 OS=Saccharomyces cerevisiae GN=ODC2 PE=1 S	ODC2_YEAST
Mitochondrial acidic protein MAM33 OS=Saccharomyces cerevisiae GN=MAM33 PE=1 SV=1	MAM33_YEAST
Mitochondrial ATPase complex subunit ATP10 OS=Saccharomyces cerevisiae GN=ATP10 P	ATP10_YEAST
Mitochondrial carrier protein RIM2 OS=Saccharomyces cerevisiae GN=RIM2 PE=2 SV=1	RIM2_YEAST
Mitochondrial chaperone TCM62 OS=Saccharomyces cerevisiae GN=TCM62 PE=1 SV=2	TCM62_YEAST
Mitochondrial clpX-like chaperone MCX1 OS=Saccharomyces cerevisiae GN=MCX1 PE=1 S	MCX1_YEAST
Mitochondrial DNA base excision repair N-glycosylase 1 OS=Saccharomyces cerevisiae GN=	NTG1_YEAST
Mitochondrial DNA replication protein YHM2 OS=Saccharomyces cerevisiae GN=YHM2 PE=	YHM2_YEAST
Mitochondrial escape protein 2 OS=Saccharomyces cerevisiae (strain YJM789) GN=YME2 P	YME2_YEAS7
Mitochondrial FAD-linked sulfhydryl oxidase ERV1 OS=Saccharomyces cerevisiae GN=ERV	ERV1_YEAST
Mitochondrial genome maintenance protein MGM101 OS=Saccharomyces cerevisiae GN=M	MG101_YEAST
Mitochondrial GTPase 1 OS=Saccharomyces cerevisiae GN=MTG1 PE=1 SV=1	MTG1_YEAST
Mitochondrial import inner membrane translocase subunit TIM10 OS=Saccharomyces cerevis	TIM10_YEAST
Mitochondrial import inner membrane translocase subunit TIM14 OS=Saccharomyces cerevis	TIM14_YEAST
Mitochondrial import inner membrane translocase subunit TIM16 OS=Saccharomyces cerevis	TIM16_YEAST
Mitochondrial import inner membrane translocase subunit TIM21 OS=Saccharomyces cerevis	TIM21_YEAST
Mitochondrial import inner membrane translocase subunit TIM44 OS=Saccharomyces cerevis	TIM44_YEAST
Mitochondrial import receptor subunit TOM20 OS=Saccharomyces cerevisiae GN=TOM20 PI	TOM20_YEAST
Mitochondrial import receptor subunit TOM40 OS=Saccharomyces cerevisiae GN=TOM40 PI	TOM40_YEAST
Mitochondrial import receptor subunit TOM6 OS=Saccharomyces cerevisiae GN=TOM6 PE=	TOM6_YEAST
Mitochondrial import receptor subunit TOM70 OS=Saccharomyces cerevisiae (strain YJM78	TOM70_YEAS7
Mitochondrial intermediate peptidase OS=Saccharomyces cerevisiae GN=OCT1 PE=1 SV=2	PMIP_YEAST
Mitochondrial metal transporter 1 OS=Saccharomyces cerevisiae GN=MMT1 PE=1 SV=1	MMT1_YEAST
Mitochondrial nuclease OS=Saccharomyces cerevisiae GN=NUC1 PE=1 SV=1	NUC1_YEAST
Mitochondrial outer membrane protein IML2 OS=Saccharomyces cerevisiae (strain YJM789)	IML2_YEAS7
Mitochondrial outer membrane protein OM45 OS=Saccharomyces cerevisiae GN=OM45 PE=	OM45_YEAST
Mitochondrial outer membrane protein porin 1 OS=Saccharomyces cerevisiae GN=POR1 PE	VDAC1_YEAST
Mitochondrial outer membrane protein SCY_3392 OS=Saccharomyces cerevisiae (strain YJ	YKR18_YEAS7
Mitochondrial oxaloacetate transport protein OS=Saccharomyces cerevisiae GN=OAC1 PE=	OAC1_YEAST
Mitochondrial peculiar membrane protein 1 OS=Saccharomyces cerevisiae (strain YJM789) (	MPM1_YEAS7
Mitochondrial peroxiredoxin PRX1 OS=Saccharomyces cerevisiae GN=PRX1 PE=1 SV=1	PRX1_YEAST

Mitochondrial phosphate carrier protein OS=Saccharomyces cerevisiae GN=MIR1 PE=1 SV=	MPCP_YEAST
Mitochondrial protein FMP38 OS=Saccharomyces cerevisiae GN=FMP38 PE=1 SV=1	FMP38_YEAST
Mitochondrial protein import protein MAS5 OS=Saccharomyces cerevisiae GN=YDJ1 PE=1 S	MAS5_YEAST
Mitochondrial respiratory chain complexes assembly protein AFG3 OS=Saccharomyces cere	AFG3_YEAST
Mitochondrial respiratory chain complexes assembly protein RCA1 OS=Saccharomyces cere	RCA1_YEAST
Mitochondrial Rho GTPase 1 OS=Saccharomyces cerevisiae GN=GEM1 PE=1 SV=1	GEM1_YEAST
Mitochondrial-processing peptidase subunit alpha OS=Saccharomyces cerevisiae GN=MAS2	MPPA_YEAST
Mitochondrial-processing peptidase subunit beta OS=Saccharomyces cerevisiae GN=MAS1	MPPB_YEAST
Mitogen-activated protein kinase FUS3 OS=Saccharomyces cerevisiae GN=FUS3 PE=1 SV=	FUS3_YEAST
Mitogen-activated protein kinase HOG1 OS=Saccharomyces cerevisiae GN=HOG1 PE=1 SV	HOG1_YEAST
Mitogen-activated protein kinase KSS1 OS=Saccharomyces cerevisiae GN=KSS1 PE=1 SV=	KSS1_YEAST
Mitogen-activated protein kinase SLT2/MPK1 OS=Saccharomyces cerevisiae GN=SLT2 PE=	SLT2_YEAST
Monopolin complex subunit CSM1 OS=Saccharomyces cerevisiae GN=CSM1 PE=1 SV=1	CSM1_YEAST
Monothiol glutaredoxin-5, mitochondrial OS=Saccharomyces cerevisiae GN=GRX5 PE=1 SV	GLRX5_YEAST
Morphogenesis-related protein MSB1 OS=Saccharomyces cerevisiae GN=MSB1 PE=1 SV=1	MSB1_YEAST
mRNA 3'-end-processing protein RNA15 OS=Saccharomyces cerevisiae GN=RNA15 PE=1 S	RNA15_YEAST
mRNA 3'-end-processing protein YTH1 OS=Saccharomyces cerevisiae GN=YTH1 PE=1 SV=	YTH1_YEAST
mRNA decay factor CTH1 OS=Saccharomyces cerevisiae GN=CTH1 PE=1 SV=2	CTH1_YEAST
mRNA export factor MEX67 OS=Saccharomyces cerevisiae GN=MEX67 PE=1 SV=1	MEX67_YEAST
mRNA transport factor GFD1 OS=Saccharomyces cerevisiae GN=GFD1 PE=1 SV=1	GFD1_YEAST
mRNA transport regulator MTR2 OS=Saccharomyces cerevisiae GN=MTR2 PE=1 SV=1	MTR2_YEAST
mRNA turnover protein 4 OS=Saccharomyces cerevisiae GN=MRT4 PE=1 SV=1	MRT4_YEAST
mRNA-binding protein PUF2 OS=Saccharomyces cerevisiae GN=PUF2 PE=1 SV=1	PUF2_YEAST
mRNA-binding protein PUF3 OS=Saccharomyces cerevisiae GN=PUF3 PE=1 SV=1	PUF3_YEAST
mRNA-decapping enzyme subunit 1 OS=Saccharomyces cerevisiae GN=DCP1 PE=1 SV=1	DCP1_YEAST
mRNA-decapping enzyme subunit 2 OS=Saccharomyces cerevisiae (strain YJM789) GN=DC	DCP2_YEAS7
Multicopy enhancer of UAS2 OS=Saccharomyces cerevisiae GN=MEU1 PE=1 SV=1	MEU1_YEAST
Multifunctional methyltransferase subunit TRM112 OS=Saccharomyces cerevisiae GN=TRM	TR112_YEAST
Multiple RNA-binding domain-containing protein 1 OS=Saccharomyces cerevisiae GN=MRD	MRD1_YEAST
Multiprotein-bridging factor 1 OS=Saccharomyces cerevisiae GN=MBF1 PE=1 SV=2	MBF1_YEAST
Myosin light chain 1 OS=Saccharomyces cerevisiae GN=MLC1 PE=1 SV=1	MLC1_YEAST
Myosin tail region-interacting protein MTI1 OS=Saccharomyces cerevisiae GN=BBC1 PE=1 S	BBC1_YEAST
Myosin-1 OS=Saccharomyces cerevisiae GN=MYO1 PE=1 SV=3	MYO1_YEAST
Myosin-2 OS=Saccharomyces cerevisiae GN=MYO2 PE=1 SV=1	MYO2_YEAST
Myosin-3 OS=Saccharomyces cerevisiae GN=MYO3 PE=1 SV=3	MYO3_YEAST
Myosin-5 OS=Saccharomyces cerevisiae (strain YJM789) GN=MYO5 PE=3 SV=1	MYO5_YEAS7
N(2),N(2)-dimethylguanosine tRNA methyltransferase, mitochondrial OS=Saccharomyces cei	TRM1_YEAST
N-(5'-phosphoribosyl)anthranilate isomerase OS=Saccharomyces cerevisiae GN=TRP1 PE=	TRPF_YEAST
N(6)-adenine-specific DNA methyltransferase-like 1 OS=Saccharomyces cerevisiae GN=AMI	AML1_YEAST
Na(+)/H(+) antiporter OS=Saccharomyces cerevisiae GN=NHA1 PE=1 SV=1	NAH1_YEAST
N-acetyltransferase HPA3 OS=Saccharomyces cerevisiae GN=HPA3 PE=1 SV=1	HPA3_YEAST
NAD-dependent deacetylase HST2 OS=Saccharomyces cerevisiae GN=HST2 PE=1 SV=1	HST2_YEAST
NAD-dependent histone deacetylase SIR2 OS=Saccharomyces cerevisiae GN=SIR2 PE=1 S	SIR2_YEAST
NAD-dependent malic enzyme, mitochondrial OS=Saccharomyces cerevisiae GN=MAE1 PE=	MAOM_YEAST
NADH pyrophosphatase OS=Saccharomyces cerevisiae GN=NPY1 PE=1 SV=1	NPY1_YEAST
NADH-cytochrome b5 reductase 1 OS=Saccharomyces cerevisiae (strain YJM789) GN=CBR	NCB5R_YEAS7
NADH-cytochrome b5 reductase 1 OS=Saccharomyces cerevisiae GN=CBR1 PE=1 SV=2	NCB5R_YEAST

NADH-cytochrome b5 reductase 2 OS=Saccharomyces cerevisiae (strain YJM789) GN=MCR	MCR1_YEAS7
NADP-dependent alcohol dehydrogenase 6 OS=Saccharomyces cerevisiae GN=ADH6 PE=1	ADH6_YEAST
NADPH dehydrogenase 2 OS=Saccharomyces cerevisiae GN=OYE2 PE=1 SV=3	OYE2_YEAST
NADPH dehydrogenase 3 OS=Saccharomyces cerevisiae GN=OYE3 PE=1 SV=2	OYE3_YEAST
NADPH--cytochrome P450 reductase OS=Saccharomyces cerevisiae GN=NCP1 PE=1 SV=3	NCPR_YEAST
NADPH-dependent aldose reductase GRE3 OS=Saccharomyces cerevisiae GN=GRE3 PE=1	GRE3_YEAST
NADPH-dependent alpha-keto amide reductase OS=Saccharomyces cerevisiae GN=YDL124	KAR_YEAST
NADPH-dependent methylglyoxal reductase GRE2 OS=Saccharomyces cerevisiae GN=GRE	GRE2_YEAST
NADP-specific glutamate dehydrogenase 1 OS=Saccharomyces cerevisiae GN=GDH1 PE=1	DHE4_YEAST
NADP-specific glutamate dehydrogenase 2 OS=Saccharomyces cerevisiae GN=GDH3 PE=1	DHE5_YEAST
NAP1-binding protein OS=Saccharomyces cerevisiae GN=NBP1 PE=1 SV=1	NBP1_YEAST
Nascent polypeptide-associated complex subunit alpha OS=Saccharomyces cerevisiae GN=I	NACA_YEAST
Nascent polypeptide-associated complex subunit beta-1 OS=Saccharomyces cerevisiae (stra	NACB1_YEAS7
Negative RAS protein regulator protein OS=Saccharomyces cerevisiae GN=RPI1 PE=1 SV=2	RPI1_YEAST
Negative regulator of sporulation PMD1 OS=Saccharomyces cerevisiae GN=PMD1 PE=1 SV	PMD1_YEAST
NET1-associated nuclear protein 1 OS=Saccharomyces cerevisiae GN=NAN1 PE=1 SV=1	UTP17_YEAST
Neutral trehalase OS=Saccharomyces cerevisiae GN=NTH1 PE=1 SV=3	TREA_YEAST
NGG1-interacting factor 3 OS=Saccharomyces cerevisiae GN=NIF3 PE=1 SV=1	NIF3_YEAST
Nicotinamidase OS=Saccharomyces cerevisiae GN=PNC1 PE=1 SV=1	PNC1_YEAST
Nicotinamide riboside kinase OS=Saccharomyces cerevisiae GN=NRK1 PE=1 SV=1	NRK1_YEAST
Nicotinamide-nucleotide adenylyltransferase 1 OS=Saccharomyces cerevisiae GN=NMA1 PE	NMA1_YEAST
Nicotinate phosphoribosyltransferase OS=Saccharomyces cerevisiae GN=NPT1 PE=1 SV=3	NPT1_YEAST
Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Saccharomyces cerevisiae GN=	NADC_YEAST
NifU-like protein, mitochondrial OS=Saccharomyces cerevisiae GN=NFU1 PE=1 SV=2	NFU1_YEAST
Nitrogen permease reactivator protein OS=Saccharomyces cerevisiae GN=NPR1 PE=1 SV=2	NPR1_YEAST
Nitrosoguanidine resistance protein SNG1 OS=Saccharomyces cerevisiae GN=SNG1 PE=1 S	SNG1_YEAST
Non-classical export protein 1 OS=Saccharomyces cerevisiae GN=NCE101 PE=2 SV=1	NCE1_YEAST
Non-classical export protein 2 OS=Saccharomyces cerevisiae GN=NCE102 PE=1 SV=1	NCE2_YEAST
Non-histone chromosomal protein 6B OS=Saccharomyces cerevisiae GN=NHP6B PE=1 SV=	NHP6B_YEAST
Nonsense-mediated mRNA decay protein 3 OS=Saccharomyces cerevisiae GN=UPF3 PE=1	UPF3_YEAST
N-terminal acetyltransferase A complex catalytic subunit ARD1 OS=Saccharomyces cerevisia	ARD1_YEAST
N-terminal acetyltransferase A complex subunit NAT1 OS=Saccharomyces cerevisiae GN=N	NAT1_YEAST
N-terminal acetyltransferase B complex subunit MDM20 OS=Saccharomyces cerevisiae GN=	MDM20_YEAST
N-terminal acetyltransferase C complex catalytic subunit MAK3 OS=Saccharomyces cerevisia	MAK3_YEAST
Nuclear GTP-binding protein NUG1 OS=Saccharomyces cerevisiae GN=NUG1 PE=1 SV=1	NUG1_YEAST
Nuclear localization sequence-binding protein OS=Saccharomyces cerevisiae GN=NSR1 PE	NSR1_YEAST
Nuclear migration protein NUM1 OS=Saccharomyces cerevisiae GN=NUM1 PE=1 SV=2	NUM1_YEAST
Nuclear polyadenylated RNA-binding protein NAB2 OS=Saccharomyces cerevisiae GN=NAB	NAB2_YEAST
Nuclear protein SNF4 OS=Saccharomyces cerevisiae GN=SNF4 PE=1 SV=1	SNF4_YEAST
Nuclear protein STH1/NPS1 OS=Saccharomyces cerevisiae GN=STH1 PE=1 SV=1	STH1_YEAST
Nuclear segregation protein BFR1 OS=Saccharomyces cerevisiae GN=BFR1 PE=1 SV=1	BFR1_YEAST
Nuclear transport factor 2 OS=Saccharomyces cerevisiae GN=NTF2 PE=1 SV=2	NTF2_YEAST
Nucleolar complex protein 14 OS=Saccharomyces cerevisiae GN=NOP14 PE=1 SV=1	NOP14_YEAST
Nucleolar complex protein 2 OS=Saccharomyces cerevisiae GN=NOC2 PE=1 SV=2	NOC2_YEAST
Nucleolar complex protein 4 OS=Saccharomyces cerevisiae GN=NOC4 PE=1 SV=1	NOC4_YEAST
Nucleolar complex-associated protein 3 OS=Saccharomyces cerevisiae GN=NOC3 PE=1 SV	NOC3_YEAST
Nucleolar GTP-binding protein 1 OS=Saccharomyces cerevisiae GN=NOG1 PE=1 SV=1	NOG1_YEAST

Nucleolar GTP-binding protein 2 OS=Saccharomyces cerevisiae GN=NOG2 PE=1 SV=1	NOG2_YEAST
Nucleolar pre-ribosomal-associated protein 1 OS=Saccharomyces cerevisiae GN=URB1 PE=	URB1_YEAST
Nucleolar pre-ribosomal-associated protein 2 OS=Saccharomyces cerevisiae GN=URB2 PE=	URB2_YEAST
Nucleolar protein 12 OS=Saccharomyces cerevisiae GN=NOP12 PE=1 SV=1	NOP12_YEAST
Nucleolar protein 13 OS=Saccharomyces cerevisiae GN=NOP13 PE=1 SV=1	NOP13_YEAST
Nucleolar protein 3 OS=Saccharomyces cerevisiae GN=NPL3 PE=1 SV=1	NOP3_YEAST
Nucleolar protein 4 OS=Saccharomyces cerevisiae GN=NOP4 PE=1 SV=1	NOP4_YEAST
Nucleolar protein 56 OS=Saccharomyces cerevisiae GN=NOP56 PE=1 SV=1	NOP56_YEAST
Nucleolar protein 58 OS=Saccharomyces cerevisiae (strain YJM789) GN=NOP58 PE=3 SV=	NOP58_YEAS7
Nucleolar protein 6 OS=Saccharomyces cerevisiae GN=NOP6 PE=1 SV=1	NOP6_YEAST
Nucleolar protein NET1 OS=Saccharomyces cerevisiae GN=NET1 PE=1 SV=1	NET1_YEAST
Nucleoporin ASM4 OS=Saccharomyces cerevisiae GN=ASM4 PE=1 SV=1	NUP59_YEAST
Nucleoporin GLE2 OS=Saccharomyces cerevisiae GN=GLE2 PE=1 SV=1	GLE2_YEAST
Nucleoporin NDC1 OS=Saccharomyces cerevisiae GN=NDC1 PE=1 SV=1	NDC1_YEAST
Nucleoporin NIC96 OS=Saccharomyces cerevisiae GN=NIC96 PE=1 SV=2	NIC96_YEAST
Nucleoporin NSP1 OS=Saccharomyces cerevisiae GN=NSP1 PE=1 SV=1	NSP1_YEAST
Nucleoporin NUP100/NSP100 OS=Saccharomyces cerevisiae GN=NUP100 PE=1 SV=1	NU100_YEAST
Nucleoporin NUP116/NSP116 OS=Saccharomyces cerevisiae GN=NUP116 PE=1 SV=2	NU116_YEAST
Nucleoporin NUP133 OS=Saccharomyces cerevisiae GN=NUP133 PE=1 SV=1	NU133_YEAST
Nucleoporin NUP145 OS=Saccharomyces cerevisiae GN=NUP145 PE=1 SV=1	NU145_YEAST
Nucleoporin NUP157 OS=Saccharomyces cerevisiae GN=NUP157 PE=1 SV=1	NU157_YEAST
Nucleoporin NUP159 OS=Saccharomyces cerevisiae GN=NUP159 PE=1 SV=1	NU159_YEAST
Nucleoporin NUP170 OS=Saccharomyces cerevisiae GN=NUP170 PE=1 SV=1	NU170_YEAST
Nucleoporin NUP188 OS=Saccharomyces cerevisiae GN=NUP188 PE=1 SV=1	NU188_YEAST
Nucleoporin NUP192 OS=Saccharomyces cerevisiae GN=NUP192 PE=1 SV=1	NU192_YEAST
Nucleoporin NUP2 OS=Saccharomyces cerevisiae GN=NUP2 PE=1 SV=2	NUP2_YEAST
Nucleoporin NUP49/NSP49 OS=Saccharomyces cerevisiae GN=NUP49 PE=1 SV=1	NUP49_YEAST
Nucleoporin NUP57 OS=Saccharomyces cerevisiae GN=NUP57 PE=1 SV=1	NUP57_YEAST
Nucleoporin NUP60 OS=Saccharomyces cerevisiae GN=NUP60 PE=1 SV=1	NUP60_YEAST
Nucleoporin NUP82 OS=Saccharomyces cerevisiae GN=NUP82 PE=1 SV=2	NUP82_YEAST
Nucleoporin POM152 OS=Saccharomyces cerevisiae GN=POM152 PE=1 SV=1	PO152_YEAST
Nucleoporin POM34 OS=Saccharomyces cerevisiae GN=POM34 PE=1 SV=1	POM34_YEAST
Nucleoporin SEH1 OS=Saccharomyces cerevisiae GN=SEH1 PE=1 SV=1	SEH1_YEAST
Nucleoside diphosphate kinase OS=Saccharomyces cerevisiae GN=YNK1 PE=1 SV=1	NDK_YEAST
Nucleosome assembly protein OS=Saccharomyces cerevisiae GN=NAP1 PE=1 SV=2	NAP1_YEAST
Oligo-1,6-glucosidase OS=Saccharomyces cerevisiae GN=FSP2 PE=1 SV=1	MALX3_YEAST
Oligomycin resistance ATP-dependent permease YOR1 OS=Saccharomyces cerevisiae GN=	YOR1_YEAST
Oligoribonuclease, mitochondrial OS=Saccharomyces cerevisiae GN=REX2 PE=1 SV=1	ORN_YEAST
Ornithine aminotransferase OS=Saccharomyces cerevisiae GN=CAR2 PE=1 SV=2	OAT_YEAST
Osmotic growth protein 1 OS=Saccharomyces cerevisiae GN=OSM1 PE=1 SV=3	OSM1_YEAST
Oxysterol-binding protein homolog 2 OS=Saccharomyces cerevisiae GN=OSH2 PE=1 SV=1	OSH2_YEAST
Oxysterol-binding protein homolog 3 OS=Saccharomyces cerevisiae GN=OSH3 PE=1 SV=1	OSH3_YEAST
Oxysterol-binding protein homolog 6 OS=Saccharomyces cerevisiae GN=OSH6 PE=1 SV=1	OSH6_YEAST
PAB1-binding protein 1 OS=Saccharomyces cerevisiae GN=PBP1 PE=1 SV=1	PBP1_YEAST
PAB1-binding protein 2 OS=Saccharomyces cerevisiae GN=PBP2 PE=1 SV=1	PBP2_YEAST
PAB-dependent poly(A)-specific ribonuclease subunit PAN3 OS=Saccharomyces cerevisiae (	PAN3_YEAST
Partitioning protein REP1 OS=Saccharomyces cerevisiae GN=REP1 PE=1 SV=1	REP1_YEAST

Partitioning protein REP2 OS=Saccharomyces cerevisiae GN=REP2 PE=1 SV=1	REP2_YEAST
Pentafunctional AROM polypeptide OS=Saccharomyces cerevisiae GN=ARO1 PE=1 SV=1	ARO1_YEAST
Peptide methionine sulfoxide reductase OS=Saccharomyces cerevisiae GN=MXR1 PE=1 SV	MSRA_YEAST
Peptide transporter PTR2 OS=Saccharomyces cerevisiae GN=PTR2 PE=1 SV=2	PTR2_YEAST
Peptidyl-prolyl cis-trans isomerase CPR6 OS=Saccharomyces cerevisiae GN=CPR6 PE=1 S	PPID_YEAST
Peptidyl-prolyl cis-trans isomerase ESS1 OS=Saccharomyces cerevisiae GN=ESS1 PE=1 S	ESS1_YEAST
Peptidyl-prolyl cis-trans isomerase OS=Saccharomyces cerevisiae GN=CPR1 PE=1 SV=3	CYPH_YEAST
Peptidyl-tRNA hydrolase 2 OS=Saccharomyces cerevisiae GN=PTH2 PE=1 SV=1	PTH2_YEAST
Periodic tryptophan protein 1 OS=Saccharomyces cerevisiae GN=PWP1 PE=1 SV=1	PWP1_YEAST
Periodic tryptophan protein 2 OS=Saccharomyces cerevisiae GN=PWP2 PE=1 SV=2	PWP2_YEAST
Peroxiredoxin DOT5 OS=Saccharomyces cerevisiae GN=DOT5 PE=1 SV=1	DOT5_YEAST
Peroxiredoxin HYR1 OS=Saccharomyces cerevisiae GN=HYR1 PE=1 SV=1	GPX3_YEAST
Peroxiredoxin TSA1 OS=Saccharomyces cerevisiae GN=TSA1 PE=1 SV=3	TSA1_YEAST
Peroxiredoxin TSA2 OS=Saccharomyces cerevisiae GN=TSA2 PE=1 SV=3	TSA2_YEAST
Peroxiredoxin type-2 OS=Saccharomyces cerevisiae GN=AHP1 PE=1 SV=4	AHP1_YEAST
Peroxisomal 2,4-dienoyl-CoA reductase SPS19 OS=Saccharomyces cerevisiae GN=SPS19 I	SPS19_YEAST
Peroxisomal acyl-coenzyme A thioester hydrolase 1 OS=Saccharomyces cerevisiae GN=TES	PTE1_YEAST
Peroxisomal biogenesis factor 8 OS=Saccharomyces cerevisiae GN=PEX8 PE=1 SV=1	PEX8_YEAST
Peroxisomal hydratase-dehydrogenase-epimerase OS=Saccharomyces cerevisiae GN=FOX2	FOX2_YEAST
Peroxisomal membrane protein PEX17 OS=Saccharomyces cerevisiae GN=PEX17 PE=1 SV	PEX17_YEAST
Peroxisomal membrane protein PMP27 OS=Saccharomyces cerevisiae GN=PEX11 PE=1 SV	PEX11_YEAST
Peroxisomal targeting signal receptor OS=Saccharomyces cerevisiae GN=PEX5 PE=1 SV=1	PEX5_YEAST
Peroxisomal-coenzyme A synthetase OS=Saccharomyces cerevisiae GN=FAT2 PE=1 SV=1	FAT2_YEAST
Peroxisome proliferation transcriptional regulator OS=Saccharomyces cerevisiae GN=PIP2 P	PIP2_YEAST
Pescadillo homolog OS=Saccharomyces cerevisiae GN=NOP7 PE=1 SV=1	PESC_YEAST
Phenylacrylic acid decarboxylase OS=Saccharomyces cerevisiae GN=PAD1 PE=1 SV=2	PAD1_YEAST
Phenylalanyl-tRNA synthetase alpha chain OS=Saccharomyces cerevisiae GN=FRS2 PE=1	SYFA_YEAST
Phenylalanyl-tRNA synthetase beta chain OS=Saccharomyces cerevisiae GN=FRS1 PE=1 S	SYFB_YEAST
Pheromone alpha factor receptor OS=Saccharomyces cerevisiae GN=STE2 PE=1 SV=1	STE2_YEAST
Phosphate metabolism protein 7 OS=Saccharomyces cerevisiae GN=PHM7 PE=1 SV=1	PHM7_YEAST
Phosphatidylethanolamine N-methyltransferase OS=Saccharomyces cerevisiae GN=PEM1 P	PEM1_YEAST
Phosphatidylglycerol/phosphatidylinositol transfer protein OS=Saccharomyces cerevisiae GN	NPC2_YEAST
Phosphatidylinositol 3-kinase VPS34 OS=Saccharomyces cerevisiae GN=VPS34 PE=1 SV=1	VPS34_YEAST
Phosphatidylinositol 4,5-bisphosphate-binding protein SLM1 OS=Saccharomyces cerevisiae	SLM1_YEAST
Phosphatidylinositol 4,5-bisphosphate-binding protein SLM2 OS=Saccharomyces cerevisiae	SLM2_YEAST
Phosphatidylinositol 4-kinase PIK1 OS=Saccharomyces cerevisiae GN=PIK1 PE=1 SV=1	PIK1_YEAST
Phosphatidylinositol 4-kinase STT4 OS=Saccharomyces cerevisiae GN=STT4 PE=1 SV=1	STT4_YEAST
Phosphatidylinositol transfer protein CSR1 OS=Saccharomyces cerevisiae GN=CSR1 PE=1	CSR1_YEAST
Phosphatidylinositol transfer protein PDR16 OS=Saccharomyces cerevisiae GN=PDR16 PE=	PDR16_YEAST
Phosphatidylinositol transfer protein PDR17 OS=Saccharomyces cerevisiae GN=PDR17 PE=	PDR17_YEAST
Phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited OS=Saccharomyces	AROF_YEAST
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited OS=Saccharomyces cere	AROG_YEAST
Phosphoglucomutase YMR278W OS=Saccharomyces cerevisiae GN=YMR278W PE=1 SV=	PGM3_YEAST
Phosphoglucomutase-1 OS=Saccharomyces cerevisiae GN=PGM1 PE=1 SV=1	PGM1_YEAST
Phosphoglucomutase-2 OS=Saccharomyces cerevisiae GN=PGM2 PE=1 SV=1	PGM2_YEAST
Phosphoglycerate kinase OS=Saccharomyces cerevisiae GN=PGK1 PE=1 SV=2	PGK_YEAST
Phosphoglycerate mutase 1 OS=Saccharomyces cerevisiae GN=GPM1 PE=1 SV=3	PMG1_YEAST

Phosphoglycerate mutase 2 OS=Saccharomyces cerevisiae GN=GPM2 PE=1 SV=1	PMG2_YEAST
Phosphoinositide phosphatase SAC1 OS=Saccharomyces cerevisiae GN=SAC1 PE=1 SV=1	SAC1_YEAST
Phospholipase D1 OS=Saccharomyces cerevisiae GN=SPO14 PE=1 SV=3	SPO14_YEAST
Phosphomannomutase OS=Saccharomyces cerevisiae GN=SEC53 PE=1 SV=1	PMM_YEAST
Phosphoribosylaminoimidazole carboxylase OS=Saccharomyces cerevisiae GN=ADE2 PE=1	PUR6_YEAST
Phosphoribosylformylglycinamidine synthase OS=Saccharomyces cerevisiae GN=ADE6 PE=	PUR4_YEAST
pH-response regulator protein palA/RIM20 OS=Saccharomyces cerevisiae GN=RIM20 PE=1	PALA_YEAST
PKHD-type hydroxylase TPA1 OS=Saccharomyces cerevisiae GN=TPA1 PE=1 SV=1	TPA1_YEAST
Plasma membrane ATPase 1 OS=Saccharomyces cerevisiae GN=PMA1 PE=1 SV=2	PMA1_YEAST
Plasma membrane iron permease OS=Saccharomyces cerevisiae GN=FTR1 PE=1 SV=1	FTR1_YEAST
Pleiotropic ABC efflux transporter of multiple drugs OS=Saccharomyces cerevisiae GN=PDR	PDR5_YEAST
Polarity protein SNI1 OS=Saccharomyces cerevisiae GN=SNI1 PE=1 SV=1	SNI1_YEAST
Polarized growth chromatin-associated controller 1 OS=Saccharomyces cerevisiae GN=PCC	PCC1_YEAST
Poly(A) polymerase OS=Saccharomyces cerevisiae GN=PAP1 PE=1 SV=1	PAP_YEAST
Poly(A) ribonuclease POP2 OS=Saccharomyces cerevisiae GN=POP2 PE=1 SV=2	POP2_YEAST
Poly(A) RNA polymerase protein 2 OS=Saccharomyces cerevisiae GN=PAP2 PE=1 SV=1	PAP2_YEAST
Polyadenylate-binding protein, cytoplasmic and nuclear OS=Saccharomyces cerevisiae GN=	PABP_YEAST
Polyamine N-acetyltransferase 1 OS=Saccharomyces cerevisiae GN=PAA1 PE=1 SV=1	PAA1_YEAST
Polyamine oxidase FMS1 OS=Saccharomyces cerevisiae GN=FMS1 PE=1 SV=1	FMS1_YEAST
Polyamine transporter 1 OS=Saccharomyces cerevisiae GN=TPO1 PE=1 SV=1	TPO1_YEAST
Polyamine transporter 2 OS=Saccharomyces cerevisiae GN=TPO2 PE=1 SV=1	TPO2_YEAST
Polyamine transporter 3 OS=Saccharomyces cerevisiae GN=TPO3 PE=1 SV=1	TPO3_YEAST
Polyamine transporter 4 OS=Saccharomyces cerevisiae GN=TPO4 PE=1 SV=1	TPO4_YEAST
Polynucleotide 3'-phosphatase OS=Saccharomyces cerevisiae GN=TPP1 PE=2 SV=1	TPP1_YEAST
Porphobilinogen deaminase OS=Saccharomyces cerevisiae GN=HEM3 PE=1 SV=1	HEM3_YEAST
Potassium-activated aldehyde dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae	ALDH4_YEAST
Prefoldin subunit 3 OS=Saccharomyces cerevisiae GN=PAC10 PE=1 SV=1	PFD3_YEAST
Prefoldin subunit 4 OS=Saccharomyces cerevisiae GN=GIM3 PE=1 SV=1	PFD4_YEAST
Prefoldin subunit 5 OS=Saccharomyces cerevisiae GN=GIM5 PE=1 SV=1	PFD5_YEAST
Pre-mRNA leakage protein 1 OS=Saccharomyces cerevisiae GN=PML1 PE=1 SV=1	PML1_YEAST
Pre-mRNA leakage protein 39 OS=Saccharomyces cerevisiae GN=PML39 PE=1 SV=2	PML39_YEAST
Pre-mRNA-splicing factor 19 OS=Saccharomyces cerevisiae GN=PRP19 PE=1 SV=2	PRP19_YEAST
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 OS=Saccharomyces cerevis	PRP16_YEAST
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP22 OS=Saccharomyces cerevis	PRP22_YEAST
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43 OS=Saccharomyces cerevis	PRP43_YEAST
Pre-mRNA-splicing factor ATP-dependent RNA helicase-like protein PRP2 OS=Saccharomyc	PRP2_YEAST
Pre-mRNA-splicing factor ISY1 OS=Saccharomyces cerevisiae GN=ISY1 PE=1 SV=2	ISY1_YEAST
Pre-mRNA-splicing factor RDS3 OS=Saccharomyces cerevisiae GN=RDS3 PE=1 SV=1	RDS3_YEAST
Pre-mRNA-splicing factor URN1 OS=Saccharomyces cerevisiae GN=URN1 PE=1 SV=1	URN1_YEAST
Pre-rRNA-processing protein ESF1 OS=Saccharomyces cerevisiae GN=ESF1 PE=1 SV=1	ESF1_YEAST
Pre-rRNA-processing protein PNO1 OS=Saccharomyces cerevisiae GN=PNO1 PE=1 SV=1	PNO1_YEAST
Pre-rRNA-processing protein RIX1 OS=Saccharomyces cerevisiae (strain YJM789) GN=RIX1	RIX1_YEAS7
Probable (R,R)-butanediol dehydrogenase 2 OS=Saccharomyces cerevisiae GN=BDH2 PE=	BDH2_YEAST
Probable 1,3-beta-glucanosyltransferase GAS3 OS=Saccharomyces cerevisiae GN=GAS3 P	GAS3_YEAST
Probable 1-acyl-sn-glycerol-3-phosphate acyltransferase OS=Saccharomyces cerevisiae GN	PLSC_YEAST
Probable 26S proteasome regulatory subunit p27 OS=Saccharomyces cerevisiae GN=NAS2	PSMD9_YEAST
Probable 26S proteasome regulatory subunit p28 OS=Saccharomyces cerevisiae GN=NAS6	PSD10_YEAST

Probable 2-methylcitrate dehydratase OS=Saccharomyces cerevisiae GN=PDH1 PE=1 SV=1	PRPD_YEAST
Probable aconitate hydratase 2 OS=Saccharomyces cerevisiae GN=ACO2 PE=1 SV=1	ACON2_YEAST
Probable ADP-ribose 1''-phosphate phosphatase YML087W OS=Saccharomyces cerevisiae	YMX7_YEAST
Probable alanine aminotransferase OS=Saccharomyces cerevisiae GN=ALT2 PE=1 SV=1	ALAT_YEAST
Probable alanine aminotransferase, mitochondrial OS=Saccharomyces cerevisiae GN=ALT1	ALAM_YEAST
Probable alpha-1,6-mannosyltransferase MNN10 OS=Saccharomyces cerevisiae GN=MNN1	MNN10_YEAST
Probable alpha-1,6-mannosyltransferase MNN11 OS=Saccharomyces cerevisiae GN=MNN1	MNN11_YEAST
Probable ATP-dependent RNA helicase DHR1 OS=Saccharomyces cerevisiae GN=ECM16 F	DHR1_YEAST
Probable ATP-dependent RNA helicase DHR2 OS=Saccharomyces cerevisiae GN=DHR2 PE	DHR2_YEAST
Probable dipeptidyl peptidase 3 OS=Saccharomyces cerevisiae GN=YOL057W PE=1 SV=1	DPP3_YEAST
Probable DNA-binding protein SNT1 OS=Saccharomyces cerevisiae GN=SNT1 PE=1 SV=2	SNT1_YEAST
Probable electron transfer flavoprotein subunit alpha, mitochondrial OS=Saccharomyces cere	ETFA_YEAST
Probable electron transfer flavoprotein subunit beta OS=Saccharomyces cerevisiae GN=YGF	ETFB_YEAST
Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Sacch	ETFD_YEAST
Probable family 17 glucosidase SCW4 OS=Saccharomyces cerevisiae GN=SCW4 PE=1 SV=	SCW4_YEAST
Probable glycosidase CRH2 OS=Saccharomyces cerevisiae GN=UTR2 PE=1 SV=3	CRH2_YEAST
Probable histone deacetylase HOS2 OS=Saccharomyces cerevisiae GN=HOS2 PE=1 SV=1	HOS2_YEAST
Probable hydrolase NIT3 OS=Saccharomyces cerevisiae GN=NIT3 PE=1 SV=1	NIT3_YEAST
Probable inosine-5'-monophosphate dehydrogenase IMD3 OS=Saccharomyces cerevisiae G	IMDH3_YEAST
Probable inosine-5'-monophosphate dehydrogenase IMD4 OS=Saccharomyces cerevisiae G	IMDH4_YEAST
Probable mannosyltransferase ALG9 OS=Saccharomyces cerevisiae GN=ALG9 PE=1 SV=1	ALG9_YEAST
Probable mannosyltransferase KTR3 OS=Saccharomyces cerevisiae GN=KTR3 PE=1 SV=1	KTR3_YEAST
Probable metalloprotease ARX1 OS=Saccharomyces cerevisiae GN=ARX1 PE=1 SV=1	ARX1_YEAST
Probable mitochondrial transport protein FSF1 OS=Saccharomyces cerevisiae GN=FSF1 PE	FSF1_YEAST
Probable NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Saccharomyces cerevisiae	ADRO_YEAST
Probable phosphatidylinositol-4-phosphate 5-kinase MSS4 OS=Saccharomyces cerevisiae G	MSS4_YEAST
Probable phospholipid-transporting ATPase DNF1 OS=Saccharomyces cerevisiae GN=DNF	ATC5_YEAST
Probable phospholipid-transporting ATPase DNF2 OS=Saccharomyces cerevisiae GN=DNF	ATC4_YEAST
Probable prolyl-tRNA synthetase, mitochondrial OS=Saccharomyces cerevisiae GN=AIM10 F	SYPM_YEAST
Probable quinone oxidoreductase OS=Saccharomyces cerevisiae GN=ZTA1 PE=1 SV=1	QOR_YEAST
Probable serine/threonine-protein kinase HSL1 OS=Saccharomyces cerevisiae GN=HSL1 PE	HSL1_YEAST
Probable serine/threonine-protein kinase KKQ8 OS=Saccharomyces cerevisiae GN=KKQ8 P	KKQ8_YEAST
Probable serine/threonine-protein kinase YBR028C OS=Saccharomyces cerevisiae GN=YBF	KBN8_YEAST
Probable serine/threonine-protein kinase YDL025C OS=Saccharomyces cerevisiae GN=YDL	KD025_YEAST
Probable serine/threonine-protein kinase YNR047W OS=Saccharomyces cerevisiae GN=YN	KN8R_YEAST
Probable serine/threonine-protein kinase YOL045W OS=Saccharomyces cerevisiae GN=YOI	KOE5_YEAST
Probable serine/threonine-protein kinase YOL100W OS=Saccharomyces cerevisiae GN=YOI	KOK0_YEAST
Probable target of rapamycin complex 2 subunit BIT2 OS=Saccharomyces cerevisiae GN=BI	BIT2_YEAST
Probable transcription factor HMS1 OS=Saccharomyces cerevisiae GN=HMS1 PE=1 SV=1	HMS1_YEAST
Probable transcriptional regulatory protein STB4 OS=Saccharomyces cerevisiae GN=STB4 F	STB4_YEAST
Probable transporter AQR1 OS=Saccharomyces cerevisiae GN=AQR1 PE=1 SV=1	AQR1_YEAST
Prohibitin-1 OS=Saccharomyces cerevisiae GN=PHB1 PE=1 SV=2	PHB1_YEAST
Prohibitin-2 OS=Saccharomyces cerevisiae GN=PHB2 PE=1 SV=2	PHB2_YEAST
Proline-rich protein LAS17 OS=Saccharomyces cerevisiae GN=LAS17 PE=1 SV=1	LAS17_YEAST
Prospore formation at selected spindle poles protein 1 OS=Saccharomyces cerevisiae GN=P	ADY1_YEAST
Proteasome chaperone 1 OS=Saccharomyces cerevisiae GN=PBA1 PE=1 SV=2	POC1_YEAST
Proteasome chaperone 2 OS=Saccharomyces cerevisiae GN=ADD66 PE=1 SV=1	POC2_YEAST

Proteasome component C1 OS=Saccharomyces cerevisiae GN=PRE10 PE=1 SV=2	PSA3_YEAST
Proteasome component C11 OS=Saccharomyces cerevisiae GN=PRE1 PE=1 SV=2	PSB2_YEAST
Proteasome component C5 OS=Saccharomyces cerevisiae GN=PRE7 PE=1 SV=1	PSB1_YEAST
Proteasome component C7-alpha OS=Saccharomyces cerevisiae GN=SCL1 PE=1 SV=1	PSA6_YEAST
Proteasome component PRE2 OS=Saccharomyces cerevisiae GN=PRE2 PE=1 SV=3	PSB5_YEAST
Proteasome component PRE3 OS=Saccharomyces cerevisiae GN=PRE3 PE=1 SV=2	PSB6_YEAST
Proteasome component PRE4 OS=Saccharomyces cerevisiae GN=PRE4 PE=1 SV=1	PSB4_YEAST
Proteasome component PRE5 OS=Saccharomyces cerevisiae GN=PRE5 PE=1 SV=1	PSA1_YEAST
Proteasome component PRE6 OS=Saccharomyces cerevisiae GN=PRE6 PE=1 SV=1	PSA7_YEAST
Proteasome component PUP1 OS=Saccharomyces cerevisiae GN=PUP1 PE=1 SV=1	PSB7_YEAST
Proteasome component PUP2 OS=Saccharomyces cerevisiae GN=PUP2 PE=1 SV=2	PSA5_YEAST
Proteasome component PUP3 OS=Saccharomyces cerevisiae GN=PUP3 PE=1 SV=1	PSB3_YEAST
Proteasome component Y13 OS=Saccharomyces cerevisiae GN=PRE9 PE=1 SV=1	PSA4_YEAST
Proteasome component Y7 OS=Saccharomyces cerevisiae GN=PRE8 PE=1 SV=1	PSA2_YEAST
Proteasome-interacting protein CIC1 OS=Saccharomyces cerevisiae GN=CIC1 PE=1 SV=1	CIC1_YEAST
Protein AFR1 OS=Saccharomyces cerevisiae GN=AFR1 PE=1 SV=1	AFR1_YEAST
Protein AIM2 OS=Saccharomyces cerevisiae GN=AIM2 PE=1 SV=1	AIM2_YEAST
Protein AIR2 OS=Saccharomyces cerevisiae GN=AIR2 PE=1 SV=1	AIR2_YEAST
Protein APA1 OS=Saccharomyces cerevisiae GN=APA1 PE=1 SV=4	APA1_YEAST
Protein ARG5,6, mitochondrial OS=Saccharomyces cerevisiae GN=ARG5,6 PE=1 SV=1	ARG56_YEAST
Protein ASK10 OS=Saccharomyces cerevisiae GN=ASK10 PE=1 SV=2	ASK10_YEAST
Protein AST1 OS=Saccharomyces cerevisiae GN=AST1 PE=1 SV=2	AST1_YEAST
Protein AST2 OS=Saccharomyces cerevisiae GN=AST2 PE=1 SV=1	AST2_YEAST
Protein ATP11, mitochondrial OS=Saccharomyces cerevisiae GN=ATP11 PE=1 SV=1	ATP11_YEAST
Protein ATP13, mitochondrial OS=Saccharomyces cerevisiae GN=ATP13 PE=1 SV=3	ATP13_YEAST
Protein BCH2 OS=Saccharomyces cerevisiae GN=BCH2 PE=1 SV=1	BCH2_YEAST
Protein BCP1 OS=Saccharomyces cerevisiae GN=BCP1 PE=1 SV=1	BCP1_YEAST
Protein BFR2 OS=Saccharomyces cerevisiae GN=BFR2 PE=1 SV=1	BFR2_YEAST
Protein BIM1 OS=Saccharomyces cerevisiae GN=BIM1 PE=1 SV=1	BIM1_YEAST
Protein BMH1 OS=Saccharomyces cerevisiae GN=BMH1 PE=1 SV=4	BMH1_YEAST
Protein BMH2 OS=Saccharomyces cerevisiae GN=BMH2 PE=1 SV=3	BMH2_YEAST
Protein BNI1 OS=Saccharomyces cerevisiae GN=BNI1 PE=1 SV=2	BNI1_YEAST
Protein BOB1 OS=Saccharomyces cerevisiae GN=BOI1 PE=1 SV=1	BOB1_YEAST
Protein BOI2 OS=Saccharomyces cerevisiae GN=BOI2 PE=1 SV=1	BOI2_YEAST
Protein BSP1 OS=Saccharomyces cerevisiae GN=BSP1 PE=1 SV=1	BSP1_YEAST
Protein BTN2 OS=Saccharomyces cerevisiae GN=BTN2 PE=1 SV=1	BTN2_YEAST
Protein BUR2 OS=Saccharomyces cerevisiae GN=BUR2 PE=1 SV=1	BUR2_YEAST
Protein BZZ1 OS=Saccharomyces cerevisiae GN=BZZ1 PE=1 SV=1	BZZ1_YEAST
Protein CAF130 OS=Saccharomyces cerevisiae GN=CAF130 PE=1 SV=1	CF130_YEAST
Protein CAJ1 OS=Saccharomyces cerevisiae GN=CAJ1 PE=1 SV=1	CAJ1_YEAST
Protein CBP3, mitochondrial OS=Saccharomyces cerevisiae GN=CBP3 PE=1 SV=1	CBP3_YEAST
Protein CGI121 OS=Saccharomyces cerevisiae GN=CGI121 PE=1 SV=1	CG121_YEAST
Protein CMS1 OS=Saccharomyces cerevisiae GN=CMS1 PE=1 SV=1	CMS1_YEAST
Protein CSF1 OS=Saccharomyces cerevisiae GN=CSF1 PE=2 SV=1	CSF1_YEAST
Protein CWH43 OS=Saccharomyces cerevisiae GN=CWH43 PE=1 SV=2	CWH43_YEAST
Protein DCS2 OS=Saccharomyces cerevisiae GN=DCS2 PE=1 SV=3	DCS2_YEAST
Protein disulfide-isomerase MPD1 OS=Saccharomyces cerevisiae GN=MPD1 PE=1 SV=1	MPD1_YEAST

Protein dopey OS=Saccharomyces cerevisiae GN=DOP1 PE=1 SV=1	DOP1_YEAST
Protein DSE1 OS=Saccharomyces cerevisiae GN=DSE1 PE=1 SV=1	DSE1_YEAST
Protein EAP1 OS=Saccharomyces cerevisiae GN=EAP1 PE=1 SV=1	EAP1_YEAST
Protein EBS1 OS=Saccharomyces cerevisiae GN=EBS1 PE=1 SV=1	EBS1_YEAST
Protein ECM30 OS=Saccharomyces cerevisiae GN=ECM30 PE=1 SV=1	ECM30_YEAST
Protein EFR3 OS=Saccharomyces cerevisiae GN=EFR3 PE=1 SV=1	EFR3_YEAST
Protein FAF1 OS=Saccharomyces cerevisiae GN=FAF1 PE=1 SV=1	FAF1_YEAST
Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha OS=Saccharomy	FNTA_YEAST
Protein FMP27, mitochondrial OS=Saccharomyces cerevisiae GN=FMP27 PE=1 SV=1	FMP27_YEAST
Protein FMP52, mitochondrial OS=Saccharomyces cerevisiae GN=FMP52 PE=1 SV=1	FMP52_YEAST
Protein FYV10 OS=Saccharomyces cerevisiae GN=FYV10 PE=1 SV=1	FYV10_YEAST
Protein GCN20 OS=Saccharomyces cerevisiae GN=GCN20 PE=1 SV=1	GCN20_YEAST
Protein GCY OS=Saccharomyces cerevisiae GN=GCY1 PE=1 SV=1	GCY_YEAST
Protein GDS1 OS=Saccharomyces cerevisiae GN=GDS1 PE=1 SV=1	GDS1_YEAST
Protein GVP36 OS=Saccharomyces cerevisiae GN=GVP36 PE=1 SV=1	GVP36_YEAST
Protein HAM1 OS=Saccharomyces cerevisiae GN=HAM1 PE=1 SV=1	HAM1_YEAST
Protein HBT1 OS=Saccharomyces cerevisiae GN=HBT1 PE=1 SV=1	HBT1_YEAST
Protein HGH1 OS=Saccharomyces cerevisiae GN=HGH1 PE=1 SV=2	HGH1_YEAST
Protein HIR1 OS=Saccharomyces cerevisiae GN=HIR1 PE=1 SV=2	HIR1_YEAST
Protein HIR2 OS=Saccharomyces cerevisiae GN=HIR2 PE=1 SV=2	HIR2_YEAST
Protein HIT1 OS=Saccharomyces cerevisiae GN=HIT1 PE=1 SV=1	HIT1_YEAST
Protein HLJ1 OS=Saccharomyces cerevisiae GN=HLJ1 PE=1 SV=1	HLJ1_YEAST
Protein IGO2 OS=Saccharomyces cerevisiae GN=IGO2 PE=1 SV=3	IGO2_YEAST
Protein interacting with Hsp90 1 OS=Saccharomyces cerevisiae GN=PIH1 PE=1 SV=1	PIH1_YEAST
Protein ISD11 OS=Saccharomyces cerevisiae GN=ISD11 PE=1 SV=1	ISD11_YEAST
Protein IVY1 OS=Saccharomyces cerevisiae GN=IVY1 PE=1 SV=1	IVY1_YEAST
Protein KES1 OS=Saccharomyces cerevisiae GN=KES1 PE=1 SV=1	KES1_YEAST
Protein kinase C-like 1 OS=Saccharomyces cerevisiae GN=PKC1 PE=1 SV=2	KPC1_YEAST
Protein kinase MCK1 OS=Saccharomyces cerevisiae GN=MCK1 PE=1 SV=1	MCK1_YEAST
Protein kinase-like protein SCY1 OS=Saccharomyces cerevisiae GN=SCY1 PE=1 SV=1	SCY1_YEAST
Protein KRI1 OS=Saccharomyces cerevisiae GN=KRI1 PE=1 SV=1	KRI1_YEAST
Protein LDB16 OS=Saccharomyces cerevisiae GN=LDB16 PE=1 SV=2	LDB16_YEAST
Protein LDB19 OS=Saccharomyces cerevisiae GN=LDB19 PE=1 SV=1	LDB19_YEAST
Protein LSM12 OS=Saccharomyces cerevisiae GN=LSM12 PE=1 SV=1	LSM12_YEAST
Protein LTV1 OS=Saccharomyces cerevisiae GN=LTV1 PE=1 SV=2	LTV1_YEAST
Protein MAK11 OS=Saccharomyces cerevisiae GN=MAK11 PE=1 SV=1	MAK11_YEAST
Protein MAK16 OS=Saccharomyces cerevisiae GN=MAK16 PE=1 SV=1	MAK16_YEAST
Protein midA homolog OS=Saccharomyces cerevisiae GN=YKL162C PE=1 SV=1	MIDA_YEAST
Protein MKT1 OS=Saccharomyces cerevisiae GN=MKT1 PE=1 SV=2	MKT1_YEAST
Protein MLP1 OS=Saccharomyces cerevisiae GN=MLP1 PE=1 SV=2	MLP1_YEAST
Protein MLP2 OS=Saccharomyces cerevisiae GN=MLP2 PE=1 SV=1	MLP2_YEAST
Protein MMF1, mitochondrial OS=Saccharomyces cerevisiae GN=MMF1 PE=1 SV=1	MMF1_YEAST
Protein MON2 OS=Saccharomyces cerevisiae GN=MON2 PE=1 SV=1	MON2_YEAST
Protein MRH1 OS=Saccharomyces cerevisiae GN=MRH1 PE=1 SV=1	MRH1_YEAST
Protein MSF1 OS=Saccharomyces cerevisiae GN=AIM30 PE=1 SV=1	MSF1_YEAST
Protein MSO1 OS=Saccharomyces cerevisiae GN=MSO1 PE=1 SV=1	MSO1_YEAST
Protein MSS18 OS=Saccharomyces cerevisiae GN=MSS18 PE=1 SV=1	MSS18_YEAST

Protein MUK1 OS=Saccharomyces cerevisiae GN=MUK1 PE=1 SV=1	MUK1_YEAST
Protein NAM1, mitochondrial OS=Saccharomyces cerevisiae GN=NAM1 PE=1 SV=1	NAM1_YEAST
Protein NAM8 OS=Saccharomyces cerevisiae GN=NAM8 PE=1 SV=2	NAM8_YEAST
Protein NBA1 OS=Saccharomyces cerevisiae GN=NBA1 PE=1 SV=1	NBA1_YEAST
Protein NIP100 OS=Saccharomyces cerevisiae GN=NIP100 PE=1 SV=2	NIP80_YEAST
Protein NIP29 OS=Saccharomyces cerevisiae GN=NIP29 PE=1 SV=1	NIP29_YEAST
Protein NIS1 OS=Saccharomyces cerevisiae GN=NIS1 PE=1 SV=1	NIS1_YEAST
Protein NNF2 OS=Saccharomyces cerevisiae GN=NNF2 PE=1 SV=1	NNF2_YEAST
Protein NSG1 OS=Saccharomyces cerevisiae GN=NSG1 PE=1 SV=1	NSG1_YEAST
Protein N-terminal amidase OS=Saccharomyces cerevisiae GN=NTA1 PE=1 SV=1	NTA1_YEAST
Protein NUD1 OS=Saccharomyces cerevisiae GN=NUD1 PE=1 SV=2	NUD1_YEAST
Protein NUF1 OS=Saccharomyces cerevisiae GN=NUF1 PE=1 SV=1	NUF1_YEAST
Protein OCA4 OS=Saccharomyces cerevisiae GN=OCA4 PE=1 SV=1	OCA4_YEAST
Protein OPY1 OS=Saccharomyces cerevisiae GN=OPY1 PE=1 SV=1	OPY1_YEAST
Protein PAM1 OS=Saccharomyces cerevisiae GN=PAM1 PE=1 SV=2	PAM1_YEAST
Protein PAR32 OS=Saccharomyces cerevisiae GN=PAR32 PE=1 SV=1	PAR32_YEAST
Protein PBP4 OS=Saccharomyces cerevisiae GN=PBP4 PE=1 SV=1	PBP4_YEAST
Protein PCF11 OS=Saccharomyces cerevisiae GN=PCF11 PE=1 SV=2	PCF11_YEAST
Protein PDC2 OS=Saccharomyces cerevisiae GN=PDC2 PE=1 SV=1	PDC2_YEAST
Protein PET54 OS=Saccharomyces cerevisiae GN=PET54 PE=1 SV=1	PET54_YEAST
Protein phosphatase 1 regulatory subunit SDS22 OS=Saccharomyces cerevisiae GN=SDS22	SDS22_YEAST
Protein phosphatase 2C homolog 1 OS=Saccharomyces cerevisiae GN=PTC1 PE=1 SV=1	PP2C1_YEAST
Protein phosphatase 2C homolog 2 OS=Saccharomyces cerevisiae GN=PTC2 PE=1 SV=1	PP2C2_YEAST
Protein phosphatase PP2A regulatory subunit B OS=Saccharomyces cerevisiae GN=CDC55	2ABA_YEAST
Protein PSP2 OS=Saccharomyces cerevisiae GN=PSP2 PE=1 SV=2	PSP2_YEAST
Protein PXR1 OS=Saccharomyces cerevisiae (strain YJM789) GN=PXR1 PE=3 SV=1	PXR1_YEAS7
Protein PXR1 OS=Saccharomyces cerevisiae GN=PXR1 PE=1 SV=1	PXR1_YEAST
Protein RFS1 OS=Saccharomyces cerevisiae GN=RFS1 PE=1 SV=1	RFS1_YEAST
Protein ROD1 OS=Saccharomyces cerevisiae GN=ROD1 PE=1 SV=1	ROD1_YEAST
Protein SCD6 OS=Saccharomyces cerevisiae GN=SCD6 PE=1 SV=1	SCD6_YEAST
Protein SCP160 OS=Saccharomyces cerevisiae GN=SCP160 PE=1 SV=3	SC160_YEAST
Protein SDA1 OS=Saccharomyces cerevisiae GN=SDA1 PE=1 SV=1	SDA1_YEAST
Protein SDS23 OS=Saccharomyces cerevisiae (strain YJM789) GN=SDS23 PE=3 SV=1	SDS23_YEAS7
Protein SDS23 OS=Saccharomyces cerevisiae GN=SDS23 PE=1 SV=1	SDS23_YEAST
Protein SFK1 OS=Saccharomyces cerevisiae GN=SFK1 PE=1 SV=1	SFK1_YEAST
Protein SIP3 OS=Saccharomyces cerevisiae GN=SIP3 PE=1 SV=1	SIP3_YEAST
Protein SIP5 OS=Saccharomyces cerevisiae GN=SIP5 PE=1 SV=1	SIP5_YEAST
Protein SIS1 OS=Saccharomyces cerevisiae GN=SIS1 PE=1 SV=1	SIS1_YEAST
Protein SKG3 OS=Saccharomyces cerevisiae GN=SKG3 PE=1 SV=1	SKG3_YEAST
Protein SKT5 OS=Saccharomyces cerevisiae GN=SKT5 PE=1 SV=1	SKT5_YEAST
Protein SLA2 OS=Saccharomyces cerevisiae GN=SLA2 PE=1 SV=3	SLA2_YEAST
Protein SLM4 OS=Saccharomyces cerevisiae GN=SLM4 PE=1 SV=1	SLM4_YEAST
Protein SNI2 OS=Saccharomyces cerevisiae GN=SNI2 PE=1 SV=1	SNI2_YEAST
Protein SNQ2 OS=Saccharomyces cerevisiae GN=SNQ2 PE=1 SV=2	SNQ2_YEAST
Protein SOF1 OS=Saccharomyces cerevisiae GN=SOF1 PE=1 SV=1	DCA13_YEAST
Protein SPA2 OS=Saccharomyces cerevisiae GN=SPA2 PE=1 SV=1	SPA2_YEAST
Protein SPT2 OS=Saccharomyces cerevisiae GN=SPT2 PE=1 SV=1	SPT2_YEAST

Protein SPT3 OS=Saccharomyces cerevisiae GN=SPT3 PE=1 SV=1	SPT3_YEAST
Protein SRN2 OS=Saccharomyces cerevisiae GN=SRN2 PE=1 SV=1	SRN2_YEAST
Protein SSD1 OS=Saccharomyces cerevisiae GN=SSD1 PE=1 SV=1	SSD1_YEAST
Protein SSO1 OS=Saccharomyces cerevisiae GN=SSO1 PE=1 SV=2	SSO1_YEAST
Protein SSO2 OS=Saccharomyces cerevisiae GN=SSO2 PE=1 SV=2	SSO2_YEAST
Protein SST2 OS=Saccharomyces cerevisiae GN=SST2 PE=1 SV=2	SST2_YEAST
Protein STB6 OS=Saccharomyces cerevisiae GN=STB6 PE=1 SV=1	STB6_YEAST
Protein SUR7 OS=Saccharomyces cerevisiae GN=SUR7 PE=1 SV=1	SUR7_YEAST
Protein TEX1 OS=Saccharomyces cerevisiae GN=TEX1 PE=1 SV=1	TEX1_YEAST
Protein THO1 OS=Saccharomyces cerevisiae GN=THO1 PE=1 SV=1	THO1_YEAST
Protein TIF31 OS=Saccharomyces cerevisiae GN=TIF31 PE=1 SV=1	TIF31_YEAST
Protein TMA23 OS=Saccharomyces cerevisiae GN=TMA23 PE=1 SV=2	TMA23_YEAST
Protein transport protein GOS1 OS=Saccharomyces cerevisiae GN=GOS1 PE=1 SV=1	GOS1_YEAST
Protein transport protein SEC1 OS=Saccharomyces cerevisiae GN=SEC1 PE=1 SV=1	SEC1_YEAST
Protein transport protein SEC13 OS=Saccharomyces cerevisiae GN=SEC13 PE=1 SV=1	SEC13_YEAST
Protein transport protein SEC23 OS=Saccharomyces cerevisiae GN=SEC23 PE=1 SV=1	SEC23_YEAST
Protein transport protein SEC24 OS=Saccharomyces cerevisiae GN=SEC24 PE=1 SV=1	SEC24_YEAST
Protein transport protein SEC31 OS=Saccharomyces cerevisiae GN=SEC31 PE=1 SV=2	SEC31_YEAST
Protein transport protein SSS1 OS=Saccharomyces cerevisiae GN=SSS1 PE=1 SV=2	SC61G_YEAST
Protein UPS1 OS=Saccharomyces cerevisiae GN=UPS1 PE=1 SV=1	UPS1_YEAST
Protein URA1 OS=Saccharomyces cerevisiae GN=URA2 PE=1 SV=4	PYR1_YEAST
Protein URE2 OS=Saccharomyces cerevisiae GN=URE2 PE=1 SV=1	URE2_YEAST
Protein VAB2 OS=Saccharomyces cerevisiae (strain YJM789) GN=VAB2 PE=3 SV=1	VAB2_YEAS7
Protein WHI3 OS=Saccharomyces cerevisiae GN=WHI3 PE=1 SV=1	WHI3_YEAST
Protein WHI4 OS=Saccharomyces cerevisiae GN=WHI4 PE=1 SV=1	WHI4_YEAST
Protein YGP1 OS=Saccharomyces cerevisiae GN=YGP1 PE=1 SV=2	YGP1_YEAST
Protein YOP1 OS=Saccharomyces cerevisiae GN=YOP1 PE=1 SV=3	YOP1_YEAST
Protein YRO2 OS=Saccharomyces cerevisiae GN=YRO2 PE=1 SV=1	YRO2_YEAST
Protein YSC84 OS=Saccharomyces cerevisiae GN=YSC84 PE=1 SV=2	YSC84_YEAST
Protein YSP1 OS=Saccharomyces cerevisiae GN=YSP1 PE=1 SV=1	YSP1_YEAST
Protein ZPS1 OS=Saccharomyces cerevisiae GN=ZPS1 PE=2 SV=1	ZPS1_YEAST
Protoplast secreted protein 2 OS=Saccharomyces cerevisiae GN=PST2 PE=1 SV=1	PST2_YEAST
Protoporphyrinogen oxidase OS=Saccharomyces cerevisiae GN=HEM14 PE=1 SV=1	PPOX_YEAST
Pumilio domain-containing protein YJL010C OS=Saccharomyces cerevisiae GN=YJL010C P	YJB0_YEAST
Pumilio homology domain family member 6 OS=Saccharomyces cerevisiae GN=PUF6 PE=1	PUF6_YEAST
Purine nucleoside phosphorylase OS=Saccharomyces cerevisiae GN=PNP1 PE=1 SV=1	PNPH_YEAST
Putative 2-hydroxyacid dehydrogenase YNL274C OS=Saccharomyces cerevisiae GN=YNL2	YN14_YEAST
Putative 2-hydroxyacyl-CoA lyase OS=Saccharomyces cerevisiae GN=YEL020C PE=1 SV=1	YEC0_YEAST
Putative adenylate kinase FAP7 OS=Saccharomyces cerevisiae GN=FAP7 PE=1 SV=1	KAD6_YEAST
Putative aryl-alcohol dehydrogenase YPL088W OS=Saccharomyces cerevisiae GN=YPL088	YP088_YEAST
Putative ATP-dependent helicase IRC3 OS=Saccharomyces cerevisiae GN=IRC3 PE=1 SV=	IRC3_YEAST
Putative ATP-dependent RNA helicase ECM32 OS=Saccharomyces cerevisiae GN=ECM32 I	ECM32_YEAST
Putative ATP-dependent RNA helicase YLR419W OS=Saccharomyces cerevisiae GN=YLR4	YL419_YEAST
Putative carboxymethylenebutenolidase OS=Saccharomyces cerevisiae GN=YDL086W PE=:	DLHH_YEAST
Putative cystathionine gamma-synthase YML082W OS=Saccharomyces cerevisiae GN=YML	METX_YEAST
Putative cysteine synthase OS=Saccharomyces cerevisiae GN=YGR012W PE=1 SV=1	CYSK_YEAST
Putative DNA helicase INO80 OS=Saccharomyces cerevisiae (strain YJM789) GN=INO80 PE	INO80_YEAS7

Putative DNA helicase INO80 OS=Saccharomyces cerevisiae GN=INO80 PE=1 SV=1	INO80_YEAST
Putative elongation factor 1 gamma homolog OS=Saccharomyces cerevisiae GN=YGR201C	YG4D_YEAST
Putative fatty aldehyde dehydrogenase HFD1 OS=Saccharomyces cerevisiae GN=HFD1 PE=	HFD1_YEAST
Putative flavin carrier protein 3 OS=Saccharomyces cerevisiae GN=FLC3 PE=1 SV=1	FLC3_YEAST
Putative glucokinase-2 OS=Saccharomyces cerevisiae GN=EMI2 PE=1 SV=1	EMI2_YEAST
Putative glutamine amidotransferase YLR126C OS=Saccharomyces cerevisiae GN=YLR126(	YL126_YEAST
Putative glycosyltransferase HOC1 OS=Saccharomyces cerevisiae GN=HOC1 PE=1 SV=3	HOC1_YEAST
Putative GTP-binding protein YLF2 OS=Saccharomyces cerevisiae GN=YLF2 PE=1 SV=1	YLF2_YEAST
Putative magnesium-dependent phosphatase YER134C OS=Saccharomyces cerevisiae GN=	MGDP1_YEAST
Putative mitochondrial carrier protein YHM1/SHM1 OS=Saccharomyces cerevisiae GN=YHM	YHM1_YEAST
Putative mitochondrial translation system component PET127 OS=Saccharomyces cerevisiae	PT127_YEAST
Putative phosphoglycerate mutase DET1 OS=Saccharomyces cerevisiae GN=DET1 PE=1 S\	DET1_YEAST
Putative prolyl-tRNA synthetase YHR020W OS=Saccharomyces cerevisiae GN=YHR020W F	YHI0_YEAST
Putative protease AXL1 OS=Saccharomyces cerevisiae GN=AXL1 PE=1 SV=1	AXL1_YEAST
Putative pterin-4-alpha-carbinolamine dehydratase OS=Saccharomyces cerevisiae GN=YHL(	PHS_YEAST
Putative pyridoxal kinase BUD16 OS=Saccharomyces cerevisiae GN=BUD16 PE=1 SV=1	BUD16_YEAST
Putative pyridoxal reductase OS=Saccharomyces cerevisiae GN=YPR127W PE=1 SV=1	PLR1_YEAST
Putative redox protein FMP46, mitochondrial OS=Saccharomyces cerevisiae GN=FMP46 PE	FMP46_YEAST
Putative reductase 1 OS=Saccharomyces cerevisiae GN=YPR1 PE=1 SV=1	YPR1_YEAST
Putative ribonuclease YLR143W OS=Saccharomyces cerevisiae GN=YLR143W PE=1 SV=1	YL143_YEAST
Putative ribosomal RNA methyltransferase Nop2 OS=Saccharomyces cerevisiae GN=NOP2 I	NOP2_YEAST
Putative thiamine transporter YOR071C OS=Saccharomyces cerevisiae GN=YOR071C PE=1	THIX_YEAST
Putative thiosulfate sulfurtransferase OS=Saccharomyces cerevisiae GN=YOR251C PE=1 S\	THTR_YEAST
Putative transcription factor SEF1 OS=Saccharomyces cerevisiae GN=SEF1 PE=1 SV=4	SEF1_YEAST
Putative uncharacterized hydrolase YKL033W-A OS=Saccharomyces cerevisiae GN=YKL03:	YKD3A_YEAST
Putative uncharacterized hydrolase YOR131C OS=Saccharomyces cerevisiae GN=YOR131(	YOR31_YEAST
Putative uncharacterized oxidoreductase YGL039W OS=Saccharomyces cerevisiae GN=YGI	YGD9_YEAST
Putative uncharacterized oxidoreductase YGL157W OS=Saccharomyces cerevisiae GN=YGI	YGP7_YEAST
Putative uncharacterized protein API2 OS=Saccharomyces cerevisiae GN=API2 PE=5 SV=1	API2_YEAST
Putative uncharacterized protein YCL042W OS=Saccharomyces cerevisiae GN=YCL042W F	YCE2_YEAST
Putative uncharacterized protein YGR137W OS=Saccharomyces cerevisiae GN=YGR137W	YG3E_YEAST
Putative uncharacterized protein YIR020W-A OS=Saccharomyces cerevisiae GN=YIR020W-	YI20A_YEAST
Putative uncharacterized protein YOR318C OS=Saccharomyces cerevisiae GN=YOR318C P	YO318_YEAST
Putative uridine kinase YDR020C OS=Saccharomyces cerevisiae GN=YDR020C PE=1 SV=1	YD020_YEAST
Putative Xaa-Pro aminopeptidase OS=Saccharomyces cerevisiae GN=YLL029W PE=1 SV=1	XPP_YEAST
Putative zinc metalloproteinase YIL108W OS=Saccharomyces cerevisiae GN=YIL108W PE=	YIK8_YEAST
PWWP domain-containing protein YLR455W OS=Saccharomyces cerevisiae GN=YLR455W	YL455_YEAST
Pyridoxamine 5'-phosphate oxidase OS=Saccharomyces cerevisiae GN=PDX3 PE=1 SV=1	PDX3_YEAST
Pyrroline-5-carboxylate reductase OS=Saccharomyces cerevisiae GN=PRO3 PE=1 SV=1	P5CR_YEAST
Pyruvate carboxylase 1 OS=Saccharomyces cerevisiae GN=PYC1 PE=1 SV=2	PYC1_YEAST
Pyruvate decarboxylase isozyme 1 OS=Saccharomyces cerevisiae GN=PDC1 PE=1 SV=7	PDC1_YEAST
Pyruvate decarboxylase isozyme 3 OS=Saccharomyces cerevisiae GN=PDC6 PE=1 SV=3	PDC6_YEAST
Pyruvate dehydrogenase complex protein X component, mitochondrial OS=Saccharomyces c	ODPX_YEAST
Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=Saccharomyces ce	ODPA_YEAST
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Saccharomyces cer	ODPB_YEAST
Pyruvate kinase 1 OS=Saccharomyces cerevisiae GN=PYK1 PE=1 SV=2	KPYK1_YEAST
Pyruvate kinase 2 OS=Saccharomyces cerevisiae GN=PYK2 PE=1 SV=1	KPYK2_YEAST

Quinidine resistance protein 2 OS=Saccharomyces cerevisiae GN=QDR2 PE=1 SV=1	QDR2_YEAST
Rab GDP-dissociation inhibitor OS=Saccharomyces cerevisiae GN=GDI1 PE=1 SV=1	GDI1_YEAST
Ran-specific GTPase-activating protein 1 OS=Saccharomyces cerevisiae GN=YRB1 PE=1 S'	YRB1_YEAST
Ras-like protein 2 OS=Saccharomyces cerevisiae GN=RAS2 PE=1 SV=4	RAS2_YEAST
Ras-related protein RSR1 OS=Saccharomyces cerevisiae GN=RSR1 PE=1 SV=1	RSR1_YEAST
RAT1-interacting protein OS=Saccharomyces cerevisiae GN=RAI1 PE=1 SV=3	DOM3Z_YEAST
RecQ-mediated genome instability protein 1 OS=Saccharomyces cerevisiae GN=RMI1 PE=1	RMI1_YEAST
Recyclin-1 OS=Saccharomyces cerevisiae GN=RCY1 PE=1 SV=4	RCY1_YEAST
Reduced viability upon starvation protein 161 OS=Saccharomyces cerevisiae GN=RVS161 P	RV161_YEAST
Reduced viability upon starvation protein 167 OS=Saccharomyces cerevisiae GN=RVS167 P	RV167_YEAST
Regulator of chromosome condensation OS=Saccharomyces cerevisiae GN=PRP20 PE=1 S'	RCC1_YEAST
Regulator of Ty1 transposition protein 103 OS=Saccharomyces cerevisiae GN=RTT103 PE=.	RT103_YEAST
Regulatory protein ADR1 OS=Saccharomyces cerevisiae GN=ADR1 PE=1 SV=2	ADR1_YEAST
Regulatory protein PHO2 OS=Saccharomyces cerevisiae GN=PHO2 PE=1 SV=1	PHO2_YEAST
Regulatory protein SIR3 OS=Saccharomyces cerevisiae GN=SIR3 PE=1 SV=6	SIR3_YEAST
Regulatory protein SIR4 OS=Saccharomyces cerevisiae GN=SIR4 PE=1 SV=1	SIR4_YEAST
Replication factor A protein 2 OS=Saccharomyces cerevisiae GN=RFA2 PE=1 SV=1	RFA2_YEAST
Replication factor A protein 3 OS=Saccharomyces cerevisiae GN=RFA3 PE=1 SV=1	RFA3_YEAST
Replication factor C subunit 1 OS=Saccharomyces cerevisiae GN=RFC1 PE=1 SV=1	RFC1_YEAST
Replication factor C subunit 2 OS=Saccharomyces cerevisiae GN=RFC2 PE=1 SV=1	RFC2_YEAST
Replication factor C subunit 3 OS=Saccharomyces cerevisiae GN=RFC3 PE=1 SV=1	RFC3_YEAST
Replication factor C subunit 4 OS=Saccharomyces cerevisiae GN=RFC4 PE=1 SV=1	RFC4_YEAST
Replication factor C subunit 5 OS=Saccharomyces cerevisiae GN=RFC5 PE=1 SV=1	RFC5_YEAST
Reticulon-like protein 1 OS=Saccharomyces cerevisiae GN=RTN1 PE=1 SV=1	RTN1_YEAST
Reticulon-like protein 2 OS=Saccharomyces cerevisiae GN=RTN2 PE=1 SV=1	RTN2_YEAST
RFX-like DNA-binding protein RFX1 OS=Saccharomyces cerevisiae GN=RFX1 PE=1 SV=2	RFX1_YEAST
Rheb-like protein RHB1 OS=Saccharomyces cerevisiae GN=RHB1 PE=1 SV=2	RHEB_YEAST
RHO GTPase-activating protein RGD1 OS=Saccharomyces cerevisiae GN=RGD1 PE=1 SV=	RGD1_YEAST
RHO1 GDP-GTP exchange protein 2 OS=Saccharomyces cerevisiae GN=ROM2 PE=1 SV=1	ROM2_YEAST
Rho-GTPase-activating protein LRG1 OS=Saccharomyces cerevisiae GN=LRG1 PE=1 SV=2	LRG1_YEAST
Rho-GTPase-activating protein RGD2 OS=Saccharomyces cerevisiae GN=RGD2 PE=1 SV=:	RGD2_YEAST
Ribonuclease 3 OS=Saccharomyces cerevisiae GN=RNT1 PE=1 SV=1	RNT1_YEAST
Ribonuclease MRP protein subunit RMP1 OS=Saccharomyces cerevisiae GN=	RMP1_YEAST
Ribonuclease P protein component, mitochondrial OS=Saccharomyces cerevisiae GN=RPM2	RPM2_YEAST
Ribonuclease P/MRP protein subunit RPP1 OS=Saccharomyces cerevisiae GN=RPP1 PE=1	RPP1_YEAST
Ribonuclease T2-like OS=Saccharomyces cerevisiae GN=RNY1 PE=1 SV=1	RNY1_YEAST
Ribonucleases P/MRP protein subunit POP8 OS=Saccharomyces cerevisiae GN=POP8 PE=	POP8_YEAST
Ribonucleoside-diphosphate reductase large chain 1 OS=Saccharomyces cerevisiae GN=RN	RIR1_YEAST
Ribonucleoside-diphosphate reductase small chain 1 OS=Saccharomyces cerevisiae GN=RN	RIR2_YEAST
Ribonucleoside-diphosphate reductase small chain 2 OS=Saccharomyces cerevisiae GN=RN	RIR4_YEAST
Ribonucleotide reductase inhibitor protein SML1 OS=Saccharomyces cerevisiae GN=SML1 F	SML1_YEAST
Ribose-phosphate pyrophosphokinase 1 OS=Saccharomyces cerevisiae GN=PRS1 PE=1 SV	KPR1_YEAST
Ribose-phosphate pyrophosphokinase 3 OS=Saccharomyces cerevisiae GN=PRS3 PE=1 SV	KPR3_YEAST
Ribose-phosphate pyrophosphokinase 5 OS=Saccharomyces cerevisiae GN=PRS5 PE=1 SV	KPR5_YEAST
Ribosomal N-lysine methyltransferase 1 OS=Saccharomyces cerevisiae GN=RKM1 PE=1 SV	RKM1_YEAST
Ribosomal N-lysine methyltransferase 3 OS=Saccharomyces cerevisiae GN=RKM3 PE=1 SV	RKM3_YEAST
Ribosomal protein VAR1, mitochondrial OS=Saccharomyces cerevisiae GN=VAR1 PE=1 SV=	RMAR_YEAST

Ribosomal RNA assembly protein KRR1 OS=Saccharomyces cerevisiae GN=KRR1 PE=1 SV	KRR1_YEAST
Ribosomal RNA-processing protein 1 OS=Saccharomyces cerevisiae GN=RRP1 PE=1 SV=2	RRP1_YEAST
Ribosomal RNA-processing protein 12 OS=Saccharomyces cerevisiae GN=RRP12 PE=1 SV	RRP12_YEAST
Ribosomal RNA-processing protein 15 OS=Saccharomyces cerevisiae GN=RRP15 PE=1 SV	RRP15_YEAST
Ribosomal RNA-processing protein 7 OS=Saccharomyces cerevisiae GN=RRP7 PE=1 SV=1	RRP7_YEAST
Ribosomal RNA-processing protein 8 OS=Saccharomyces cerevisiae GN=RRP8 PE=1 SV=2	RRP8_YEAST
Ribosomal RNA-processing protein 9 OS=Saccharomyces cerevisiae GN=RRP9 PE=1 SV=1	RRP9_YEAST
Ribosome assembly protein 3 OS=Saccharomyces cerevisiae GN=RSA3 PE=1 SV=1	RSA3_YEAST
Ribosome assembly protein RRB1 OS=Saccharomyces cerevisiae GN=RRB1 PE=1 SV=1	RRB1_YEAST
Ribosome assembly protein SQT1 OS=Saccharomyces cerevisiae GN=SQT1 PE=1 SV=2	SQT1_YEAST
Ribosome biogenesis ATPase RIX7 OS=Saccharomyces cerevisiae GN=RIX7 PE=1 SV=1	RIX7_YEAST
Ribosome biogenesis protein 15 OS=Saccharomyces cerevisiae GN=NOP15 PE=1 SV=1	NOP15_YEAST
Ribosome biogenesis protein ALB1 OS=Saccharomyces cerevisiae (strain YJM789) GN=ALE	ALB1_YEAS7
Ribosome biogenesis protein BMS1 OS=Saccharomyces cerevisiae GN=BMS1 PE=1 SV=1	BMS1_YEAST
Ribosome biogenesis protein BRX1 OS=Saccharomyces cerevisiae GN=BRX1 PE=1 SV=1	BRX1_YEAST
Ribosome biogenesis protein ENP2 OS=Saccharomyces cerevisiae GN=ENP2 PE=1 SV=1	NOL10_YEAST
Ribosome biogenesis protein ERB1 OS=Saccharomyces cerevisiae (strain YJM789) GN=ER	ERB1_YEAS7
Ribosome biogenesis protein MAK21 OS=Saccharomyces cerevisiae GN=MAK21 PE=1 SV=	MAK21_YEAST
Ribosome biogenesis protein NOP53 OS=Saccharomyces cerevisiae GN=NOP53 PE=1 SV=	NOP53_YEAST
Ribosome biogenesis protein NSA2 OS=Saccharomyces cerevisiae (strain YJM789) GN=NS.	NSA2_YEAS7
Ribosome biogenesis protein RLP24 OS=Saccharomyces cerevisiae GN=RLP24 PE=1 SV=1	RLP24_YEAST
Ribosome biogenesis protein RLP7 OS=Saccharomyces cerevisiae GN=RLP7 PE=1 SV=1	RLP7_YEAST
Ribosome biogenesis protein SLX9 OS=Saccharomyces cerevisiae GN=SLX9 PE=1 SV=1	SLX9_YEAST
Ribosome biogenesis protein SSF2 OS=Saccharomyces cerevisiae GN=SSF2 PE=1 SV=1	SSF2_YEAST
Ribosome biogenesis protein UTP30 OS=Saccharomyces cerevisiae GN=UTP30 PE=1 SV=1	RL1D1_YEAST
Ribosome biogenesis protein YTM1 OS=Saccharomyces cerevisiae (strain YJM789) GN=YTI	YTM1_YEAS7
Ribosome maturation protein SDO1 OS=Saccharomyces cerevisiae GN=SDO1 PE=1 SV=1	SDO1_YEAST
Ribosome production factor 1 OS=Saccharomyces cerevisiae GN=RPF1 PE=1 SV=1	RPF1_YEAST
Ribosome-associated complex subunit SSZ1 OS=Saccharomyces cerevisiae GN=SSZ1 PE=.	SSZ1_YEAST
Ribosome-recycling factor, mitochondrial OS=Saccharomyces cerevisiae GN=RRF1 PE=1 S	RRF1_YEAST
RING-box protein HRT1 OS=Saccharomyces cerevisiae GN=HRT1 PE=1 SV=1	RBX1_YEAST
RNA 3'-terminal phosphate cyclase-like protein OS=Saccharomyces cerevisiae GN=RCL1 PE	RCL1_YEAST
RNA annealing protein YRA1 OS=Saccharomyces cerevisiae GN=YRA1 PE=1 SV=2	YRA1_YEAST
RNA exonuclease 4 OS=Saccharomyces cerevisiae GN=REX4 PE=1 SV=1	REXO4_YEAST
RNA exonuclease NGL2 OS=Saccharomyces cerevisiae GN=NGL2 PE=1 SV=1	NGL2_YEAST
RNA polymerase II subunit A C-terminal domain phosphatase SSU72 OS=Saccharomyces ce	SSU72_YEAST
RNA polymerase II transcription factor B subunit 3 OS=Saccharomyces cerevisiae GN=TFB3	TFB3_YEAST
RNA-binding protein NAB6 OS=Saccharomyces cerevisiae GN=NAB6 PE=1 SV=1	NAB6_YEAST
RNA-binding protein SRO9 OS=Saccharomyces cerevisiae GN=SRO9 PE=1 SV=2	SRO9_YEAST
Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial OS=Saccharomyces (	NDI1_YEAST
rRNA 2'-O-methyltransferase fibrillarin OS=Saccharomyces cerevisiae GN=NOP1 PE=1 SV=	FBRL_YEAST
rRNA biogenesis protein RRP5 OS=Saccharomyces cerevisiae GN=RRP5 PE=1 SV=1	RRP5_YEAST
rRNA-processing protein EBP2 OS=Saccharomyces cerevisiae GN=EBP2 PE=1 SV=1	EBP2_YEAST
rRNA-processing protein FCF1 OS=Saccharomyces cerevisiae GN=FCF1 PE=1 SV=1	FCF1_YEAST
rRNA-processing protein FYV7 OS=Saccharomyces cerevisiae GN=FYV7 PE=1 SV=1	FYV7_YEAST
rRNA-processing protein UTP23 OS=Saccharomyces cerevisiae GN=UTP23 PE=1 SV=1	UTP23_YEAST
RuvB-like protein 1 OS=Saccharomyces cerevisiae GN=RVB1 PE=1 SV=1	RUVB1_YEAST

RuvB-like protein 2 OS=Saccharomyces cerevisiae GN=RVB2 PE=1 SV=1	RUVB2_YEAST
Saccharolysin OS=Saccharomyces cerevisiae GN=PRD1 PE=1 SV=1	PRTD_YEAST
Saccharopepsin OS=Saccharomyces cerevisiae GN=PEP4 PE=1 SV=1	CARP_YEAST
Saccharopine dehydrogenase [NAD+, L-lysine-forming] OS=Saccharomyces cerevisiae GN=	LYS1_YEAST
S-adenosylmethionine permease SAM3 OS=Saccharomyces cerevisiae GN=SAM3 PE=1 SV	SAM3_YEAST
S-adenosylmethionine synthetase 1 OS=Saccharomyces cerevisiae GN=SAM1 PE=1 SV=2	METK1_YEAST
SAGA-associated factor 29 OS=Saccharomyces cerevisiae GN=SGF29 PE=1 SV=2	SGF29_YEAST
Scavenger mRNA-decapping enzyme DcpS OS=Saccharomyces cerevisiae GN=DCS1 PE=1	DCPS_YEAST
SEC14 cytosolic factor OS=Saccharomyces cerevisiae GN=SEC14 PE=1 SV=3	SEC14_YEAST
SED5-binding protein 2 OS=Saccharomyces cerevisiae GN=SFB2 PE=1 SV=1	SFB2_YEAST
SED5-binding protein 3 OS=Saccharomyces cerevisiae GN=SFB3 PE=1 SV=1	SFB3_YEAST
Separin OS=Saccharomyces cerevisiae GN=ESP1 PE=1 SV=2	ESP1_YEAST
Serine hydrolase YJU3 OS=Saccharomyces cerevisiae GN=YJU3 PE=1 SV=1	YJU3_YEAST
Serine hydroxymethyltransferase, cytosolic OS=Saccharomyces cerevisiae GN=SHM2 PE=1	GLYC_YEAST
Serine hydroxymethyltransferase, mitochondrial OS=Saccharomyces cerevisiae GN=SHM1 F	GLYM_YEAST
Serine palmitoyltransferase 1 OS=Saccharomyces cerevisiae GN=LCB1 PE=1 SV=2	LCB1_YEAST
Serine/threonine protein kinase KIN1 OS=Saccharomyces cerevisiae GN=KIN1 PE=1 SV=3	KIN1_YEAST
Serine/threonine-protein kinase AKL1 OS=Saccharomyces cerevisiae GN=AKL1 PE=1 SV=1	AKL1_YEAST
Serine/threonine-protein kinase BCK1/SLK1/SSP31 OS=Saccharomyces cerevisiae GN=BCI	BCK1_YEAST
Serine/threonine-protein kinase BUR1 OS=Saccharomyces cerevisiae GN=SGV1 PE=1 SV=	BUR1_YEAST
Serine/threonine-protein kinase CBK1 OS=Saccharomyces cerevisiae GN=CBK1 PE=1 SV=	CBK1_YEAST
Serine/threonine-protein kinase CHK1 OS=Saccharomyces cerevisiae GN=CHK1 PE=1 SV=	CHK1_YEAST
Serine/threonine-protein kinase CLA4 OS=Saccharomyces cerevisiae GN=CLA4 PE=1 SV=1	CLA4_YEAST
Serine/threonine-protein kinase DBF20 OS=Saccharomyces cerevisiae GN=DBF20 PE=1 SV	DBF20_YEAST
Serine/threonine-protein kinase GCN2 OS=Saccharomyces cerevisiae GN=GCN2 PE=1 SV=	GCN2_YEAST
Serine/threonine-protein kinase GIN4 OS=Saccharomyces cerevisiae GN=GIN4 PE=1 SV=1	GIN4_YEAST
Serine/threonine-protein kinase HAL5 OS=Saccharomyces cerevisiae GN=HAL5 PE=1 SV=2	HAL5_YEAST
Serine/threonine-protein kinase HRK1 OS=Saccharomyces cerevisiae GN=HRK1 PE=1 SV=	HRK1_YEAST
Serine/threonine-protein kinase KIC1 OS=Saccharomyces cerevisiae GN=KIC1 PE=1 SV=1	KIC1_YEAST
Serine/threonine-protein kinase KIN2 OS=Saccharomyces cerevisiae GN=KIN2 PE=1 SV=3	KIN2_YEAST
Serine/threonine-protein kinase KIN4 OS=Saccharomyces cerevisiae GN=KIN4 PE=1 SV=1	KIN4_YEAST
Serine/threonine-protein kinase KSP1 OS=Saccharomyces cerevisiae GN=KSP1 PE=1 SV=1	KSP1_YEAST
Serine/threonine-protein kinase MEC1 OS=Saccharomyces cerevisiae GN=MEC1 PE=1 SV=	ATR_YEAST
Serine/threonine-protein kinase PKH1 OS=Saccharomyces cerevisiae GN=PKH1 PE=1 SV=	PKH1_YEAST
Serine/threonine-protein kinase PKH3 OS=Saccharomyces cerevisiae GN=PKH3 PE=1 SV=	PKH3_YEAST
Serine/threonine-protein kinase PTK2/STK2 OS=Saccharomyces cerevisiae GN=PTK2 PE=1	PTK2_YEAST
Serine/threonine-protein kinase RIO2 OS=Saccharomyces cerevisiae GN=RIO2 PE=1 SV=1	RIO2_YEAST
Serine/threonine-protein kinase SCH9 OS=Saccharomyces cerevisiae GN=SCH9 PE=1 SV=	SCH9_YEAST
Serine/threonine-protein kinase TOR1 OS=Saccharomyces cerevisiae GN=TOR1 PE=1 SV=	TOR1_YEAST
Serine/threonine-protein kinase TOR2 OS=Saccharomyces cerevisiae GN=TOR2 PE=1 SV=	TOR2_YEAST
Serine/threonine-protein kinase VPS15 OS=Saccharomyces cerevisiae GN=VPS15 PE=1 SV	VPS15_YEAST
Serine/threonine-protein kinase YPK1 OS=Saccharomyces cerevisiae GN=YPK1 PE=1 SV=2	YPK1_YEAST
Serine/threonine-protein phosphatase PP1-1 OS=Saccharomyces cerevisiae GN=SIT4 PE=1	PP11_YEAST
Serine/threonine-protein phosphatase PP1-2 OS=Saccharomyces cerevisiae GN=GLC7 PE=	PP12_YEAST
Serine/threonine-protein phosphatase PP2A-1 catalytic subunit OS=Saccharomyces cerevisi	PP2A1_YEAST
Serine/threonine-protein phosphatase PP2A-2 catalytic subunit OS=Saccharomyces cerevisi	PP2A2_YEAST
Serine/threonine-protein phosphatase PP-Z1 OS=Saccharomyces cerevisiae GN=PPZ1 PE=	PPZ1_YEAST

Serine-rich protein TYE7 OS=Saccharomyces cerevisiae GN=TYE7 PE=1 SV=1	TYE7_YEAST
Seryl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=SES1 PE=1 SV=2	SYSC_YEAST
Seventh homolog of septin 1 OS=Saccharomyces cerevisiae GN=SHS1 PE=1 SV=1	SHS1_YEAST
S-formylglutathione hydrolase OS=Saccharomyces cerevisiae GN=YJL068C PE=1 SV=1	SFGH_YEAST
Signal recognition particle receptor subunit alpha homolog OS=Saccharomyces cerevisiae G	SRPR_YEAST
Signal recognition particle subunit SRP54 OS=Saccharomyces cerevisiae GN=SRP54 PE=1	SRP54_YEAST
Signal recognition particle subunit SRP68 OS=Saccharomyces cerevisiae GN=SRP68 PE=1	SRP68_YEAST
Signal recognition particle subunit SRP72 OS=Saccharomyces cerevisiae GN=SRP72 PE=1	SRP72_YEAST
Single-strand telomeric DNA-binding protein GBP2 OS=Saccharomyces cerevisiae GN=GBP	GBP2_YEAST
Single-stranded DNA-binding protein RIM1, mitochondrial OS=Saccharomyces cerevisiae GN	RIM1_YEAST
Sister chromatid cohesion protein PDS5 OS=Saccharomyces cerevisiae GN=PDS5 PE=1 SV	PDS5_YEAST
Small COPII coat GTPase SAR1 OS=Saccharomyces cerevisiae GN=SAR1 PE=1 SV=1	SAR1_YEAST
Small glutamine-rich tetratricopeptide repeat-containing protein 2 OS=Saccharomyces cerevi	SGT2_YEAST
Small nuclear ribonucleoprotein E OS=Saccharomyces cerevisiae GN=SME1 PE=1 SV=1	RUXE_YEAST
Small nuclear ribonucleoprotein Sm D1 OS=Saccharomyces cerevisiae GN=SMD1 PE=1 SV=	SMD1_YEAST
Small nuclear ribonucleoprotein Sm D2 OS=Saccharomyces cerevisiae GN=SMD2 PE=1 SV=	SMD2_YEAST
Small nuclear ribonucleoprotein Sm D3 OS=Saccharomyces cerevisiae GN=SMD3 PE=1 SV=	SMD3_YEAST
Small nuclear ribonucleoprotein-associated protein B OS=Saccharomyces cerevisiae GN=SM	RSMB_YEAST
Sm-like protein LSm1 OS=Saccharomyces cerevisiae GN=LSM1 PE=1 SV=1	LSM1_YEAST
Sodium transport ATPase 1 OS=Saccharomyces cerevisiae GN=ENA1 PE=1 SV=1	ATN1_YEAST
Sodium transport ATPase 2 OS=Saccharomyces cerevisiae GN=ENA2 PE=1 SV=1	ATN2_YEAST
Something about silencing protein 10 OS=Saccharomyces cerevisiae GN=SAS10 PE=1 SV=	SAS10_YEAST
Something about silencing protein 4 OS=Saccharomyces cerevisiae GN=SAS4 PE=1 SV=1	SAS4_YEAST
Something about silencing protein 5 OS=Saccharomyces cerevisiae GN=SAS5 PE=1 SV=1	SAS5_YEAST
Sorting nexin MVP1 OS=Saccharomyces cerevisiae GN=MVP1 PE=1 SV=2	MVP1_YEAST
Sorting nexin-3 OS=Saccharomyces cerevisiae GN=SNX3 PE=1 SV=1	SNX3_YEAST
Spermidine synthase OS=Saccharomyces cerevisiae GN=SPE3 PE=1 SV=1	SPEE_YEAST
Sphingoid long chain base kinase 4 OS=Saccharomyces cerevisiae GN=LCB4 PE=1 SV=1	LCB4_YEAST
Sphingoid long chain base kinase 5 OS=Saccharomyces cerevisiae GN=LCB5 PE=1 SV=1	LCB5_YEAST
Sphingolipid long chain base-responsive protein LSP1 OS=Saccharomyces cerevisiae GN=L	LSP1_YEAST
Sphingolipid long chain base-responsive protein PIL1 OS=Saccharomyces cerevisiae GN=PI	PIL1_YEAST
Sphingosine-1-phosphate lyase OS=Saccharomyces cerevisiae GN=DPL1 PE=1 SV=1	SGPL_YEAST
Spindle pole body component SPC42 OS=Saccharomyces cerevisiae GN=SPC42 PE=1 SV=	SPC42_YEAST
Sporulation protein RMD1 OS=Saccharomyces cerevisiae GN=RMD1 PE=1 SV=1	RMD1_YEAST
Sporulation protein RMD8 OS=Saccharomyces cerevisiae GN=RMD8 PE=1 SV=1	RMD8_YEAST
Sporulation-specific protein 73 OS=Saccharomyces cerevisiae GN=SPO73 PE=2 SV=1	SPO73_YEAST
Sporulation-specific protein 77 OS=Saccharomyces cerevisiae GN=SPO77 PE=2 SV=1	SPO77_YEAST
Stationary phase protein 5 OS=Saccharomyces cerevisiae GN=SPG5 PE=1 SV=3	SPG5_YEAST
Sterol 24-C-methyltransferase OS=Saccharomyces cerevisiae GN=ERG6 PE=1 SV=4	ERG6_YEAST
Sterol uptake protein 1 OS=Saccharomyces cerevisiae GN=SUT1 PE=1 SV=1	SUT1_YEAST
Structural maintenance of chromosomes protein 1 OS=Saccharomyces cerevisiae GN=SMC1	SMC1_YEAST
Structural maintenance of chromosomes protein 2 OS=Saccharomyces cerevisiae GN=SMC2	SMC2_YEAST
Structural maintenance of chromosomes protein 3 OS=Saccharomyces cerevisiae GN=SMC3	SMC3_YEAST
Structural maintenance of chromosomes protein 4 OS=Saccharomyces cerevisiae GN=SMC4	SMC4_YEAST
Structural maintenance of chromosomes protein 6 OS=Saccharomyces cerevisiae GN=SMC6	SMC6_YEAST
Structure-specific endonuclease RAD27 OS=Saccharomyces cerevisiae GN=RAD27 PE=1 S	RAD27_YEAST
Styryl dye vacuolar localization protein 3 OS=Saccharomyces cerevisiae GN=SVL3 PE=1 SV	SVL3_YEAST

Succinate dehydrogenase [ubiquinone] flavoprotein subunit 2, mitochondrial OS=Saccharom	DHSX_YEAST
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Saccharomyc	DHSA_YEAST
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Saccharomyce:	DHSB_YEAST
Succinate dehydrogenase assembly factor 1 homolog, mitochondrial OS=Saccharomyces cei	SDHF1_YEAS7
Succinate dehydrogenase assembly factor 2, mitochondrial OS=Saccharomyces cerevisiae (:	SDHF2_YEAS1
Succinate-semialdehyde dehydrogenase [NADP+] OS=Saccharomyces cerevisiae GN=UGA:	UGA2_YEAST
Succinyl-CoA ligase [ADP-forming] subunit alpha, mitochondrial OS=Saccharomyces cerevis	SUCA_YEAST
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Saccharomyces cerevisia	SUCB_YEAST
Sulfate adenylyltransferase OS=Saccharomyces cerevisiae GN=MET3 PE=1 SV=2	MET3_YEAST
Superkiller protein 3 OS=Saccharomyces cerevisiae GN=SKI3 PE=1 SV=2	SKI3_YEAST
Superoxide dismutase [Cu-Zn] OS=Saccharomyces cerevisiae GN=SOD1 PE=1 SV=2	SODC_YEAST
Superoxide dismutase [Mn], mitochondrial OS=Saccharomyces cerevisiae GN=SOD2 PE=1 S	SODM_YEAST
Suppressor of glycerol defect protein 1 OS=Saccharomyces cerevisiae GN=SGD1 PE=1 SV=	SGD1_YEAST
Suppressor of mar1-1 protein OS=Saccharomyces cerevisiae GN=SUM1 PE=1 SV=2	SUM1_YEAST
Suppressor of yeast profilin deletion OS=Saccharomyces cerevisiae GN=SYP1 PE=1 SV=3	SYP1_YEAST
Suppressor protein MPT5 OS=Saccharomyces cerevisiae GN=MPT5 PE=1 SV=2	MPT5_YEAST
Suppressor protein SRP40 OS=Saccharomyces cerevisiae GN=SRP40 PE=1 SV=2	SRP40_YEAST
Suppressor protein STM1 OS=Saccharomyces cerevisiae GN=STM1 PE=1 SV=3	STM1_YEAST
SUR7 family protein FMP45 OS=Saccharomyces cerevisiae GN=FMP45 PE=1 SV=1	FMP45_YEAST
SVP1-like protein 2 OS=Saccharomyces cerevisiae GN=HSV2 PE=1 SV=1	HSV2_YEAST
SWI/SNF chromatin-remodeling complex subunit SNF5 OS=Saccharomyces cerevisiae GN=!	SNF5_YEAST
SWIRM domain-containing protein YOR338W OS=Saccharomyces cerevisiae GN=YOR338V	YO338_YEAST
SWR1-complex protein 3 OS=Saccharomyces cerevisiae GN=SWC3 PE=1 SV=2	SWC3_YEAST
SWR1-complex protein 4 OS=Saccharomyces cerevisiae GN=SWC4 PE=1 SV=1	SWC4_YEAST
Target of rapamycin complex 1 subunit KOG1 OS=Saccharomyces cerevisiae GN=KOG1 PE	KOG1_YEAST
Target of rapamycin complex 1 subunit TCO89 OS=Saccharomyces cerevisiae GN=TCO89 F	TCO89_YEAST
Target of rapamycin complex 2 subunit AVO1 OS=Saccharomyces cerevisiae GN=AVO1 PE=	AVO1_YEAST
Target of rapamycin complex 2 subunit AVO2 OS=Saccharomyces cerevisiae GN=AVO2 PE=	AVO2_YEAST
Target of rapamycin complex subunit LST8 OS=Saccharomyces cerevisiae GN=LST8 PE=1 !	LST8_YEAST
TATA-binding protein-associated factor MOT1 OS=Saccharomyces cerevisiae GN=MOT1 PE	MOT1_YEAST
TATA-box-binding protein OS=Saccharomyces cerevisiae GN=SPT15 PE=1 SV=3	TBP_YEAST
Tat-binding homolog 7 OS=Saccharomyces cerevisiae GN=YTA7 PE=1 SV=2	TBP7_YEAST
T-complex protein 1 subunit beta OS=Saccharomyces cerevisiae GN=CCT2 PE=1 SV=1	TCPB_YEAST
T-complex protein 1 subunit delta OS=Saccharomyces cerevisiae GN=CCT4 PE=1 SV=2	TCPD_YEAST
T-complex protein 1 subunit epsilon OS=Saccharomyces cerevisiae GN=CCT5 PE=1 SV=3	TCPE_YEAST
T-complex protein 1 subunit gamma OS=Saccharomyces cerevisiae GN=CCT3 PE=1 SV=2	TCPG_YEAST
T-complex protein 1 subunit theta OS=Saccharomyces cerevisiae GN=CCT8 PE=1 SV=1	TCPQ_YEAST
T-complex protein 1 subunit zeta OS=Saccharomyces cerevisiae GN=CCT6 PE=1 SV=1	TCPZ_YEAST
Telomerase reverse transcriptase OS=Saccharomyces cerevisiae GN=EST2 PE=1 SV=1	TERT_YEAST
Telomere length regulator protein RIF1 OS=Saccharomyces cerevisiae GN=RIF1 PE=1 SV=:	RIF1_YEAST
Temperature shock-inducible protein 1 OS=Saccharomyces cerevisiae GN=TIP1 PE=1 SV=1	TIP1_YEAST
Thiamine biosynthetic bifunctional enzyme OS=Saccharomyces cerevisiae GN=THI6 PE=2 S	THI6_YEAST
Thiamine transporter OS=Saccharomyces cerevisiae GN=THI7 PE=1 SV=1	THI7_YEAST
Thiamine transporter THI72 OS=Saccharomyces cerevisiae GN=THI72 PE=1 SV=1	THI72_YEAST
Thioredoxin reductase 1 OS=Saccharomyces cerevisiae GN=TRR1 PE=1 SV=3	TRXB1_YEAST
Thioredoxin-3, mitochondrial OS=Saccharomyces cerevisiae GN=TRX3 PE=1 SV=1	TRX3_YEAST
THO complex subunit 2 OS=Saccharomyces cerevisiae GN=THO2 PE=1 SV=1	THO2_YEAST

Threo-3-hydroxyaspartate ammonia-lyase OS=Saccharomyces cerevisiae GN=SRY1 PE=1 S	SRY1_YEAST
Threonine dehydratase, mitochondrial OS=Saccharomyces cerevisiae GN=ILV1 PE=1 SV=2	THDH_YEAST
Threonyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=THS1 PE=1 SV=	SYTC_YEAST
Threonyl-tRNA synthetase, mitochondrial OS=Saccharomyces cerevisiae GN=MST1 PE=1 S	SYTM_YEAST
Thymidylate synthase OS=Saccharomyces cerevisiae GN=TMP1 PE=1 SV=1	TYSY_YEAST
Topoisomerase 1-associated factor 2 OS=Saccharomyces cerevisiae GN=TOF2 PE=1 SV=1	TOF2_YEAST
Trans-acting factor D OS=Saccharomyces cerevisiae GN=RAF1 PE=2 SV=1	RAF_YEAST
Transaldolase NQM1 OS=Saccharomyces cerevisiae GN=NQM1 PE=1 SV=1	TAL2_YEAST
Transaldolase OS=Saccharomyces cerevisiae GN=TAL1 PE=1 SV=4	TAL1_YEAST
Transcription corepressor MIG3 OS=Saccharomyces cerevisiae GN=MIG3 PE=1 SV=1	MIG3_YEAST
Transcription elongation factor S-II OS=Saccharomyces cerevisiae GN=DST1 PE=1 SV=4	TFS2_YEAST
Transcription elongation factor SPT5 OS=Saccharomyces cerevisiae GN=SPT5 PE=1 SV=1	SPT5_YEAST
Transcription factor IWS1 OS=Saccharomyces cerevisiae GN=IWS1 PE=1 SV=1	IWS1_YEAST
Transcription factor PDR1 OS=Saccharomyces cerevisiae GN=PDR1 PE=1 SV=2	PDR1_YEAST
Transcription factor tau 138 kDa subunit OS=Saccharomyces cerevisiae GN=TFC3 PE=1 SV	TFC3_YEAST
Transcription factor tau 55 kDa subunit OS=Saccharomyces cerevisiae GN=TFC7 PE=1 SV=	TFC7_YEAST
Transcription initiation factor IIA small subunit OS=Saccharomyces cerevisiae GN=TOA2 PE=	TOA2_YEAST
Transcription initiation factor IIB OS=Saccharomyces cerevisiae GN=SUA7 PE=1 SV=1	TF2B_YEAST
Transcription initiation factor TFIID subunit 1 OS=Saccharomyces cerevisiae GN=TAF1 PE=:	TAF1_YEAST
Transcription initiation factor TFIID subunit 11 OS=Saccharomyces cerevisiae GN=TAF11 PE	TAF11_YEAST
Transcription initiation factor TFIID subunit 4 OS=Saccharomyces cerevisiae (strain YJM789)	TAF4_YEAS7
Transcription initiation factor TFIID subunit 6 OS=Saccharomyces cerevisiae GN=TAF6 PE=:	TAF6_YEAST
Transcription initiation factor TFIID subunit 9 OS=Saccharomyces cerevisiae GN=TAF9 PE=:	TAF9_YEAST
Transcription regulatory protein SNF2 OS=Saccharomyces cerevisiae GN=SNF2 PE=1 SV=1	SNF2_YEAST
Transcriptional activator/repressor MOT3 OS=Saccharomyces cerevisiae GN=MOT3 PE=1 S	MOT3_YEAST
Transcriptional adapter 2 OS=Saccharomyces cerevisiae GN=ADA2 PE=1 SV=1	ADA2_YEAST
Transcriptional modulator WTM1 OS=Saccharomyces cerevisiae GN=WTM1 PE=1 SV=1	WTM1_YEAST
Transcriptional modulator WTM2 OS=Saccharomyces cerevisiae GN=WTM2 PE=1 SV=1	WTM2_YEAST
Transcriptional regulatory protein ASH1 OS=Saccharomyces cerevisiae GN=ASH1 PE=1 SV:	ASH1_YEAST
Transcriptional regulatory protein DOT6 OS=Saccharomyces cerevisiae GN=DOT6 PE=1 SV	DOT6_YEAST
Transcriptional regulatory protein GAT1 OS=Saccharomyces cerevisiae GN=GAT1 PE=1 SV	GAT1_YEAST
Transcriptional regulatory protein RXT2 OS=Saccharomyces cerevisiae GN=RXT2 PE=1 SV=	RXT2_YEAST
Transcriptional regulatory protein RXT3 OS=Saccharomyces cerevisiae GN=RXT3 PE=1 SV=	RXT3_YEAST
Transcriptional regulatory protein UME1 OS=Saccharomyces cerevisiae GN=UME1 PE=1 SV	UME1_YEAST
Transcriptional repressor OPI1 OS=Saccharomyces cerevisiae GN=OPI1 PE=1 SV=1	OPI1_YEAST
Transcription-associated protein 1 OS=Saccharomyces cerevisiae GN=TRA1 PE=1 SV=1	TRA1_YEAST
Transgelin OS=Saccharomyces cerevisiae GN=SCP1 PE=1 SV=1	SCP1_YEAST
Transketolase 1 OS=Saccharomyces cerevisiae GN=TKL1 PE=1 SV=4	TKT1_YEAST
Transketolase 2 OS=Saccharomyces cerevisiae GN=TKL2 PE=1 SV=1	TKT2_YEAST
Translation initiation factor eIF-2B subunit alpha OS=Saccharomyces cerevisiae GN=GCN3 I	EI2BA_YEAST
Translation initiation factor eIF-2B subunit beta OS=Saccharomyces cerevisiae GN=GCD7 P	EI2BB_YEAST
Translation initiation factor eIF-2B subunit delta OS=Saccharomyces cerevisiae GN=GCD2 F	EI2BD_YEAST
Translation initiation factor eIF-2B subunit gamma OS=Saccharomyces cerevisiae GN=GCD:	EI2BG_YEAST
Translation initiation factor RLI1 OS=Saccharomyces cerevisiae GN=RLI1 PE=1 SV=1	RLI1_YEAST
Translation machinery-associated protein 10 OS=Saccharomyces cerevisiae GN=TMA10 PE	TMA10_YEAST
Translation machinery-associated protein 20 OS=Saccharomyces cerevisiae GN=TMA20 PE	TMA20_YEAST
Translation machinery-associated protein 22 OS=Saccharomyces cerevisiae GN=TMA22 PE	DENR_YEAST

Translation machinery-associated protein 46 OS=Saccharomyces cerevisiae GN=TMA46 PE	TMA46_YEAST
Translation machinery-associated protein 7 OS=Saccharomyces cerevisiae GN=TMA7 PE=1	TMA7_YEAST
Translational activator GCN1 OS=Saccharomyces cerevisiae GN=GCN1 PE=1 SV=1	GCN1_YEAST
Translationally-controlled tumor protein homolog OS=Saccharomyces cerevisiae GN=TMA19	TCTP_YEAST
Translocation protein SEC62 OS=Saccharomyces cerevisiae GN=SEC62 PE=1 SV=2	SEC62_YEAST
Translocation protein SEC72 OS=Saccharomyces cerevisiae GN=SEC72 PE=1 SV=3	SEC72_YEAST
Transmembrane 9 superfamily member 2 OS=Saccharomyces cerevisiae GN=TMN2 PE=1 S	TMN2_YEAST
Transport protein particle 120 kDa subunit OS=Saccharomyces cerevisiae GN=TRS120 PE=	TR120_YEAST
Transport protein particle 130 kDa subunit OS=Saccharomyces cerevisiae GN=TRS130 PE=	TR130_YEAST
Transport protein particle 20 kDa subunit OS=Saccharomyces cerevisiae GN=TRS20 PE=1 S	TRS20_YEAST
Transport protein particle 22 kDa subunit OS=Saccharomyces cerevisiae GN=BET3 PE=1 SV	BET3_YEAST
Transport protein particle 23 kDa subunit OS=Saccharomyces cerevisiae GN=TRS23 PE=1 S	TRS23_YEAST
Transport protein particle 31 kDa subunit OS=Saccharomyces cerevisiae GN=TRS31 PE=1 S	TRS31_YEAST
Transport protein particle 33 kDa subunit OS=Saccharomyces cerevisiae GN=TRS33 PE=1 S	TRS33_YEAST
Transposon Ty1-A/Ty1-PR1 Gag polyprotein OS=Saccharomyces cerevisiae GN=TY1A-A PE	YA11A_YEAST
Transposon Ty1-BL Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY1B-BL PE=1	YB11B_YEAST
Transposon Ty1-BR Gag polyprotein OS=Saccharomyces cerevisiae GN=TY1A-BR PE=1 SV	YB12A_YEAST
Transposon Ty1-DR1 Gag polyprotein OS=Saccharomyces cerevisiae GN=TY1A-DR1 PE=1	YD11A_YEAST
Transposon Ty1-DR1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY1B-DR1 PI	YD11B_YEAST
Transposon Ty1-DR2 Gag polyprotein OS=Saccharomyces cerevisiae GN=TY1A-DR2 PE=3	YD17A_YEAST
Transposon Ty1-DR3 Gag polyprotein OS=Saccharomyces cerevisiae GN=TY1A-DR3 PE=1	YD12A_YEAST
Transposon Ty1-DR3 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY1B-DR3 PI	YD12B_YEAST
Transposon Ty1-DR6/Ty1-ER1/Ty1-LR2/Ty1-PL Gag polyprotein OS=Saccharomyces cerevi	YD15A_YEAST
Transposon Ty1-GR2 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY1B-GR2 P	YG12B_YEAST
Transposon Ty1-JR2 Gag polyprotein OS=Saccharomyces cerevisiae GN=TY1A-JR2 PE=1 S	YJ12A_YEAST
Transposon Ty1-JR2 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY1B-JR2 PE	YJ12B_YEAST
Transposon Ty1-ML1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY1B-ML1 PE	YM11B_YEAST
Transposon Ty1-MR2 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY1B-MR2 P	YM14B_YEAST
Transposon Ty1-NL1 Gag polyprotein OS=Saccharomyces cerevisiae GN=TY1A-NL1 PE=2 S	YN11A_YEAST
Transposon Ty1-NL1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY1B-NL1 PE	YN11B_YEAST
Transposon Ty1-NL2 Gag polyprotein OS=Saccharomyces cerevisiae GN=TY1A-NL2 PE=2 S	YN12A_YEAST
Transposon Ty1-OL Gag polyprotein OS=Saccharomyces cerevisiae GN=TY1A-OL PE=1 SV	YO11A_YEAST
Transposon Ty1-OL Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY1B-OL PE=3	YO11B_YEAST
Transposon Ty1-PR2 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY1B-PR2 PE	YP13B_YEAST
Transposon Ty1-PR3 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY1B-PR3 PE	YP14B_YEAST
Transposon Ty2-B Gag polyprotein OS=Saccharomyces cerevisiae GN=TY2A-B PE=1 SV=1	YB21A_YEAST
Transposon Ty2-B Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY2B-B PE=1 S	YB21B_YEAST
Transposon Ty2-DR1 Gag polyprotein OS=Saccharomyces cerevisiae GN=TY2A-DR1 PE=1	YD21A_YEAST
Transposon Ty2-DR3 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY2B-DR3 PI	YD23B_YEAST
Transposon Ty2-F/Ty2-GR2 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY2B-	YF21B_YEAST
Transposon Ty2-GR1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY2B-GR1 P	YG21B_YEAST
Transposon Ty3-I Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY3B-I PE=3 SV	YI31B_YEAST
Transposon Ty4-J Gag-Pol polyprotein OS=Saccharomyces cerevisiae GN=TY4B-J PE=3 SV	YJ41B_YEAST
Trehalose synthase complex regulatory subunit TPS3 OS=Saccharomyces cerevisiae GN=TI	TPS3_YEAST
Trehalose synthase complex regulatory subunit TSL1 OS=Saccharomyces cerevisiae GN=TS	TSL1_YEAST
Trehalose-phosphatase OS=Saccharomyces cerevisiae GN=TPS2 PE=1 SV=3	TPS2_YEAST
Tricalbin-1 OS=Saccharomyces cerevisiae GN=TCB1 PE=1 SV=1	TCB1_YEAST

Tricalbin-2 OS=Saccharomyces cerevisiae GN=TCB2 PE=1 SV=1	TCB2_YEAST
Tricalbin-3 OS=Saccharomyces cerevisiae GN=TCB3 PE=1 SV=1	TCB3_YEAST
Trimethylguanosine synthase OS=Saccharomyces cerevisiae GN=TGS1 PE=1 SV=1	TGS1_YEAST
Triosephosphate isomerase OS=Saccharomyces cerevisiae GN=TPI1 PE=1 SV=2	TPIS_YEAST
tRNA (guanine-N(7)-)-methyltransferase subunit TRM82 OS=Saccharomyces cerevisiae (stra	TRM82_YEAS1
tRNA (guanine-N(7)-)-methyltransferase subunit TRM82 OS=Saccharomyces cerevisiae (stra	TRM82_YEAS7
tRNA 2'-phosphotransferase OS=Saccharomyces cerevisiae GN=TPT1 PE=1 SV=1	TPT1_YEAST
tRNA A64-2'-O-ribosylphosphate transferase OS=Saccharomyces cerevisiae GN=RIT1 PE=1	RIT1_YEAST
tRNA wybutosine-synthesizing protein 1 OS=Saccharomyces cerevisiae GN=TYW1 PE=1 SV	TYW1_YEAST
tRNA wybutosine-synthesizing protein 2 OS=Saccharomyces cerevisiae GN=TRM12 PE=1 S	TYW2_YEAST
tRNA-dihydrouridine synthase 3 OS=Saccharomyces cerevisiae (strain YJM789) GN=DUS3 I	DUS3_YEAS7
tRNA-specific adenosine deaminase 1 OS=Saccharomyces cerevisiae GN=TAD1 PE=1 SV=1	TAD1_YEAST
Tryptophan synthase OS=Saccharomyces cerevisiae GN=TRP5 PE=1 SV=1	TRP_YEAST
Tryptophanyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=WRS1 PE=1	SYWC_YEAST
Tryptophanyl-tRNA synthetase, mitochondrial OS=Saccharomyces cerevisiae GN=MSW1 PE	SYWM_YEAST
Tubulin alpha-1 chain OS=Saccharomyces cerevisiae GN=TUB1 PE=1 SV=2	TBA1_YEAST
Tubulin alpha-3 chain OS=Saccharomyces cerevisiae GN=TUB3 PE=1 SV=1	TBA3_YEAST
Tubulin beta chain OS=Saccharomyces cerevisiae GN=TUB2 PE=1 SV=2	TBB_YEAST
Tyrosine-protein phosphatase 3 OS=Saccharomyces cerevisiae GN=PTP3 PE=1 SV=1	PTP3_YEAST
Tyrosine-protein phosphatase CDC14 OS=Saccharomyces cerevisiae GN=CDC14 PE=1 SV=	CDC14_YEAST
Tyrosine-protein phosphatase YVH1 OS=Saccharomyces cerevisiae GN=YVH1 PE=1 SV=1	PVH1_YEAST
Tyrosyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae GN=TYS1 PE=1 SV=3	SYYC_YEAST
Tyrosyl-tRNA synthetase, mitochondrial OS=Saccharomyces cerevisiae GN=MSY1 PE=1 SV	SYYM_YEAST
U2 snRNP component HSH155 OS=Saccharomyces cerevisiae GN=HSH155 PE=1 SV=1	SF3B1_YEAST
U3 small nucleolar ribonucleoprotein protein IMP3 OS=Saccharomyces cerevisiae GN=IMP3	IMP3_YEAST
U3 small nucleolar ribonucleoprotein protein IMP4 OS=Saccharomyces cerevisiae GN=IMP4	IMP4_YEAST
U3 small nucleolar RNA-associated protein 10 OS=Saccharomyces cerevisiae GN=UTP10 P	UTP10_YEAST
U3 small nucleolar RNA-associated protein 11 OS=Saccharomyces cerevisiae (strain AWRI1	UTP11_YEAS6
U3 small nucleolar RNA-associated protein 12 OS=Saccharomyces cerevisiae GN=DIP2 PE=	UTP12_YEAST
U3 small nucleolar RNA-associated protein 13 OS=Saccharomyces cerevisiae GN=UTP13 P	UTP13_YEAST
U3 small nucleolar RNA-associated protein 14 OS=Saccharomyces cerevisiae GN=UTP14 P	UTP14_YEAST
U3 small nucleolar RNA-associated protein 15 OS=Saccharomyces cerevisiae GN=UTP15 P	UTP15_YEAST
U3 small nucleolar RNA-associated protein 18 OS=Saccharomyces cerevisiae GN=UTP18 P	UTP18_YEAST
U3 small nucleolar RNA-associated protein 20 OS=Saccharomyces cerevisiae GN=UTP20 P	UTP20_YEAST
U3 small nucleolar RNA-associated protein 21 OS=Saccharomyces cerevisiae GN=UTP21 P	UTP21_YEAST
U3 small nucleolar RNA-associated protein 22 OS=Saccharomyces cerevisiae GN=UTP22 P	UTP22_YEAST
U3 small nucleolar RNA-associated protein 4 OS=Saccharomyces cerevisiae GN=UTP4 PE=	UTP4_YEAST
U3 small nucleolar RNA-associated protein 5 OS=Saccharomyces cerevisiae GN=UTP5 PE=	UTP5_YEAST
U3 small nucleolar RNA-associated protein 6 OS=Saccharomyces cerevisiae GN=UTP6 PE=	UTP6_YEAST
U3 small nucleolar RNA-associated protein 7 OS=Saccharomyces cerevisiae GN=UTP7 PE=	UTP7_YEAST
U3 small nucleolar RNA-associated protein 8 OS=Saccharomyces cerevisiae GN=UTP8 PE=	UTP8_YEAST
U3 small nucleolar RNA-associated protein 9 OS=Saccharomyces cerevisiae GN=UTP9 PE=	UTP9_YEAST
U3 small nucleolar RNA-associated protein MPP10 OS=Saccharomyces cerevisiae GN=MPF	MPP10_YEAST
U6 snRNA-associated Sm-like protein LSm2 OS=Saccharomyces cerevisiae GN=LSM2 PE=1	LSM2_YEAST
U6 snRNA-associated Sm-like protein LSm3 OS=Saccharomyces cerevisiae GN=LSM3 PE=1	LSM3_YEAST
U6 snRNA-associated Sm-like protein LSm4 OS=Saccharomyces cerevisiae GN=LSM4 PE=1	LSM4_YEAST
U6 snRNA-associated Sm-like protein LSm5 OS=Saccharomyces cerevisiae GN=LSM5 PE=1	LSM5_YEAST

U6 snRNA-associated Sm-like protein LSm6 OS=Saccharomyces cerevisiae (strain YJM789)	LSM6_YEAS7
U6 snRNA-associated Sm-like protein LSm7 OS=Saccharomyces cerevisiae GN=LSM7 PE=1	LSM7_YEAST
Ubiquinone biosynthesis methyltransferase COQ5, mitochondrial OS=Saccharomyces cerevi	COQ5_YEAST
Ubiquinone biosynthesis monooxygenase COQ6 OS=Saccharomyces cerevisiae GN=COQ6	COQ6_YEAST
Ubiquitin carboxyl-terminal hydrolase 10 OS=Saccharomyces cerevisiae GN=UBP10 PE=1 S	UBP10_YEAST
Ubiquitin carboxyl-terminal hydrolase 15 OS=Saccharomyces cerevisiae GN=UBP15 PE=1 S	UBP15_YEAST
Ubiquitin carboxyl-terminal hydrolase 3 OS=Saccharomyces cerevisiae GN=UBP3 PE=1 SV=	UBP3_YEAST
Ubiquitin carboxyl-terminal hydrolase 5 OS=Saccharomyces cerevisiae GN=UBP5 PE=1 SV=	UBP5_YEAST
Ubiquitin carboxyl-terminal hydrolase 7 OS=Saccharomyces cerevisiae GN=UBP7 PE=1 SV=	UBP7_YEAST
Ubiquitin carboxyl-terminal hydrolase YUH1 OS=Saccharomyces cerevisiae GN=YUH1 PE=1	UBL1_YEAST
Ubiquitin ligase-binding protein BUL1 OS=Saccharomyces cerevisiae GN=BUL1 PE=1 SV=1	BUL1_YEAST
Ubiquitin ligase-binding protein BUL2 OS=Saccharomyces cerevisiae GN=BUL2 PE=1 SV=1	BUL2_YEAST
Ubiquitin OS=Saccharomyces cerevisiae GN=UBI1 PE=1 SV=1	UBIQ_YEAST
Ubiquitin-activating enzyme E1 1 OS=Saccharomyces cerevisiae GN=UBA1 PE=1 SV=2	UBA1_YEAST
Ubiquitin-conjugating enzyme E2-18 kDa OS=Saccharomyces cerevisiae GN=UBC7 PE=1 S	UBC7_YEAST
Ubiquitin-like protein MDY2 OS=Saccharomyces cerevisiae GN=MDY2 PE=1 SV=1	MDY2_YEAST
Ubiquitin-like protein SMT3 OS=Saccharomyces cerevisiae GN=SMT3 PE=1 SV=1	SMT3_YEAST
Ubiquitin-like-specific protease 1 OS=Saccharomyces cerevisiae GN=ULP1 PE=1 SV=1	ULP1_YEAST
UBP3-associated protein BRE5 OS=Saccharomyces cerevisiae GN=BRE5 PE=1 SV=1	BRE5_YEAST
UBX domain-containing protein 4 OS=Saccharomyces cerevisiae GN=UBX4 PE=1 SV=1	UBX4_YEAST
UBX domain-containing protein 6 OS=Saccharomyces cerevisiae GN=UBX6 PE=1 SV=1	UBX6_YEAST
UDP-N-acetylglucosamine pyrophosphorylase OS=Saccharomyces cerevisiae GN=UAP1 PE	UAP1_YEAST
UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase OS=	GPT_YEAST
Uncharacterized ABC transporter ATP-binding protein YDR061W OS=Saccharomyces cerevi	YD061_YEAST
Uncharacterized ABC transporter ATP-binding protein/permease YNR070W OS=Saccharomy	YN99_YEAST
Uncharacterized ABC transporter ATP-binding protein/permease YOL075C OS=Saccharomy	YO075_YEAST
Uncharacterized ATP-dependent helicase FUN30 OS=Saccharomyces cerevisiae GN=FUN3	FUN30_YEAST
Uncharacterized ATP-dependent helicase YHR031C OS=Saccharomyces cerevisiae GN=YH	YHJ1_YEAST
Uncharacterized ATP-dependent helicase YLR247C OS=Saccharomyces cerevisiae GN=YLI	YL247_YEAST
Uncharacterized bolA-like protein YAL044W-A OS=Saccharomyces cerevisiae GN=YAL044V	YA044_YEAST
Uncharacterized endoplasmic reticulum membrane protein YJR015W OS=Saccharomyces ce	YJY5_YEAST
Uncharacterized glycosyl hydrolase YBR056W OS=Saccharomyces cerevisiae GN=YBR056	YBQ6_YEAST
Uncharacterized GTP-binding protein OLA1 OS=Saccharomyces cerevisiae GN=OLA1 PE=1	OLA1_YEAST
Uncharacterized GTP-binding protein YGR173W OS=Saccharomyces cerevisiae GN=YGR17	YG3Y_YEAST
Uncharacterized GTP-binding protein YGR210C OS=Saccharomyces cerevisiae GN=YGR21	YG4I_YEAST
Uncharacterized membrane protein YDL133W OS=Saccharomyces cerevisiae GN=YDL133V	YD133_YEAST
Uncharacterized membrane protein YOL019W OS=Saccharomyces cerevisiae GN=YOL019V	YOL19_YEAST
Uncharacterized membrane protein YPL041C OS=Saccharomyces cerevisiae GN=YPL041C	YP041_YEAST
Uncharacterized methyltransferase YIL064W OS=Saccharomyces cerevisiae GN=YIL064W I	YIG4_YEAST
Uncharacterized mitochondrial hydrolase FMP41 OS=Saccharomyces cerevisiae GN=FMP41	FMP41_YEAST
Uncharacterized mitochondrial protein RF1 OS=Saccharomyces cerevisiae GN=Q0255 PE=2	YMRF1_YEAST
Uncharacterized ORAOV1 family protein YNL260C OS=Saccharomyces cerevisiae GN=YNL	YN00_YEAST
Uncharacterized oxidoreductase YHL021C OS=Saccharomyces cerevisiae GN=YHL021C PE	YHC1_YEAST
Uncharacterized oxidoreductase YIR036C OS=Saccharomyces cerevisiae GN=YIR036C PE=	YIV6_YEAST
Uncharacterized oxidoreductase YJR096W OS=Saccharomyces cerevisiae GN=YJR096W P	YJ66_YEAST
Uncharacterized oxidoreductase YKL071W OS=Saccharomyces cerevisiae GN=YKL071W P	YKH1_YEAST
Uncharacterized oxidoreductase YMR226C OS=Saccharomyces cerevisiae GN=YMR226C P	YM71_YEAST

Uncharacterized peptidase YFR006W OS=Saccharomyces cerevisiae GN=YFR006W PE=1	YFH6_YEAST
Uncharacterized PH domain-containing protein YPR091C OS=Saccharomyces cerevisiae GN	YP091_YEAST
Uncharacterized PH domain-containing protein YPR115W OS=Saccharomyces cerevisiae GI	YP115_YEAST
Uncharacterized phosphatase YNL010W OS=Saccharomyces cerevisiae GN=YNL010W PE=	YNB0_YEAST
Uncharacterized plasma membrane protein YNL194C OS=Saccharomyces cerevisiae GN=YI	YNT4_YEAST
Uncharacterized protein IRC10 OS=Saccharomyces cerevisiae GN=IRC10 PE=2 SV=1	IRC10_YEAST
Uncharacterized protein JIP4 OS=Saccharomyces cerevisiae GN=JIP4 PE=1 SV=2	JIP4_YEAST
Uncharacterized protein MRP8 OS=Saccharomyces cerevisiae GN=MRP8 PE=1 SV=1	MRP8_YEAST
Uncharacterized protein RSN1 OS=Saccharomyces cerevisiae GN=RSN1 PE=1 SV=1	RSN1_YEAST
Uncharacterized protein YBL086C OS=Saccharomyces cerevisiae GN=YBL086C PE=1 SV=1	YBI6_YEAST
Uncharacterized protein YBL095W OS=Saccharomyces cerevisiae GN=YBL095W PE=1 SV=	YBJ5_YEAST
Uncharacterized protein YBR108W OS=Saccharomyces cerevisiae GN=YBR108W PE=1 SV	YBV8_YEAST
Uncharacterized protein YBR191W-A OS=Saccharomyces cerevisiae GN=YBR191W-A PE=:	YB191_YEAST
Uncharacterized protein YBR225W OS=Saccharomyces cerevisiae GN=YBR225W PE=1 SV	YB75_YEAST
Uncharacterized protein YBR246W OS=Saccharomyces cerevisiae GN=YBR246W PE=1 SV	YB96_YEAST
Uncharacterized protein YBR259W OS=Saccharomyces cerevisiae GN=YBR259W PE=1 SV	YB9F_YEAST
Uncharacterized protein YBR271W OS=Saccharomyces cerevisiae GN=YBR271W PE=1 SV	YB9P_YEAST
Uncharacterized protein YCR016W OS=Saccharomyces cerevisiae GN=YCR016W PE=1 SV	YCQ6_YEAST
Uncharacterized protein YDL012C OS=Saccharomyces cerevisiae GN=YDL012C PE=1 SV=:	YD012_YEAST
Uncharacterized protein YDL144C OS=Saccharomyces cerevisiae GN=YDL144C PE=1 SV=:	YD144_YEAST
Uncharacterized protein YDR348C OS=Saccharomyces cerevisiae GN=YDR348C PE=1 SV=	PAL1_YEAST
Uncharacterized protein YDR391C OS=Saccharomyces cerevisiae GN=YDR391C PE=1 SV=	YD391_YEAST
Uncharacterized protein YEL007W OS=Saccharomyces cerevisiae GN=YEL007W PE=1 SV=	YEA7_YEAST
Uncharacterized protein YEL043W OS=Saccharomyces cerevisiae GN=YEL043W PE=1 SV=	YEF3_YEAST
Uncharacterized protein YEL137C OS=Saccharomyces cerevisiae GN=YER137C PE=2 SV=	YEW7_YEAST
Uncharacterized protein YER041W OS=Saccharomyces cerevisiae GN=YER041W PE=1 SV	YEN1_YEAST
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Uncharacterized protein YGL082W OS=Saccharomyces cerevisiae GN=YGL082W PE=1 SV	YGI2_YEAST
Uncharacterized protein YGR110W OS=Saccharomyces cerevisiae GN=YGR110W PE=1 S\	YG2V_YEAST
Uncharacterized protein YGR117C OS=Saccharomyces cerevisiae GN=YGR117C PE=1 SV=	YG32_YEAST
Uncharacterized protein YGR127W OS=Saccharomyces cerevisiae GN=YGR127W PE=1 S\	YG37_YEAST
Uncharacterized protein YGR130C OS=Saccharomyces cerevisiae GN=YGR130C PE=1 SV=	YG3A_YEAST
Uncharacterized protein YGR203W OS=Saccharomyces cerevisiae GN=YGR203W PE=1 S\	YG4E_YEAST
Uncharacterized protein YGR266W OS=Saccharomyces cerevisiae GN=YGR266W PE=1 S\	YG5L_YEAST
Uncharacterized protein YGR283C OS=Saccharomyces cerevisiae GN=YGR283C PE=1 SV=	YG5X_YEAST
Uncharacterized protein YHR080C OS=Saccharomyces cerevisiae GN=YHR080C PE=1 SV=	YHO0_YEAST
Uncharacterized protein YHR097C OS=Saccharomyces cerevisiae GN=YHR097C PE=1 SV=	YHP7_YEAST
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Uncharacterized protein YHR146W OS=Saccharomyces cerevisiae GN=YHR146W PE=1 SV	YHU6_YEAST
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Uncharacterized protein YIL091C OS=Saccharomyces cerevisiae GN=YIL091C PE=1 SV=1	YIJ1_YEAST
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Uncharacterized protein YIR003W OS=Saccharomyces cerevisiae GN=YIR003W PE=1 SV=:	YIS3_YEAST
Uncharacterized protein YJL133C-A OS=Saccharomyces cerevisiae GN=YJL133C-A PE=1 S	YJ133_YEAST
Uncharacterized protein YJL171C OS=Saccharomyces cerevisiae GN=YJL171C PE=1 SV=1	YJR1_YEAST
Uncharacterized protein YJL217W OS=Saccharomyces cerevisiae GN=YJL217W PE=1 SV=	YJV7_YEAST
Uncharacterized protein YJR046W OS=Saccharomyces cerevisiae GN=YJR046W PE=1 SV=	YJ16_YEAST

Uncharacterized protein YJR111C OS=Saccharomyces cerevisiae GN=YJR111C PE=1 SV=1	YJ81_YEAST
Uncharacterized protein YJR142W OS=Saccharomyces cerevisiae GN=YJR142W PE=1 SV=	YJ9J_YEAST
Uncharacterized protein YKL054C OS=Saccharomyces cerevisiae GN=YKL054C PE=1 SV=1	YKF4_YEAST
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Uncharacterized protein YKL128C OS=Saccharomyces cerevisiae GN=YKL128C PE=1 SV=1	YKM8_YEAST
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Uncharacterized protein YKR011C OS=Saccharomyces cerevisiae GN=YKR011C PE=1 SV=	YKZ1_YEAST
Uncharacterized protein YKR023W OS=Saccharomyces cerevisiae GN=YKR023W PE=1 SV	YK03_YEAST
Uncharacterized protein YKR043C OS=Saccharomyces cerevisiae GN=YKR043C PE=1 SV=	YK23_YEAST
Uncharacterized protein YKR070W OS=Saccharomyces cerevisiae GN=YKR070W PE=1 SV	YK50_YEAST
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Uncharacterized protein YLR392C OS=Saccharomyces cerevisiae GN=YLR392C PE=1 SV=3	YL392_YEAST
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Uncharacterized protein YML119W OS=Saccharomyces cerevisiae GN=YML119W PE=1 SV	YML9_YEAST
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Uncharacterized protein YMR031C OS=Saccharomyces cerevisiae GN=YMR031C PE=1 SV=	YMS1_YEAST
Uncharacterized protein YMR086W OS=Saccharomyces cerevisiae GN=YMR086W PE=1 SV	YMX6_YEAST
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Uncharacterized protein YMR124W OS=Saccharomyces cerevisiae GN=YMR124W PE=1 SV	YM11_YEAST
Uncharacterized protein YMR152W OS=Saccharomyces cerevisiae GN=YMR152W PE=1 SV	YM27_YEAST
Uncharacterized protein YMR157C OS=Saccharomyces cerevisiae GN=YMR157C PE=1 SV=	YM32_YEAST
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Uncharacterized protein YMR244C-A OS=Saccharomyces cerevisiae GN=YMR244C-A PE=1	YM244_YEAST
Uncharacterized protein YMR258C OS=Saccharomyces cerevisiae GN=YMR258C PE=1 SV=	YM8A_YEAST
Uncharacterized protein YMR262W OS=Saccharomyces cerevisiae GN=YMR262W PE=1 SV	YM8C_YEAST
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Uncharacterized protein YNL134C OS=Saccharomyces cerevisiae GN=YNL134C PE=1 SV=1	YNN4_YEAST
Uncharacterized protein YNL181W OS=Saccharomyces cerevisiae GN=YNL181W PE=1 SV=	YNS1_YEAST
Uncharacterized protein YNL193W OS=Saccharomyces cerevisiae GN=YNL193W PE=2 SV=	YNT3_YEAST

Uncharacterized protein YNL200C OS=Saccharomyces cerevisiae GN=YNL200C PE=1 SV=:	YNU0_YEAST
Uncharacterized protein YNL208W OS=Saccharomyces cerevisiae GN=YNL208W PE=1 SV	YNU8_YEAST
Uncharacterized protein YNL313C OS=Saccharomyces cerevisiae GN=YNL313C PE=1 SV=:	YN53_YEAST
Uncharacterized protein YOL022C OS=Saccharomyces cerevisiae GN=YOL022C PE=1 SV=	YO022_YEAST
Uncharacterized protein YOL083W OS=Saccharomyces cerevisiae GN=YOL083W PE=1 SV	YO083_YEAST
Uncharacterized protein YOL086W-A OS=Saccharomyces cerevisiae GN=YOL086W-A PE=:	YO086_YEAST
Uncharacterized protein YOR051C OS=Saccharomyces cerevisiae GN=YOR051C PE=1 SV=	YO051_YEAST
Uncharacterized protein YOR112W OS=Saccharomyces cerevisiae GN=YOR112W PE=1 S\	YO112_YEAST
Uncharacterized protein YOR227W OS=Saccharomyces cerevisiae GN=YOR227W PE=1 S\	YO227_YEAST
Uncharacterized protein YOR289W OS=Saccharomyces cerevisiae GN=YOR289W PE=1 S\	YO289_YEAST
Uncharacterized protein YOR304C-A OS=Saccharomyces cerevisiae GN=YOR304C-A PE=1	YO304_YEAST
Uncharacterized protein YOR316C-A OS=Saccharomyces cerevisiae GN=YOR316C-A PE=2	YO316_YEAST
Uncharacterized protein YPL034W OS=Saccharomyces cerevisiae GN=YPL034W PE=2 SV=	YP034_YEAST
Uncharacterized protein YPL245W OS=Saccharomyces cerevisiae GN=YPL245W PE=1 SV=	YP245_YEAST
Uncharacterized protein YPR074W-A OS=Saccharomyces cerevisiae GN=YPR074W-A PE=:	YP074_YEAST
Uncharacterized RNA-binding protein YGR250C OS=Saccharomyces cerevisiae GN=YGR25	YG5B_YEAST
Uncharacterized RNA-binding protein YPL184C OS=Saccharomyces cerevisiae GN=YPL184	YP184_YEAST
Uncharacterized transcriptional regulatory protein TBS1 OS=Saccharomyces cerevisiae GN=	TBS1_YEAST
Uncharacterized transcriptional regulatory protein YKR064W OS=Saccharomyces cerevisiae	YK44_YEAST
Uncharacterized transporter ESBP6 OS=Saccharomyces cerevisiae GN=ESBP6 PE=1 SV=1	ESBP6_YEAST
Uncharacterized WD repeat-containing protein YOL087C OS=Saccharomyces cerevisiae GN	YO087_YEAST
UPF0061 protein FMP40 OS=Saccharomyces cerevisiae GN=FMP40 PE=1 SV=1	FMP40_YEAST
UPF0067 GAF domain-containing protein YKL069W OS=Saccharomyces cerevisiae GN=YKI	YKG9_YEAST
UPF0082 protein YGR021W OS=Saccharomyces cerevisiae GN=YGR021W PE=1 SV=1	YG1D_YEAST
UPF0103 protein YJR008W OS=Saccharomyces cerevisiae GN=YJR008W PE=1 SV=1	YJX8_YEAST
UPF0121 membrane protein YLL023C OS=Saccharomyces cerevisiae GN=YLL023C PE=1 S	YL023_YEAST
UPF0121 membrane protein YLR064W OS=Saccharomyces cerevisiae GN=YLR064W PE=1	YL064_YEAST
UPF0160 protein YER156C OS=Saccharomyces cerevisiae GN=YER156C PE=1 SV=1	YEY6_YEAST
UPF0202 protein KRE33 OS=Saccharomyces cerevisiae GN=KRE33 PE=1 SV=1	KRE33_YEAST
UPF0303 protein YBR137W OS=Saccharomyces cerevisiae GN=YBR137W PE=1 SV=2	YBY7_YEAST
UPF0327 protein YCL057C-A OS=Saccharomyces cerevisiae GN=YCL057C-A PE=2 SV=1	YCF7_YEAST
UPF0368 protein YPL225W OS=Saccharomyces cerevisiae GN=YPL225W PE=1 SV=1	YP225_YEAST
UPF0399 protein YOR287C OS=Saccharomyces cerevisiae GN=YOR287C PE=1 SV=1	YO287_YEAST
UPF0587 protein YCR090C OS=Saccharomyces cerevisiae GN=YCR090C PE=1 SV=1	YCY0_YEAST
UPF0642 protein YBL028C OS=Saccharomyces cerevisiae GN=YBL028C PE=1 SV=1	YBC8_YEAST
UPF0646 protein YGL250W OS=Saccharomyces cerevisiae GN=YGL250W PE=1 SV=2	YGZA_YEAST
UPF0647 protein YCL047C OS=Saccharomyces cerevisiae GN=YCL047C PE=1 SV=1	YCE7_YEAST
UPF0657 nucleolar protein YBR141C OS=Saccharomyces cerevisiae GN=YBR141C PE=1 S	YBZ1_YEAST
UPF0661 TPR repeat-containing protein YDR161W OS=Saccharomyces cerevisiae GN=YDI	YD161_YEAST
UPF0666 protein YPR045C OS=Saccharomyces cerevisiae GN=YPR045C PE=1 SV=1	YP045_YEAST
UPF0673 membrane protein YHR009C OS=Saccharomyces cerevisiae GN=YHR009C PE=1	YHG9_YEAST
UPF0674 endoplasmic reticulum membrane protein YNR021W OS=Saccharomyces cerevisi	YN8B_YEAST
UPF0675 protein YKR021W OS=Saccharomyces cerevisiae GN=YKR021W PE=1 SV=1	YK01_YEAST
UPF0743 protein YCR087C-A OS=Saccharomyces cerevisiae GN=YCR087C-A PE=1 SV=1	YC16_YEAST
Uracil phosphoribosyltransferase OS=Saccharomyces cerevisiae GN=FUR1 PE=1 SV=2	UPP_YEAST
Uroporphyrinogen decarboxylase OS=Saccharomyces cerevisiae GN=HEM12 PE=1 SV=1	DCUP_YEAST
Uroporphyrinogen-III synthase OS=Saccharomyces cerevisiae GN=HEM4 PE=1 SV=2	HEM4_YEAST

UTP--glucose-1-phosphate uridylyltransferase OS=Saccharomyces cerevisiae GN=UGP1 PE	UGPA1_YEAST
Vacuolar acid trehalase OS=Saccharomyces cerevisiae GN=ATH1 PE=1 SV=1	ATH1_YEAST
Vacuolar aminopeptidase 1 OS=Saccharomyces cerevisiae GN=APE1 PE=1 SV=2	AMPL_YEAST
Vacuolar ATPase assembly protein VMA22 OS=Saccharomyces cerevisiae GN=VMA22 PE=	VMA22_YEAST
Vacuolar import and degradation protein 30 OS=Saccharomyces cerevisiae GN=VID30 PE=1	VID30_YEAST
Vacuolar membrane protein PEP3 OS=Saccharomyces cerevisiae GN=PEP3 PE=1 SV=1	PEP3_YEAST
Vacuolar membrane protein PEP5 OS=Saccharomyces cerevisiae GN=PEP5 PE=1 SV=2	PEP5_YEAST
Vacuolar membrane-associated protein IML1 OS=Saccharomyces cerevisiae GN=IML1 PE=1	IML1_YEAST
Vacuolar morphogenesis protein 7 OS=Saccharomyces cerevisiae GN=VAM7 PE=1 SV=1	VAM7_YEAST
Vacuolar protein 8 OS=Saccharomyces cerevisiae GN=VAC8 PE=1 SV=3	VAC8_YEAST
Vacuolar protein sorting-associated protein 1 OS=Saccharomyces cerevisiae GN=VPS1 PE=	VPS1_YEAST
Vacuolar protein sorting-associated protein 13 OS=Saccharomyces cerevisiae GN=VPS13 P	VPS13_YEAST
Vacuolar protein sorting-associated protein 20 OS=Saccharomyces cerevisiae GN=VPS20 P	VPS20_YEAST
Vacuolar protein sorting-associated protein 21 OS=Saccharomyces cerevisiae GN=VPS21 P	VPS21_YEAST
Vacuolar protein sorting-associated protein 26 OS=Saccharomyces cerevisiae GN=VPS26 P	VPS26_YEAST
Vacuolar protein sorting-associated protein 29 OS=Saccharomyces cerevisiae GN=VPS29 P	PEP11_YEAST
Vacuolar protein sorting-associated protein 3 OS=Saccharomyces cerevisiae GN=VPS3 PE=	VPS3_YEAST
Vacuolar protein sorting-associated protein 30 OS=Saccharomyces cerevisiae GN=VPS30 P	VPS30_YEAST
Vacuolar protein sorting-associated protein 33 OS=Saccharomyces cerevisiae GN=VPS33 P	VPS33_YEAST
Vacuolar protein sorting-associated protein 35 OS=Saccharomyces cerevisiae GN=VPS35 P	VPS35_YEAST
Vacuolar protein sorting-associated protein 41 OS=Saccharomyces cerevisiae GN=VPS41 P	VPS41_YEAST
Vacuolar protein sorting-associated protein 5 OS=Saccharomyces cerevisiae GN=VPS5 PE=	VPS5_YEAST
Vacuolar protein sorting-associated protein 54 OS=Saccharomyces cerevisiae GN=VPS54 P	VPS54_YEAST
Vacuolar protein sorting-associated protein 66 OS=Saccharomyces cerevisiae GN=VPS66 P	VPS66_YEAST
Vacuolar protein-sorting-associated protein 46 OS=Saccharomyces cerevisiae GN=DID2 PE=	DID2_YEAST
Vacuolar transporter chaperone 2 OS=Saccharomyces cerevisiae GN=VTC2 PE=1 SV=1	VTC2_YEAST
Vacuolar-sorting protein SNF7 OS=Saccharomyces cerevisiae GN=SNF7 PE=1 SV=1	SNF7_YEAST
Vacuolar-sorting protein SNF8 OS=Saccharomyces cerevisiae GN=SNF8 PE=1 SV=1	SNF8_YEAST
Valine/tyrosine/tryptophan amino-acid permease OS=Saccharomyces cerevisiae GN=VAP1 P	VAL1_YEAST
Valyl-tRNA synthetase, mitochondrial OS=Saccharomyces cerevisiae GN=VAS1 PE=1 SV=2	SYV_YEAST
Verprolin OS=Saccharomyces cerevisiae GN=VRP1 PE=1 SV=2	VRP1_YEAST
Very long-chain fatty acid transport protein OS=Saccharomyces cerevisiae GN=FAT1 PE=1 S	FAT1_YEAST
Vesicle-associated membrane protein-associated protein SCS2 OS=Saccharomyces cerevisi	SCS2_YEAST
Vesicular-fusion protein SEC18 OS=Saccharomyces cerevisiae GN=SEC18 PE=1 SV=2	SEC18_YEAST
V-type proton ATPase catalytic subunit A OS=Saccharomyces cerevisiae GN=TFP1 PE=1 SV	VATA_YEAST
V-type proton ATPase subunit a, vacuolar isoform OS=Saccharomyces cerevisiae GN=VPH1	VPH1_YEAST
V-type proton ATPase subunit B OS=Saccharomyces cerevisiae GN=VMA2 PE=1 SV=2	VATB_YEAST
V-type proton ATPase subunit C OS=Saccharomyces cerevisiae GN=VMA5 PE=1 SV=4	VATC_YEAST
V-type proton ATPase subunit d OS=Saccharomyces cerevisiae GN=VMA6 PE=1 SV=2	VA0D_YEAST
V-type proton ATPase subunit D OS=Saccharomyces cerevisiae GN=VMA8 PE=1 SV=1	VATD_YEAST
V-type proton ATPase subunit E OS=Saccharomyces cerevisiae GN=VMA4 PE=1 SV=4	VATE_YEAST
V-type proton ATPase subunit G OS=Saccharomyces cerevisiae GN=VMA10 PE=1 SV=1	VATG_YEAST
WD repeat-containing protein YBL104C OS=Saccharomyces cerevisiae GN=YBL104C/YBL1	YBK4_YEAST
WD repeat-containing protein YCR072C OS=Saccharomyces cerevisiae GN=YCR072C PE=	YCW2_YEAST
WD repeat-containing protein YMR102C OS=Saccharomyces cerevisiae GN=YMR102C PE=	YMZ2_YEAST
WD repeat-containing protein YPL247C OS=Saccharomyces cerevisiae GN=YPL247C PE=1	YP247_YEAST
WW domain-containing protein YFL010C OS=Saccharomyces cerevisiae GN=YFL010C PE=	YFB0_YEAST

Y' element ATP-dependent helicase protein 1 copies 1/5/8 OS=Saccharomyces cerevisiae G	YRF11_YEAST
Y' element ATP-dependent helicase protein 1 copies 3/7 OS=Saccharomyces cerevisiae GN=	YRF13_YEAST
YAP1-binding protein 2 OS=Saccharomyces cerevisiae GN=YBP2 PE=1 SV=1	YBP2_YEAST
Zinc finger protein GIS2 OS=Saccharomyces cerevisiae GN=GIS2 PE=1 SV=1	GIS2_YEAST
Zinc finger protein RME1 OS=Saccharomyces cerevisiae GN=RME1 PE=1 SV=1	RME1_YEAST
Zinc finger protein RTS2 OS=Saccharomyces cerevisiae GN=RTS2 PE=1 SV=1	RTS2_YEAST
Zinc finger protein SFP1 OS=Saccharomyces cerevisiae GN=SFP1 PE=1 SV=1	SFP1_YEAST
Zinc finger protein STP3 OS=Saccharomyces cerevisiae GN=STP3 PE=1 SV=1	STP3_YEAST
Zinc finger protein YPR022C OS=Saccharomyces cerevisiae GN=YPR022C PE=1 SV=1	YP022_YEAST
Zuotin OS=Saccharomyces cerevisiae GN=ZUO1 PE=1 SV=1	ZUO1_YEAST

Raw Results from Mascot									
emPAI Scores									
Replicate A						Replicate B			
WT-GR	**KO-GR**	**MT-GR**	**WT-HS**	**KO-HS**	**MT-HS**	**WT-GR**	**KO-GR**	**MT-GR**	**WT-HS**
0.13	0.13	0.13	1.08	1.08	0.84	0.13	0.28	0.13	1.66
									1.37
			0.09	0.18	0.09				0.09
0.56	0.68	0.4	0.23	0.44	0.56	0.26	0.64	0.17	0.37
0.28	0.38	0.18	0.28	0.28	1.07		0.08	0.38	0.63
0.08	0.14	0.24	0.14		0.18	0.08	0.12	0.32	0.12
				0.07					
0.42	0.34	0.59	0.42	0.26	0.34	0.34	0.42	0.42	0.26
0.22	0.4	0.4	0.14	0.14	0.14	0.07	0.22	0.22	0.14
		0.04	0.35	0.47	0.82			0.09	0.54
	0.79		0.34	0.34	0.79		0.34	0.34	0.79
				0.33	0.76			0.33	
0.63	1.09	0.63	1.09	1.67	2.41	1.67	0.63	0.63	2.41
0.07			0.07		0.07				0.07
					0.15				0.07
			0.15	0.24	0.15		0.15	0.07	0.15
			0.15	0.33	0.15				0.24
0.14	0.39		0.39	0.59	0.82	0.14			0.22
	0.08		0.36	0.16	0.26				0.46
			0.15	0.23	0.07				0.15
0.03		0.03	0.03	0.03	0.03				
			0.22	0.49	0.22				0.35
				0.21					
	0.03	0.03	0.03	0.03	0.03	0.03			
	0.09		0.09	0.2	0.2				0.09
			0.08	0.08	0.08				0.08
			0.29	0.13					
				0.05	0.11				
			0.11						0.16
			0.06	0.03	0.13	0.03		0.03	
				0.16	0.16				0.16
			0.09	0.09	0.09	0.09			0.09
			0.45	0.74	0.91		0.1		0.59
		0.1	0.32	0.32	0.32		0.1	0.1	0.21
			0.09		0.09				
0.25		0.25	0.56	0.25	0.56	0.25			0.25
			0.63	0.28	0.63				0.28
			0.08	0.17	0.17	0.08	0.08	0.08	0.08
	0.09	0.09	0.09	0.19	0.3		0.09		0.09
			0.06		0.13				0.06
			0.1	0.1	0.1				0.1
						0.09			

			0.16	0.16	0.16				0.16
0.22		0.22		0.22			0.22		
			0.45	0.28	0.28			0.13	0.13
			0.15	0.52	0.15		0.15		0.15
		0.37	0.37	0.37	0.37		0.37		
	0.06			0.13	0.06		0.06		0.13
				0.1					
					0.12				
			0.12	0.25	0.12				0.12
	0.11		0.23	0.11	0.51				0.11
					0.09		0.09		0.09
			0.22	0.34	0.22				0.22
			0.13	0.28					0.28
			1.16	0.47	0.47				0.47
			0.11	0.11	0.11		0.11		0.11
	0.23	0.23	0.23		0.23	0.23			0.23
			0.03						
		0.03				0.03			0.03
				0.18					
				0.06					
			0.22	0.04					0.22
	0.09	0.19		1.89	1.89		0.19	0.3	
0.09		0.09	0.09	0.09	0.09				
0.09	0.09			0.09		0.09	0.09	0.09	
		0.44				0.63		0.84	
0.44	0.44		1.35	1.35	1.08		0.84		1.35
0.3	2.66	5.16	3.75	0.68	6.98	1.83	3.75	9.35	1.83
7.04	8.72	16.16	4.51	4.51	8.72	4.51	8.72	7.04	2.77
1.96	1.38	2.67	1.96	4.67	3.56	1.38	1.38	1.38	1.96
2.99	4.93	7.81	2.28	3.87	3.87	6.23	3.87	7.81	2.99
38.3			18.75	18.75	30.24				14.7
	37.28	47.07				59.36	18.33	37.28	
1.31	1.85	1.85	1.85	0.88	1.85	7.14	7.14	9.04	4.35
7.25	4.41	7.25	5.68	4.41	7.25	5.68	7.25	5.68	9.19
14.83	14.83	28.95	14.83	28.95	23.22	18.58	18.58	28.95	11.8
9.74	14.95	14.95	18.44	12.09	18.44	6.23	7.81	12.09	4.93
1.87	4.41	3.38	2.55	3.38	3.38	0.88	7.25	4.41	2.55
18.53	21	30.43	7.5	7.5	18.53	4.95	14.4	26.9	6.55
16.34	26.9	38.86	6.55	5.7	12.67	4.28	11.14	30.43	5.7
2.93	2.93	6.33	2.07	2.47	2.47	0.86	2.47	6.33	1.71
7.66	7.66	13	4.36	16.8	7.66	5.82	7.66	7.66	10.01
4.3	13.44	13.44	6.41	27.14		1.72		6.41	6.41
				27.14	13.44	1.72	9.34	6.41	6.41
8.76	18.33	47.07	11.25	6.77	29.48	14.39	18.33	149.15	6.77
1.31	0.52	1.85	0.88	0.88	0.52	0.52	0.52	1.31	0.88
6.14	7.88	7.88	7.88	6.14	10.04	6.14	10.04	10.04	4.74
4.22	4.22	5.88	5.88	2.01	5.88	5.88	2.96	2.96	2.96

0.63	2.41	2.41	1.67	0.28			0.28		2.41
					1.69	1.69		2.45	
11.83	5.19	11.83	7.91	3.3	7.91	3.3	7.91	11.83	3.3
4.43	18.34	11.67	18.34	44.08	44.08	2.56	18.34		2.56
		11.67	18.34	44.08	44.08	2.56		44.08	
5.66	0.61	3.15	0.61	1.58	0.61	3.15	1.58	1.58	
	0.6	1.54				1.54	0.6		
5.88	5.88	5.88	3.68	2.62	4.32	3.68	3.11	6.82	3.11
34.77	54.93	54.93	13.63	13.63	21.87	13.63	21.87	34.77	21.87
1.11	12.63	3.45	1.11	2.06	2.06	0.45	5.46	1.11	8.38
2.2	2.59	6.22	1.53	2.2	5.42	2.2	4.09	13.5	4.09
0.73	0.98	1.6	0.73	1.27	1.27	0.98	0.73	1.27	0.98
19.82	22.63	56.29	10.06	13.25	13.25	10.06	17.35	49.49	6.57
3.79	4.6	3.79	2.5	2.5	5.55	3.09	6.66	6.66	2.5
1.99	5.55	3.79	2.5	1.99	3.79	2.5	9.48	13.33	2.5
3.54	2.36	7.32	3.54	3.54	4.29	1.89	1.89	4.29	1.13
2.36	3.54	5.15	1.89	2.36	5.15	1.48	1.89	2.91	1.89
			0.69	0.48	0.39	0.07	0.07		0.92
				0.1					
0.08	0.22	0.15	0.17	0.17	0.38	0.1	0.17	0.1	0.22
0.03	0.06	0.06	0.06				0.03		
		1	1.39	0.42	1.84		0.19	0.42	1.39
			0.25	0.12	0.12				0.12
					0.13				
0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18
		0.12							
					0.13				
0.11			0.11						0.11
			0.5	0.5	0.83				0.83
			0.08	0.08	0.17				
			0.2	0.2	0.2			0.2	
							0.26		
		0.21	0.21	0.47	0.21		0.21		0.21
			0.08	0.08	0.17				0.08
		0.41	0.98	0.98	0.98			0.41	0.41
				0.32	0.32		0.32		
0.08			0.17	0.08	0.27	0.17			0.17
			0.18					0.18	
0.25	0.25	0.25		0.25		0.25	0.25	0.57	0.25
				0.2					0.1
				0.11					0.11
0.33	0.33	0.33	0.33	0.78	0.33		0.33	0.33	
			0.2	0.2	0.2				
			0.23						
			0.15		0.33				
		0.13	0.13	0.29	0.13		0.13	0.29	0.13

									0.12
			0.15		0.33				
0.04		0.04	0.18	0.28	0.44				0.28
			0.73		0.2		0.2		
0.36	0.84	0.84	1.26	1.04	1.76	0.84	1.04	1.5	0.84
0.36		0.36		0.36	0.36	0.36		0.36	
	0.36	0.36	0.36	0.36	0.84	3.59	1.49	3.59	1.49
	0.82				0.35		0.82	0.35	
0.06			0.12	0.19					0.06
1.31	1.01	0.75	2.05	1.65	3.63	2.05	1.01	1.31	1.65
3.4	1.57	5.58	1.94	3.4	2.84	1.24	0.96	3.4	0.71
1.79	1.35		0.98		2.31	1.35	0.41		0.67
		3.66		2.31				1.79	
1.13	1.58	2.12	2.12	3.55	3.55	3.55	4.51	4.51	5.65
	0.57		0.83	0.83	1.47	1.12	0.57	0.83	0.83
0.35		0.83		0.83		1.12	0.57		
4.81	2.74		6.23	4.81	2.74	2.74	2	2.74	1.41
		3.71							
4.32	1.65	3.03	2.05	3.63	3.03	1.31	1.01	1.31	1.31
1.15	1.91	1.91	0.84	0.84	0.84	0.84	1.5	0.84	0.84
1.5	1.5	1.91	1.15	1.15	1.5	1.15	1.5	1.15	0.36
10.85	7.52	10.85	4.2	4.2	6.23	4.2	4.2	12.97	2.17
10.85	7.52	10.85	4.2	5.13	6.23		3.41	12.97	2.17
2.74	1.69	2.17	1.69	1.69	2.17	0.64	1.28	0.64	1.28
3.09	0.87	5.55	0.87	1.56	2.5	1.99	0.87	3.79	0.6
0.86	0.86	1.71	1.39	1.39	1.71	2.47	1.39	2.93	1.39
11	6.3	11	6.3	9.17	7.62	4.24	5.19	4.24	2.19
2.04	3.4	4.29	4.29	3.4	4.29	1.52	2.04	2.04	1.52
1.51	1.51	2.63	2.63	3.36	2.02		2.02	2.02	1.51
	0.28	0.63	0.63	0.63	0.63	0.63	0.63	0.63	0.28
63.1	49.87	160.58	49.87	39.37	255.53	31.04	79.77	512.19	19.18
4.56	4.56	8.86	3.6	4.56	5.73	5.73	4.56	5.73	2.8
2.83	2.83	5.81	2.16	3.64	3.64	5.81	2.16	5.81	
3.43	5.77	3.43	4.47	4.47	7.37	3.43	4.47	5.77	5.77
12.2	12.2	9.44	15.69	7.26	3.09	4.17	5.53	41.65	5.53
		5.95	3.52	4.6	7.62	4.6	4.6	4.6	3.52
5.95	4.6								
5.07	3.06	3.97	3.06	3.06	3.06	1.72	2.33	3.97	2.33
0.88	1.38	2.53	1.58	1.2	2.01	1.2	1.58	3.13	1.38
2.17	1.37	0.78	3.22	3.22	6.51	0.78	1.37	3.22	1.37
1.15	0.29	1.15	0.29	0.67	0.67	1.15	0.67	0.67	0.29
1.47	0.97	2.1	1.47	2.1	2.88	3.87	2.1	3.87	2.1
4.15	4.15	5.77	4.15	4.15	1.98	1.98	2.92	4.15	1.98
4.08	4.08		4.08	4.08	2.87		1.95		
3.31	1.65	3.31	1.65	1.65	2.38	1.65	1.08		1.08
								2.38	

5.82	7.66	7.66	4.36	5.82	7.66	3.22	4.36	7.66	5.82
6.95		6.95	9.69	4.91	6.95	2.27	4.91	4.91	4.91
	24.99								
8.14	26.64	82.56	82.56	18.11	56.79	38.97	38.97	38.97	26.64
0.64		1.7		1.7	0.64	0.64		0.64	
									0.68
0.72	0.31	0.72	1.25	0.72	1.95	0.72	1.25	0.72	1.25
2.65	1.64	4.04	1.64	1.64	1.64	1.64	0.91	2.65	0.38
2.14	2.14	2.43	1.21	1.63	2.43	1.21	2.75	2.14	1.63
0.23	0.36	0.11	0.23	0.11	0.36	0.23	0.11	0.11	0.23
			1.76						
1.76	2.87	2.87	2.27	3.59	2.87	0.97	3.59	1.76	2.27
1.37	0.85	2.04	1.69	1.37		0.85	1.1	1.1	1.1
					2.04				
2.37	2.81	3.86	2.81	1.34	2.37	2.37	2.37	2.37	1.34
2.81	3.86	4.49	2.81	2.37	3.86	2.81	2.81	4.49	1.65
	1.2	1.2	2.52	2.01	2.52	3.12	2.52	5.61	
1.99		1.19	1.99	1.56	2.5	1.56	1.99	4.6	1.99
			0.16	0.33	0.16				0.16
0.18	0.4		0.4	0.4	0.65	0.18	0.65	0.18	0.65
0.13	0.06		0.13	0.13					0.06
0.14	0.07	0.18	0.34	0.57	0.43	0.14	0.14	0.14	0.38
0.22	0.26	0.26	0.7	0.76	0.76		0.11	0.14	0.54
	0.07	0.07	0.91	0.79	0.91				0.57
					0.47				0.21
			0.82	1.06	1.32				0.82
				0.1					
0.32	0.45	0.26	0.92	0.67	1.11	0.15	0.32	0.21	1.01
0.29	0.29	0.16	0.66	0.75	0.5	0.16	0.22	0.16	0.75
0.06									
0.38	0.59	0.45	0.52	0.52	0.83	0.26	0.59	0.66	0.52
0.35	0.35	0.5	0.5	1.03	1.75		0.35	0.22	0.83
	0.18		0.18	0.64	0.64	0.09	0.18	0.18	0.64
1.48	1.48	1.41	1.19	1.1	1.55	0.9	2.01	1.62	1.25
				0.27	0.06				
0.1	0.1	0.05	0.1	0.15	0.1	0.05	0.05	0.1	0.1
				0.08	0.08				
0.04	0.04	0.18	0.18	0.33	0.44		0.04	0.18	0.28
0.09	0.09	0.09			0.09	0.19		0.09	
							0.29		
0.12	0.24	0.16			0.27	0.09	0.22	0.09	
0.08	0.05	0.11	0.05	0.03	0.23	0.05	0.2	0.05	
1.48	0.78	0.51	0.64	0.64	3.43	1.48	2.19	0.18	0.51
	0.1	0.1	0.1	0.1	0.1				0.1
0.05			0.05	0.05	0.05			0.11	0.05
			0.05	0.11	0.11				0.11

0.07	0.07		0.14	0.07	0.07		0.07		0.07
		0.04			0.17				
0.37	0.48	0.48	0.87	0.48	1.02	0.08	0.73	0.26	0.87
0.08					0.28		0.08		
0.09	0.19	0.09	0.19	0.3	0.69	0.09	0.3	0.19	0.3
0.64	0.39	0.18	0.18	0.39	0.64		0.18		0.18
0.67	0.67	0.67	0.97	1.34	0.97	0.41	0.67	0.19	0.97
0.22	0.22	0.22	0.22	0.22	0.8	0.48	0.22	0.48	0.22
0.07	0.42	0.42	0.23	0.32	0.63	0.15	0.42	0.15	0.32
					0.04				0.04
							0.05		
			0.27	0.61					0.27
	0.13							0.06	
			0.25	0.25					
				0.09	0.09				
	0.1		0.21						0.21
0.07	0.15	0.15	1.33	1.68	0.76		0.15	0.15	1.87
0.15	0.75	0.15		0.15	0.15		0.15		0.15
									0.14
			0.21	0.14	0.07	0.07	0.07	0.07	0.21
			0.07						0.07
	0.06						0.06		
			0.15						0.15
				0.07					
			0.04	0.04	0.07				0.04
1.71	2.66	3.93	2.31	1.22	5.02	0.82	2.31	6.35	2
			0.3	0.14	0.14				0.48
	0.18	0.18		0.18			0.18		0.18
0.07									
	0.11	0.11	0.11	0.11	0.11	0.11	0.37	0.11	0.11
0.19	0.09	0.09							0.09
	0.06	0.13	0.06	0.13	0.13	0.13	0.13		0.13
					0.06	0.06			
0.06	0.54	0.46	0.11	0.11	0.24	0.11	0.38	0.24	0.18
			0.03						0.07
1.54	3.05	2.06	8.38	12.62	11.4	2.69	3.88	1.79	8.38
0.09	0.09	0.09	0.53	0.67	0.41	0.09	0.09	0.53	0.53
				0.09					
			0.58	0.44					0.44
			0.18		0.12		0.06		
			1.12	0.99	1.12	0.13	0.06		0.99
			2.95	3.77	3.48	0.55	0.45	0.13	2.95
			0.06						0.06
0.08	0.16	0.08			0.08	0.08	0.16	0.08	
		0.06	0.28	0.36	0.74	0.2	0.2	0.13	0.45

0.16	0.16	0.08	0.08	0.08	0.08		0.16	0.08	0.08
0.17					0.17				0.17
					0.09			0.03	0.03
0.14	0.31	0.14	0.14	0.14	0.14		0.14		
		0.08	0.26	0.08	0.36		0.08		0.17
					0.07				
0.12	0.26	0.12	0.12	0.12		0.12	0.12	0.12	0.12
	0.04				0.04				
	0.11		0.11	0.11	0.11			0.11	0.39
			0.22	0.22	0.22				0.22
				0.05					
				0.15					
			0.09						
			0.2	0.2					0.2
	0.07		0.07	0.07	0.07				0.07
0.05	0.02	0.03	0.05		0.02		0.03		0.03
					0.04				
0.07									
0.2			0.2						
	0.06	0.03	0.03	0.03	0.06		0.03	0.03	0.03
0.06	0.06		0.06						
0.21		0.21	0.21	0.21	0.21		0.21	0.21	0.21
			0.09	0.18					
							0.03		
0.02									
	0.02							0.02	
			0.62	0.34	0.21				0.47
			0.08	0.16					0.08
			0.14	0.07					
			0.08		0.25				0.08
			0.05	0.05	0.1				0.05
								0.05	0.05
			0.54	0.64	0.45				0.54
0.17	0.17	0.17	0.6	0.37	0.17	0.37	0.17	0.17	0.37
			0.24	0.31	0.11		0.06		0.24
				0.06					0.06
	0.08		0.82	0.57	0.57				0.57
0.07	0.07	0.07	0.07	0.07	0.07		0.07		0.14
	0.09		0.55	0.84	0.19				0.69
	0.06								
	0.06		0.12	0.06	0.24				0.06
				0.05					0.05
			0.53	0.53	0.37				0.37
			0.13	0.29	0.13		0.13		
					0.35			0.16	0.16

0.19	0.51	0.51	0.7	0.92	1.29	0.13	0.27	0.51	0.81
0.37	0.77	1	4.17	3.86	4.17	0.37	1.14	1.42	3.86
				0.19				0.19	
			0.22						0.22
							0.35		
	0.34	0.34			0.34		0.34	0.34	0.34
0.29	0.29	0.29	0.29	0.29	0.29	0.29	0.29	0.29	0.29
	0.11	0.11	0.22	0.49	0.65	0.11	0.11	0.11	0.49
			0.27	0.27	0.27				0.27
							0.61	0.61	
			0.4		0.96				
0.03		0.03	0.03	0.07	0.07		0.07		0.07
					0.02				
0.04	0.6	0.24	0.83	0.91	1.36	0.09	0.29	0.24	1.17
			0.74	0.82	1.35		0.24		0.98
	0.05						0.05		
0.36	0.5	0.54	0.6	0.3	0.67	0.39	0.63	0.85	0.36
		0.36	0.18	0.3	0.38			0.38	0.22
			0.04		0.04				
					0.58				
0.1								0.03	
	0.1	0.1	0.03	0.13	0.1	0.03	0.1		0.03
1.78	1.78	1.22	1.94	2.3	1.78	0.98	1.48	1.09	1.48
0.34	0.7	0.42	0.6		0.51	0.34		0.27	
				0.7			0.6		0.51
0.04	0.08		0.13	0.08	0.13		0.13		0.13
0.14	0.14	0.14	0.21	0.14	0.47		0.14	0.07	0.14
0.05	0.05	0.05	0.05				0.05		0.05
				0.05					
0.33	0.33	0.33	0.24	0.33	0.33	0.16	0.33	0.07	0.24
0.23	0.36	0.29	0.29	0.29	0.43	0.11	0.36	0.05	0.23
2.2	2.56	3.4	5.38	4.74	7.76	3.64	5.38	5.38	5.05
0.27	0.35	0.43	0.35	0.35	0.62	0.13	0.43	0.43	0.35
0.03	0.15	0.06	0.03		0.12		0.26		0.03
0.18	0.23	0.13	0.23	0.18	0.23		0.13	0.04	0.23
0.36	0.86	0.59	0.72	0.47	0.72	0.08	0.59	0.47	0.72
0.08	0.26	0.16	0.08	0.08	0.08		0.16		0.08
0.84	1.08	0.96	1.21	0.84	1.35	0.36	0.84	0.28	0.96
0.04	0.04		0.04	0.08	0.17		0.04	0.04	
									0.08
0.51	0.44	0.51	0.31	0.31	0.73	0.26	0.51	0.44	0.58
			0.06	0.06	0.06		0.18		
0.07	0.32	0.15	0.15	0.15	0.41	0.15	0.51	0.07	0.23
						0.2			

0.45	0.36	0.54	0.74	0.54	0.54		0.45	0.36	0.45
			0.05	0.05	0.05		0.05		0.05
						0.09			
	0.22								
						0.08			
	0.02				0.02				
			0.06		0.06				0.06
			0.15	0.15					
					0.15				
									0.17
			0.06						
		0.05	0.61	0.61	0.45	0.24	0.11		0.61
			0.17	0.3	0.3	0.17	0.11		0.24
			0.18	0.38	0.13				0.18
			0.94	1.11	0.64	0.09	0.18		0.94
0.08			0.48	0.48	0.17				0.61
0.05	0.05	0.05	0.05				0.05	0.05	0.05
0.18	0.18	0.06	0.18	0.18	0.18	0.06	0.25	0.06	0.25
0.05	0.05	0.05	0.05	0.05	0.1	0.05	0.05	0.05	
0.02	0.02						0.02		
					0.04				
	0.23	0.15					0.15	0.07	
0.07	0.15	0.11	0.15	0.15	0.07	0.03	0.07	0.03	0.11
0.39	0.48	0.48	0.39	0.53	0.64	0.07	0.39	0.26	0.34
						0.15			
	0.19						0.19	0.19	0.19
			0.07	0.07					0.07
			0.17	0.17	0.17				0.17
	0.23						0.23		
0.25	0.55	0.34	0.34	0.55	0.8	0.08	0.55	0.25	0.44
									0.08
	0.08								
			0.32		0.15	0.15	0.15	0.15	0.32
						0.06			
			0.32	1.01	3.05	0.75	0.32		1.66
						0.04			0.04
	0.04								
									0.03
	0.11		0.11		0.11		0.11	0.11	
				0.06	0.06		0.06		
0.12	0.12	0.06	0.06	0.06	0.06	0.06	0.12	0.18	0.12
	0.06						0.06		
0.06	0.13	0.13	0.06	0.06	0.13	0.06	0.06	0.13	0.13
			0.11	0.11	0.24				0.11
			0.12	0.12	0.12				0.12
0.55	0.55	0.85	1.86	2.12	2.41	0.69	1.2	1.62	1.86

				0.14					
			0.81	0.81	1.49	0.11	0.11	0.11	1.36
			0.14		0.3				0.48
0.11	0.23	0.11	0.23	0.11	0.36		0.23	0.11	0.11
	0.17	0.23	0.3	0.37	0.3	0.05	0.17		0.23
0.59	0.32	0.75	0.59	0.75	0.75	0.59	0.92	0.92	0.75
0.54	0.79	0.79	0.92	1.22	1.39	0.24	0.79	0.92	0.54
1.26	1.43	2.52	1.82	2.04	2.27	0.68	1.62	1.43	1.62
			0.04		0.04				0.04
0.22			0.35	0.5	0.35		0.11	0.11	0.5
0.68	0.78	1.12	1.24	1.24	1.99	0.59	1.24	0.89	1
0.17									
0.04	0.16	0.08	0.35	0.41	0.41	0.04	0.08	0.12	0.41
	0.08	0.08	0.04	0.08	0.12		0.12	0.04	0.08
									0.03
									0.06
0.15	0.27	0.33	0.1	0.15	0.05	0.15	0.21	0.27	0.05
0.01	0.01	0.03	0.01	0.01	0.03		0.01	0.01	0.01
							0.07		
			0.12	0.12	0.12				0.25
					0.16	0.08			
								0.15	
1.2	1.2	1.2	0.73	1.03	1.03	0.73	1.03	1.03	0.6
								0.07	
				0.03	0.03				
			0.1	0.22	0.1				0.22
		0.05					0.11		
					0.15		0.05		
	0.03	0.03		0.03	0.03				
0.52	0.8	0.52	0.52	0.4	0.66	0.18	1.14	0.29	0.96
				0.08	0.08				
		0.07							
0.03		0.03	0.03	0.07	0.07		0.03	0.03	0.03
				0.06					
			0.06		0.06				
			0.05		0.05				
			0.07	0.15	0.15				0.15
			0.05	0.11	0.05				0.05
			0.07	0.07	0.15				0.15
	0.02		0.11	0.09	0.21		0.02		0.18
					0.1				
								0.07	
			0.25						
0.14	0.21	0.3	0.58	0.48	2.22	0.68	0.38	0.38	0.91
							0.06		
0.04	0.04	0.06	0.35	0.25	0.51	0.06	0.12	0.06	0.25

0.14	0.14			0.14	0.29		0.14	0.14	
0.03	0.03	0.08	0.2	0.2	0.2	0.03	0.05	0.08	0.17
	0.03		0.14	0.17	0.07				0.07
	0.11	0.04	0.04	0.04	0.07				0.04
				0.06					0.06
			0.11	0.5	0.5		0.11		0.5
					0.03				
			0.17	0.17					0.17
	0.23				0.88		0.53		
	0.1	0.1	0.1	0.2					0.1
				0.04					
				0.08					
			0.11						0.11
		0.05							
			0.19						
0.01	0.01	0.01	0.09	0.04	0.11		0.03		0.06
		0.08						0.08	
0.27	0.1	0.05			0.54	0.21	0.21	0.05	
			0.29		0.29				
			0.21	0.33	0.46				0.33
		0.06							
	0.1	0.1		0.1	0.1				0.1
0.24	0.31	0.11	0.38	0.38	0.45		0.31	0.24	0.17
			0.06	0.17	0.11				0.11
0.22	0.1	0.1				0.1			
			0.69	0.92	0.92	0.14	0.07		0.8
					0.07				
	0.13		0.06	0.2	0.13		0.06	0.06	0.2
	0.18		0.18	0.38	0.18				0.28
0.07	0.14		0.14	0.21	0.29		0.07		0.21
			0.13	0.13	0.06				
2.64	2.64	2.64	1.37	1.94	2.64	1.37	12.26	5.95	1.94
					0.1				
0.2		0.2		0.2	0.2		0.2		
			0.23	0.41	0.51				0.73
			0.67	0.53	0.67				0.53
			0.58	0.58	0.58				0.99
		0.16	0.16	0.34	0.34		0.16	0.16	0.16
			0.12						0.12
13.99	98.79	32.79	24.77	13.99	43.29	43.29	43.29	43.29	13.99
			0.22					0.22	0.22
			0.22						
			1.17	0.79	0.79				1.17

			0.57	0.57					
			0.11	0.11	0.11				0.11
0.05	0.05		0.1						
									0.04
					0.09				
						0.07			
				0.1					
				0.07	0.07				0.07
0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09		0.09
			0.19	0.7	0.3				0.43
	0.35		0.83	0.83	0.35				0.83
		0.21	0.1	0.1				0.1	
			0.06		0.06				
					0.06				
			0.31	0.58	0.1				0.2
0.34	0.34	0.34	0.1	0.1	0.34		0.47	0.1	0.34
			0.21	0.1	0.21				0.46
			0.27	0.27	0.17				0.27
		0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09
						0.05	0.05	0.05	
0.57	0.67	0.47	1.45	0.9	1.02	0.21	0.67	0.9	1.02
0.59	0.59	0.49	0.82	0.82	0.82	0.59	0.7	0.7	0.7
			0.23	0.07	0.15	0.07			0.23
				0.1					
			0.18	0.06	0.25				0.25
					0.06				
0.25	0.47	0.12	0.55	0.25	0.39	0.06	0.47	0.12	0.55
		0.1	0.21	0.1	0.1		0.1		0.1
									0.08
					0.05				
			0.06	0.12	0.12				0.26
			0.21	0.21	0.13		0.06		0.21
	0.08						0.08		
							0.04		
	0.06				0.06				
0.04									
					0.03		0.03		
0.04									0.02
0.05									
					0.06				
					0.01				0.01
	0.03								
0.02									
	0.08	0.08	0.08	0.16					0.08
0.14	0.14	0.07			0.07				
0.03	0.11		0.07	0.03	0.07	0.03	0.07	0.07	0.03

					0.04				
	0.02				0.02				
			0.08	0.17					0.08
					0.02				
0.02						0.02			
									0.04
					0.04				
			0.06	0.06					0.06
			0.04						0.04
			0.07		0.07	0.02	0.02		0.02
	0.04		0.04	0.04	0.04				
					0.11				0.11
				0.04	0.04				
0.18	0.14	0.16	0.16	0.12	0.16	0.04	0.14		0.16
0.28	0.28						0.28		0.28
0.08	0.08	0.03	0.14	0.14	0.17	0.03	0.2	0.03	0.17
0.14	0.14				0.14	0.14	0.14		
0.1	0.1						0.1		
0.16	0.08	0.08	0.08		0.25	0.08	0.16		0.08
0.02	0.02	0.02	0.14	0.16	0.22	0.02	0.06		0.16
			0.28		0.28				0.63
	0.03	0.03	0.11	0.13	0.08		0.03		0.13
				0.1	0.1				
				0.14		0.14			
			0.3						
0.03			0.03	0.03	0.03		0.03		
			0.1						0.1
			0.2	0.44	0.2				
0.58	0.9	0.58	1.08	1.28	1.49	0.2	0.9	0.44	1.08
0.23	0.52	0.52	0.23	0.23	0.23	0.23	0.23	0.23	0.23
0.15	0.15		0.15	0.15	0.15	0.15	0.15		0.15
				0.22					
0.52	0.52	0.52	1.31	1.31	0.52		0.52	0.52	0.52
	1.17	0.47	1.17	2.19			0.47		0.47
0.21	0.28	0.13	0.99	0.99	1.71	0.13	0.21	0.21	0.99
	0.07								
									0.05
0.18	0.51	0.39	0.28	0.28	0.51	0.18	0.51	0.39	0.18
	0.14	0.14						0.14	
	0.02		0.02		0.03		0.02		0.02
0.25	0.25			0.12	0.25		0.12	0.12	0.25
					0.09				
	0.26	0.26	0.26	0.26	0.26		0.26		0.26
	0.07				0.15		0.07	0.15	

				0.04	0.04				
					0.05				
			0.04				0.04		0.07
0.19	0.29	0.29	0.14	0.19	0.09		0.24	0.14	0.09
			0.08	0.08					
0.26	0.26	0.26	0.3	0.26	0.46	0.12	0.3	0.21	0.3
				0.17	0.17				0.17
0.05	0.02	0.02			0.1		0.05		
54.21	58.16	109.25	88.59	88.59	177.9	77.02	71.8	88.59	40.87
0.35	0.35	0.35	0.35	0.35	0.35	0.35	0.35	0.35	0.35
0.34	0.16	0.25	0.25	0.34	0.8	0.16	0.08		0.16
0.45		0.35	0.56	1.1	0.95	0.35	0.16	0.45	0.45
1.84	1.27	2.69	1.54	1.95	3.61	1.84	1.74	2.3	0.96
0.77	0.52	1	0.52	0.77	1	0.72	0.88	0.48	0.57
0.07	0.24	0.15	0.24	0.33	0.43		0.15	0.15	0.33
0.09	0.09			0.09			0.09	0.09	
	0.02		0.02	0.02	0.05				0.02
	0.06		0.06						0.06
0.1	0.1	0.1	0.1	0.1	0.1		0.1	0.1	0.1
	0.12		0.12		0.25				0.25
0.12	0.12	0.12	0.18	0.4	0.4	0.06	0.12	0.06	0.25
			10.44	28.87	10.44	2.26	1.09	1.09	15.55
0.56	1.42	0.56	18.05	33.34	19.51	2.25	1.81	2.5	24.58
					0.16				
							0.1		
			0.77	0.93	0.63	0.09			0.63
					0.07				
0.16	0.1	0.27	0.05	0.05	0.1	0.05	0.1	0.05	
						0.08		0.08	
	0.13		0.13	0.13	0.13		0.27		
0.08	0.08	0.08	0.08	0.08	0.16			0.08	
	0.1	0.1		0.1	0.1		0.1	0.22	
		0.08	0.08	0.08	0.08		0.08		0.08
							0.22	0.48	
	0.22	0.11		0.35		0.11			
0.13	0.28	0.13	0.44	0.85	0.44		0.13	0.28	0.28
	0.06		0.06	0.06	0.13		0.06		
	0.03		0.07	0.03	0.03				
0.03	0.07	0.03	0.03		0.1		0.07		
0.31	0.44	0.5	0.31	0.25	0.37	0.15	0.37	0.31	0.37
0.89	1.33	0.89	1.33	1.5	1.68	0.42	0.89	0.89	1.17
			0.21		0.21		0.21		0.21
0.1	0.1	0.1		0.22	0.1	0.1	0.1		
0.54	0.72	0.54	0.72	0.72	1.39	0.11	1.14	0.39	1.14

0.35	0.52	0.52	0.61	0.52	0.61	0.13	0.52	0.27	0.61
	0.05		0.1	0.16	0.16				0.16
0.25	0.56	0.46	0.13	0.17	0.42	0.1	0.33	0.17	0.17
0.27	0.32	0.27	0.08	0.13	0.37	0.04	0.22	0.04	0.22
	0.08	0.08			0.04	0.04	0.08		
0.12									
0.12	0.12	0.25	0.4	0.57		0.12	0.4	0.25	0.4
					0.4				
	0.09		0.09	0.19	0.19	0.09	0.19	0.09	0.09
	0.12						0.12		
	0.07	0.15	0.15	0.15	0.15				0.15
0.75	0.52	1.32	0.15	1.02	0.75		0.32	0.15	0.52
0.08	0.26	0.08	0.08	0.16	0.26	0.08	0.08	0.08	0.08
1.67	1.2	2.96	2.25	1.2	2.96	1.67	1.67	1.67	1.2
0.06	0.17	0.06	0.06	0.17	0.2	0.06	0.2	0.03	0.1
0.14	0.14		0.29	0.14	0.14			0.14	0.14
0.71	1.24	0.31	1.24	1.24	1.24	0.31	0.71		1.24
0.05	0.05	0.05							
			0.04	0.04	0.07				
			0.07	0.14	0.1				0.07
0.02					0.02				
					0.03		0.03		0.03
		0.04			0.04				0.04
0.06	0.06	0.06	0.03	0.12			0.06		0.03
	0.04								0.09
				0.11					
					0.29				
					0.35				
			0.15						
		0.03							
			0.18	0.06	0.32				0.12
	0.12	0.09	0.34	0.12	0.47	0.03	0.06	0.03	0.27
			0.23	0.11	0.23				
			0.13	0.28	0.13				0.28
			0.25	0.25	0.12				0.25
					0.09				
0.07	0.18	0.13	0.25	0.14	0.33	0.02	0.07	0.09	0.2
0.13	0.17	0.17	0.18	0.2	0.24	0.06	0.11	0.08	0.24
					0.04				
								0.05	
			0.08	0.08		0.08		0.08	
					0.05				0.05
0.25	0.25	0.25	0.81	1.1	0.81	0.08	0.16	0.35	0.68
				0.31	0.31				0.31
0.17	0.37	0.27	0.48	0.88	0.73		0.27		0.48
0.04	0.04				0.04		0.04	0.04	

			0.26	0.26	0.36				0.17
	0.14		0.14		0.14		0.14	0.14	
	0.42	0.19	3.38	2.68	2.68	0.42	0.84	0.42	2.37
0.07			0.22	0.22	0.3	0.07		0.07	0.38
			0.31	0.23	0.31	0.15	0.15		0.23
	0.08		0.03	0.03	0.09				0.06
				0.16					
	0.05								
									0.11
			0.04		0.04	0.04	0.04	0.04	0.04
0.07	0.07	0.07	0.22	0.07	0.31	0.07	0.14	0.07	0.07
0.11				0.22	0.22			0.11	
			0.99	0.75	1.25	0.21	0.13	0.28	1.4
	0.04	0.04	0.09	0.04	0.14				0.09
			0.06	0.2	0.2				0.2
			0.22	0.35	0.22	0.11	0.11		
	0.12		0.4	0.49	0.49				0.33
				0.07					
		0.04				0.04			0.04
0.25	0.44	0.16	0.55	0.34	0.44		0.34	0.34	0.34
			0.3	0.23	0.52				0.3
0.03	0.01	0.03	0.06	0.05	0.11				0.08
							0.05		0.05
			0.51	0.39	0.94				0.78
0.04	0.09	0.04	0.09	0.09	0.14		0.04		0.09
	0.23	0.23	0.23	0.53	0.53	0.23	0.23	0.23	0.53
	0.2			0.44	0.2				0.2
0.07	0.07	0.07	0.21	0.38	0.21			0.07	0.21
			0.14	0.14	0.47			0.14	0.14
						0.14			
									0.06
		0.78	1.61	2.49	1.37				3.23
		1.87	2.82	2.82	2.47	1.87	2.82		4.61
1.88	1.88	2.17	3.23	3.65	2.84	1.88	3.65	3.23	5.83
		0.08	0.08	0.08	0.08			0.08	0.08
	0.07	0.07		0.07	0.07		0.15		
									0.04
		0.05	0.05	0.05	0.05		0.05	0.05	0.05
									0.2
					0.06				
			0.19	0.19				0.09	0.19
	0.04	0.61	0.68	0.92	2.23	0.24	0.24	0.42	0.61
		0.08	0.02		0.3			0.08	0.06
			0.45	0.6	1.24	0.07	0.07		0.66
							0.07		

			0.38	0.32	0.51				0.38
			0.05						
	0.06		0.27	0.34	0.06				0.13
			0.03	0.03					
0.02	0.02	0.02		0.02		0.02	0.07	0.04	
				0.09					
			0.06		0.06				0.21
				0.64	0.28				0.28
			0.09	0.2					
			0.06	0.06	0.06				0.06
0.07	0.31	0.12	0.12	0.19	0.24	0.04	0.24	0.07	0.14
	0.05	0.05							
			0.05						
				0.06					
		0.05							
			0.15		0.15				0.31
				0.09					
0.53	0.81	0.4	1.33	0.81	1.33		0.66	0.53	1.33
0.8	0.55	2.24	0.55	0.8	0.55	0.34	0.55	0.8	0.34
			0.14	0.14	0.14				0.14
0.1	0.1	0.32	0.21	0.21	0.21	0.1	0.21	0.1	0.1
			0.34	0.34	0.34				0.34
				0.16					0.16
	0.09		0.09	0.09					0.09
			0.02						
			0.04		0.04		0.04		0.04
2.27	0.64	2.27	1.43	2.99	1.96	1.43	0.35	1	1
			0.69	0.69	0.69				0.69
				0.18					
0.17	0.17	0.17	0.61	0.37	0.37	0.37	0.37	0.61	0.37
0.8	1.67	0.8	1.67	0.8	1.2	1.2	2.25	0.8	1.67
1.58	1.58	1.58	3.15	1.58	3.15	0.61	3.15	0.61	5.66
0.66	1	0.56	1.14	1.27	1.42	1	1.42	0.88	1.27
			0.13						
			0.14	0.31	0.14				0.31
	0.03	0.03	0.85	1.12	1.78	0.07	0.03	0.07	0.98
			5.37	7.48	5.37	0.33	0.15	0.15	5.37
			0.38	0.62	1.06	0.17	0.17	0.08	0.76
	0.26	0.33	2.51	2.71	4.23	0.49	0.41	0.41	3.41
			0.31	0.21	0.7	0.04			0.46
0.05	0.2	0.25	0.57	0.79	0.87	0.25	0.5	0.09	1.05
			0.43	0.5	0.64	0.14		0.05	0.64
1.99	2.65	1.85	5.01	5.98	9.41	1.01	1.99	2.15	4.72
1.86	2.32	1.86	4.47	6.03	9.48	1.23	2	2.16	4.47
					0.9				
			1.99	2.15	3.24	0.35			2.31

3.77	5.51	4.29	4.57	3.3	5.86		5.18	4.29	4.02
4.02	5.86	4.57	4.87	3.53	6.23	2.49	5.18	4.29	4.29
0.34	0.8	1.2	2.25	2.25	4.32	0.1	0.72	0.99	2.59
	0.05		0.23	0.11	0.3				0.37
0.04	0.04	0.01	0.01	0.03	0.06	0.01	0.04		0.01
		0.28		0.28					
			0.02	0.07	0.02				0.02
			0.07	0.07	0.14	0.07	0.14		0.07
					0.1				
			0.67	0.57	0.57				0.67
	0.07		0.14	0.29	0.14				0.07
	0.13	0.13	0.13	0.13	0.13		0.13	0.13	0.13
	0.05	0.1					0.1	0.15	
	0.06	0.25	0.32	0.25	0.56		0.06	0.39	0.25
	0.03		0.03		0.03		0.03		
	0.04								
			0.04	0.04					0.04
			0.12	0.12	0.12				0.06
0.07	0.07	0.14			0.07			0.07	
	0.04								
				0.11					
				0.06					
					0.04				
0.19	0.09	0.25	0.09	0.09	0.14	0.09	0.19	0.09	0.14
			0.07	0.07	0.33				
0.45	0.64	0.28	0.45	0.28	0.85	0.28	0.85	0.28	0.64
0.61	0.61	1.04	0.61	0.61	1.59	0.61	1.04	2.29	1.59
1.01	1.54	1.54	1.54	1.54	2.2	1.01	1.01	1.54	2.2
			5.53	7.26		4.17	5.53		5.53
4.17	4.17	5.53	5.53	7.26	9.44		5.53	4.17	5.53
0.93	0.24	0.55	0.55	0.93	0.24	0.93	0.55		0.55
31.74	103.73	77.31	103.73	103.73	447.08	139.07	186.32	103.73	186.32
	0.03	0.03	0.03						
				0.21					
			0.05	0.05	0.05				
0.25	0.44	0.67	0.44	0.44	0.8	0.34	0.44	0.67	0.34
				0.2		0.09			
			0.19	0.19	0.09				0.19
	0.2				0.2		0.2		
0.09	0.09		0.09	0.09	0.09		0.09		0.09
0.06	0.06		0.13	0.29	0.13		0.06	0.06	0.13
				0.14					
	0.06	0.06	0.12	0.19	0.06		0.12		
	0.04		0.04	0.04	0.04		0.04		0.04
	0.03		0.03	0.03	0.06				

				0.07	0.07				0.07
	0.03	0.03	0.07	0.1	0.07		0.14	0.03	0.07
					0.07				
					0.03				
					0.02				
	0.14		0.09	0.09	0.09		0.09	0.09	0.09
									0.26
0.17	0.38	0.17	0.17	0.17	0.17		0.38	0.38	0.38
	0.1	0.1			0.1	0.1	0.1	0.1	
0.11	0.11	0.11	0.24	0.37	0.37		0.11	0.11	0.24
	0.2		0.96	0.96	0.63		0.2		0.96
	0.03				0.03				0.03
0.07	0.07	0.07	0.14	0.14	0.14		0.07		0.07
0.12	0.15	0.06	0.03	0.03	0.09	0.03	0.06		0.06
			0.06						0.06
	0.21	0.21			0.21				
							0.22		
									0.05
			0.28	0.13					0.13
0.09	0.09	0.19	0.19	0.3	0.55	0.09	0.3	0.3	0.19
0.19	0.54	0.83	1.38	1.18	3	0.41	0.68	0.83	1.59
	0.16			0.24	0.43		0.16	0.54	0.16
1.2	1.2	1.93	1.2	0.91	1.54	0.91	1.73	2.9	0.91
			0.03	0.09	0.03				0.03
			0.11	0.11					0.11
									0.03
			0.04						0.04
			0.06	0.06	0.06				0.06
			0.12	0.12	0.06				0.12
0.05	0.05	0.05	0.05	0.03	0.11		0.14		0.05
0.26	0.37	0.37	0.6	0.26	0.72		0.72	0.37	0.48
0.18	0.09	0.18	0.09	0.18	0.18	0.18	0.09		0.28
			0.04		0.04				
								0.02	
	0.03						0.03		
	0.04								
0.05			0.05	0.05	0.05				
									0.05
			0.07						
			0.15	0.15	0.07				0.15
				0.11	0.11				
			0.74	1.3	1.3		0.1	0.1	0.59
					0.06				

	0.12								
	0.06		0.12		0.06				0.06
0.1	0.1	0.1	0.05	0.05	0.21		0.05		
						0.14			
0.42	0.32	0.42	0.23	0.23	0.52	0.15	0.42	0.32	0.15
									0.09
			0.04	0.04					0.04
	0.03		0.06	0.03	0.09				0.06
	0.1	0.05			0.21		0.05	0.05	0.05
		0.05							
	0.08			0.08					0.16
0.05	0.05	0.14	0.2	0.14	0.49	0.05	0.14	0.05	0.14
				0.05					
	0.05		0.43	0.57	0.31		0.05		0.5
						0.2			
			0.5	0.91	0.62	0.18	0.08	0.08	0.62
0.31	0.24	0.64	0.18	0.06	0.31	0.24	0.31	0.55	0.18
0.25	0.47	0.65	0.12	0.12	0.32	0.47	0.32	0.65	0.18
0.05		0.05							
	0.06		0.04	0.02	0.04				0.02
	0.05			0.05					0.05
						0.05			
					0.14				
						0.04			
	0.29	0.07	1.44	1.6	1.6	0.21	0.07		1.6
			0.1	0.47	0.78				0.21
0.45	1.52	1.3	1.3	0.91	1.76	0.74	1.52	2.03	1.3
	0.06								
	0.09								
									0.03
0.07	0.07	0.07	0.07	0.07	0.07		0.07		0.07
0.08	0.08	0.08	0.08	0.08	0.08		0.08	0.08	0.08
	0.06								
0.84	1.19	0.84	1.01	1.01	1.61	0.55	1.19	1.19	1.19
	0.07		0.15	0.15	0.07				0.07
		0.06		0.06					
							0.05		
0.05	0.07	0.02	0.05		0.12		0.02		0.02
				0.25					0.25
			0.03		0.03				0.03
			0.25						
							0.03		
			0.35	0.35	0.56				0.35
0.27			0.62	0.62	0.27				0.62

0.04									
0.04	0.09	0.09	0.09	0.09	0.14	0.04	0.09		0.09
						0.04			
			0.07						0.15
0.08	0.08	0.08	1.4	1.05	1.6	0.17	0.08	0.08	1.4
			0.16	0.16	0.08	0.08	0.08	0.08	0.16
0.04	0.04		0.23	0.13	0.18	0.04	0.04	0.04	0.08
				0.14					
				0.01	0.01				0.01
		0.05							
			0.04	0.04	0.04				0.04
0.21	0.46	0.46	0.46	0.46	1.13	0.21	0.46	0.77	0.21
				0.11					0.05
	0.22	0.22					0.22	0.11	0.11
					0.12				0.26
0.11	0.11	0.11				0.11			
0.09	0.09	0.18	0.09		0.18		0.18	0.09	0.09
							0.06		
					0.06				
						0.08			
0.22	0.22	0.49	0.11	0.22	0.22	0.11	0.11	0.11	0.11
									0.37
0.41		0.12	0.26	0.26	0.58		0.41		0.12
			0.09	0.18			0.09		0.09
					0.37				0.37
					0.21	0.21			
	0.23	0.23	0.23		0.23			0.23	0.23
	0.13								
0.33	0.42	0.53	0.42	0.53	0.42	0.24	0.76	0.33	0.76
				0.18		0.18		0.18	0.18
			0.09	0.09				0.09	
				0.63					
0.05		0.16	0.1	0.05	0.1	0.05	0.22	0.22	0.05
	0.04								
0.1		0.1			0.1			0.1	
			0.04		0.04				0.04
		0.08			0.47	0.08	0.08		0.17
0.4	0.96	0.4	4.41	5.77	2.45	1.2	1.75	1.2	2.86
			0.04						
0.22			0.1						
			0.13						0.13
0.12	0.12	0.12	0.42	0.59	0.78		0.12	0.26	0.42

0.69	1.31	1.08	0.87	0.69	1.85	0.52	1.31	1.85	1.08
					0.11				
0.47	1.17	1	1.34	1.73	3.69	1.17	2.19	1.73	1.95
	0.04								
0.04	0.04	0.04	0.04		0.04		0.04	0.04	
	0.07			0.07					0.07
			0.07	0.07	0.07			0.07	0.07
0.18	0.09	0.09	0.09	0.18	0.09	0.09	0.09		0.09
			0.24	0.15					0.15
									0.08
				0.06	0.06				
			0.17						
			0.82	0.22	0.82				0.49
	0.03	0.03						0.03	
			0.11	0.11	0.11				
			0.15	0.15	0.15				0.15
			0.1	0.1					0.1
0.29	0.29	0.17	0.29	0.17	0.23	0.05	0.17	0.11	0.29
								0.17	0.17
	0.18	0.18	0.18		0.18				
	0.29	0.13	0.46	1.13	0.46	0.46	0.13		0.88
							0.03		0.03
0.04				0.07		0.04			
0.14	0.14	0.3	0.14	0.48	0.3		0.3		0.3
			0.03	0.07					
			0.72	0.72	0.72			0.2	0.72
			0.25	0.25					
	0.07			0.04	0.07				
4.12	4.12	3.18	13.22	16.45	13.22	3.18	4.12	5.28	5.28
0.5	0.5	0.23	0.23	0.85	0.5	0.5	1.78		0.5
0.42	0.54	0.5	0.35	0.28	0.39	0.28	0.68	0.63	0.35
				0.02		0.02	0.02		
0.02	0.04		0.04	0.04	0.04	0.06	0.14		
0.13	0.16	0.13	0.16	0.16	0.25	0.19	0.22	0.02	0.22
0.17	0.2	0.08	0.08	0.11	0.26	0.2	0.36	0.03	0.08
							0.06		
			0.33	0.33	0.33				0.15
				0.13					0.27
	0.03	0.07					0.03	0.07	0.03
					0.18				
			0.09	0.19	0.19				0.19
	0.06	0.06	0.06		0.12		0.06		
			0.05		0.1	0.05		0.05	0.1
			0.08		0.08				0.08
0.24	0.72		0.24	0.24			0.55	0.24	0.39
		0.54			0.39				

0.11	0.11	0.22		0.22	0.35			0.11	0.22
	0.09		0.09	0.09	0.19				0.19
	0.17		1.51	1.33	0.47	0.17	0.17	0.17	1.15
			0.05	0.05	0.05				
			0.45	1.1	1.3	0.2	0.2	0.1	1.3
			0.97	0.79	1.17	0.21	0.21	0.1	1.9
			0.09	0.09	0.09				
			0.52	0.52	0.15				1.15
						0.07			
								0.1	
0.44	0.72	0.2	0.44	0.44	0.2	0.2	0.44	0.44	0.72
					0.49		0.22		
				0.08					
0.02									
0.19	0.23	0.07	0.19	0.11	0.23	0.04	0.19	0.04	0.23
			0.44	0.56	0.56	0.08	0.08	0.04	0.76
			0.38	0.54	0.24				0.71
		0.15	0.51	0.51	0.51				0.73
			0.13		0.13				0.13
								0.08	0.08
			0.15	0.24	0.15				0.15
			0.11	0.11					0.11
			0.42	0.6	0.6				0.42
0.04	0.04	0.08				0.04	0.04		
					0.06				
		0.64							
1.04	0.43	1.43	0.43	0.7	1.43	0.43	0.43	0.7	0.43
			0.33						0.33
				0.08					
			0.45	0.64	0.85				0.85
				0.04	0.04				
0.04	0.04	0.04			0.08	0.04			
				0.39	0.39				
0.43	0.52	0.27	0.62	0.43	0.82	0.27	0.43	0.2	0.62
0.08	0.08		0.08		0.08		0.17		
0.02	0.02	0.05	0.02	0.01	0.02		0.02	0.06	
					0.06				
					0.1	0.1			
			0.05	0.05	0.09				0.07
0.56	1.59	1.28	0.56	0.37	0.88	0.29	0.77	0.66	0.56
			0.26	0.26					
0.04	0.08	0.04	0.08	0.04	0.04	0.04	0.12	0.04	0.04
0.09		0.04	0.09	0.04	0.04		0.04		0.04
				0.06	0.06			0.06	0.06
	0.05		0.1	0.1	0.1	0.05			0.1
0.15	0.15	0.21	0.52	0.26	0.21	0.1	0.15	0.05	0.32

0.21	0.65	0.65	0.28	0.65	0.55	0.37	0.55	0.45	0.45
0.03	0.07	0.03	0.03	0.15	0.09	0.03	0.09	0.02	0.03
			0.03	0.03					
0.07	0.22	0.14	0.3	0.39	0.39	0.14	0.39	0.14	0.49
0.08	0.16			0.08	0.08				
0.08	0.26	0.16	0.08	0.08	0.46	0.08	0.26	0.08	0.16
0.14	0.25	0.14	0.25	0.25	0.14	0.05	0.2	0.09	0.09
1.65	2.38	1.82	3.87	2.59	2.59	1.82	3.31	1.65	3.87
1.07	1.81	2.17	2.81	2.58	3.05	1.2	2.17	2.37	2.58
	0.31		0.14	0.31	0.72		0.31	0.14	0.97
0.15	0.21	0.18	0.21	0.18	0.15	0.06	0.28	0.03	0.24
		0.06	0.06	0.06					0.06
	0.09		0.19	0.09	0.19		0.19		0.09
					0.05				
0.2	0.08	0.2	0.16	0.11	0.2		0.08	0.11	0.08
0.04	0.04	0.04	0.08		0.08	0.04	0.08		0.04
	0.07	0.07	0.07		0.07		0.07	0.04	
0.06	0.13	0.09	0.13	0.06	0.16	0.03	0.13	0.06	0.09
0.05	0.05	0.02	0.05	0.02	0.05		0.05	0.05	0.02
0.02	0.05	0.02			0.05	0.02	0.02		0.02
0.09	0.07	0.07	0.02	0.04	0.07	0.02	0.07	0.04	0.04
	0.06		0.09	0.02	0.09		0.06	0.02	0.04
0.02	0.02	0.02		0.02	0.06		0.02		0.02
	0.02	0.02	0.04	0.04	0.04		0.02	0.02	0.02
	0.05				0.09				
						0.07			
0.06	0.06	0.06	0.06	0.06	0.13	0.06	0.06	0.06	0.06
0.06	0.06		0.06	0.06	0.06		0.06	0.06	
0.14	0.09	0.14	0.04	0.04	0.24	0.04	0.04	0.04	0.04
0.1	0.2	0.15	0.12	0.15	0.15	0.02	0.15	0.15	0.1
0.11	0.22	0.35	0.22	0.11	0.11	0.22	0.11	0.11	0.11
0.19	0.09	0.19	0.19	0.42	0.19	0.09	0.09		0.19
1.66	1.66	1.66	1.66	2.23	2.93		0.48	0.48	1.66
									0.07
				0.05	0.05				
0.21	0.49	0.52	0.4	0.37	0.49	0.23	0.59	0.76	0.31
			0.25	0.12	0.25				0.12
			0.25	0.45	0.25				0.35
					0.06			0.06	
0.07	0.15	0.15	0.1	0.13	0.27	0.05	0.1	0.13	0.07
0.06	0.13	0.06	0.06	0.06	0.06	0.03	0.06		0.06
0.07	0.22	0.07	0.07	0.07	0.14		0.14	0.07	0.07
0.09	0.25	0.14	0.19	0.3	0.19		0.19		0.05
			0.16	0.16	0.08				0.25
					0.05				
			0.08						0.08

0.11			0.23	0.23					
0.08	0.02		0.04	0.15	0.15				0.15
				0.17	0.17				
		0.05						0.11	
0.09	0.09	0.28	0.39	0.39	0.63	0.18	0.28	0.18	0.51
0.19		0.19	0.19	0.19	0.42		0.19		0.19
0.21	1.16	0.78	3.68	3.68	5.89	0.47	0.78	0.47	3.68
				0.16	0.16				
0.11		0.06		0.11					
0.07	0.03	0.07	0.11	0.03	0.11		0.11		0.07
		0.15	0.15			0.15		0.15	
								0.2	
0.6	0.6		0.6	0.88	0.6	0.88	0.88	0.17	0.88
		0.17	0.6	0.6	0.87				0.37
	0.19		0.42	1.03	1.03	0.42	0.19	0.19	0.7
					0.39			0.12	
		0.09	0.19		0.19	0.09		0.09	
			0.05	0.05	0.05				
					0.04				
			0.16						
					0.14				
			0.05	0.05					
0.12	0.33	0.41	0.41	0.33	0.33	0.12	0.41	0.33	0.33
	0.06								
0.1	0.22	0.05	0.16	0.1	0.22	0.05	0.1		0.05
0.29	0.29		0.29	0.14			0.29	0.14	
			0.13		0.13				
	0.05		0.11	0.29	0.17	0.05	0.05		0.23
0.07	0.33	0.16				0.07	0.24	0.33	
					0.06			0.03	0.03
							0.04		
1.89	3.91	2.45	2.45	2.45	3.11	4.86	7.34	3.11	3.91
0.14	0.14	0.09	0.09	0.09	0.31	0.09	0.25	0.09	0.14
	0.1						0.05		
0.02	0.02			0.03	0.03		0.02	0.02	0.02
			0.08	0.08	0.08				0.08
					0.09	0.09		0.09	
				0.09	0.09				
			0.19	0.09					
				0.1	0.05				
					0.12				
			0.64	0.55	0.64	0.06	0.12	0.06	0.47
7.66	7.66	15.04	8.35	4.45	17.72	6.42	9.91	7.02	9.1
2.04	2.04	2.04	39.69	84.4	23.83	5.38	2.44	4.64	27.09

				0.1	0.1				0.21
0.05	0.05	0.1			0.1		0.05	0.05	0.05
	0.02	0.02			0.02			0.02	
0.27	0.27	0.27	5.56	5.56	8.33	0.27	0.6		3.1
	0.06			0.12			0.06	0.12	0.06
			0.02	0.02					0.02
			0.05	0.05					0.05
0.05		0.05	0.15	0.1	0.1		0.05		0.32
7.14	7.14	16.56	10.55	11.38	17.83	5.15	7.73	16.56	7.14
								0.08	
1.67	2.22	3.56	1.79	2.64	2.71	1.96	2.35	3.75	1.73
							0.03		
			0.39	0.39	0.39				0.39
					0.06				
0.07	0.07		0.15	0.07	0.15		0.07		0.07
0.17	0.11	0.17	0.05	0.11	0.05		0.05	0.05	
1.02	1.5	1.79	1.37	0.91	1.64	0.31	1.13	0.91	1.5
			1.16	1.95	1.52	0.59	0.17	0.36	2.44
			0.06	0.13					
0.06	0.11	0.24	0.11	0.18	0.18	0.11	0.18	0.24	0.11
			0.05		0.17				0.11
	0.11	0.05	0.11		0.11		0.11	0.17	0.11
					0.05		0.05		
						0.13			
			0.1	0.21	0.1				0.1
		0.2	1.65	1.82	2	0.2	0.28	0.36	1.82
			0.16						
									0.25
	0.2		0.2		0.2				0.2
									0.15
							0.09	0.09	
	0.06	0.06				0.06			
					0.06		0.06		
					0.03				
0.43	0.49	0.32	0.37	0.49	0.55	0.27	0.61	0.37	0.32
		0.07							
			0.13						
							0.31		0.31
							0.07		
	0.05		0.1	0.05	0.21		0.05		0.1
	0.25	0.12	0.12		0.12		0.25		
				0.04	0.04		0.04		0.04
			0.25	0.08	0.25				0.25
0.36	0.36	0.36	0.13		0.13	0.36	0.36	0.28	0.13
0.11	0.11	0.11		0.22	0.22	0.11	0.22	0.36	0.11
									0.15
			0.14	0.14					0.14

							0.06		0.06
			0.04	0.04	0.13				0.08
			0.11						0.11
			0.06		0.06				0.06
					0.05				
0.08	0.08	0.08	0.08	0.08	0.08				0.08
	0.08				0.08			0.08	
0.1	0.1	0.07	0.05	0.1	0.07	0.02	0.16	0.05	0.1
0.09	0.04				0.04	0.04	0.09		
				0.04	0.04				0.04
	0.03								
			0.21	0.21	0.21				0.32
			0.61	0.43	0.61	0.27			0.43
		0.05	0.05	0.1	0.1				
			0.09	0.09	0.09				0.19
0.07	0.07						0.07		
					0.11				
0.44	0.44	0.36	2.2	1.66	2.62	0.13		0.2	2.01
0.2	0.36	0.2					0.28		0.63
								0.06	
0.16		0.16		0.08	0.08	0.08			
0.05	0.11		0.05	0.05	0.11		0.05		0.05
0.21	0.1	0.1			0.1		0.1	0.1	
	0.04	0.04							
	0.04	0.04		0.04					
0.02	0.06	0.08	0.04		0.02	0.04	0.08	0.12	
			0.05		0.11				0.05
	0.1		0.1		0.1				0.1
	0.04	0.02							
								0.04	
									0.05
		0.04							
			0.03	0.06	0.03				0.09
	0.06		0.03		0.06				
					0.06				
0.07									
0.03	0.07		0.03		0.03		0.07	0.03	0.07
	0.05	0.05					0.05	0.05	
0.55	0.72	0.55	1.15	0.55	1.15	0.24	0.39	0.55	1.39
0.22	0.49	0.35	0.65	0.49	0.82	0.1	0.1	0.49	0.82
0.05	0.11	0.11			0.05	0.05	0.23		
		0.13							
			0.12	0.12	0.12				0.12
			0.12						

			0.39	0.24	0.39		0.11		0.39
			0.16	0.16	0.35				
			0.46	0.66	0.29				0.29
0.13	0.13		0.84	1.66	0.63		0.13		2
			1.38	1.95	0.54	0.24	0.11		1.65
			0.54	0.78	0.54				0.33
				0.26		0.12	0.12	0.12	0.12
0.14	0.14	0.14	1.22	1.54	1.22	0.49	0.49	0.49	1.22
0.27	0.27	0.13	0.27	0.43	0.43		0.27	0.13	0.62
			0.13	0.13					
			0.61	0.82	0.13				0.82
			0.35	0.57	0.82	0.35	0.35	0.35	0.57
			0.43	0.61	0.43	0.13	0.13		0.43
			0.87	0.65	1.12				1.12
				0.08	0.18		0.18		0.18
0.05	0.05	0.05	0.05	0.05	0.05		0.05	0.05	
				0.13					0.13
			0.09				0.09		
			0.1	0.46	0.21	0.1	0.1		0.1
0.08	0.08		0.04		0.08				
0.03	0.03	0.03	0.03		0.15		0.03		0.06
0.07	0.15	0.24	0.15	0.24	0.24		0.15		0.24
					0.07				
								0.1	
					0.05				
					0.04				
			0.23	0.37					0.52
0.06	0.06	0.06	0.06	0.06	0.06		0.06	0.06	0.12
	0.77	0.41	0.58		0.77	0.12	0.26	0.26	0.98
0.25	0.55			0.39	0.55	0.12			0.73
	0.03	0.02	0.05		0.03		0.03		
0.03	0.07	0.1	0.07	0.1	0.14		0.1	0.03	0.03
			0.03		0.03		0.03		0.09
0.06	0.11	0.06	0.06		0.17	0.06	0.11		0.11
			0.8	0.67	0.8				0.93
		0.08							
		0.05	0.05	0.05	0.1	0.05	0.05		
									0.08
0.19	0.09	0.19	0.09		0.09			0.09	0.09
			0.64	0.64	0.39				1.27
0.23	0.23	0.23	0.36	0.23	0.36	0.11	0.11	0.36	0.36
				0.02					
0.03									
			0.4	0.29	0.66	0.09			0.4
0.33	0.21	0.21	1.13	1.13	0.6		0.21	0.1	0.76

0.02	0.04	0.02	0.06	0.06	0.09		0.04	0.02	0.06
				0.06	0.06				
		0.05			0.05				
	0.04						0.07		
			0.02	0.02					
0.04	0.04	0.04	0.08	0.08	0.12	0.08	0.04	0.04	0.04
	0.09								
			0.1						0.1
	0.02				0.02		0.02		
			0.72	0.31	0.72				0.72
0.04	0.04	0.04	0.09	0.04	0.09		0.04	0.04	0.04
			0.1	0.34	0.63	0.22	0.1	0.22	0.34
			0.93	0.6	0.21				0.6
			0.17	0.17					0.17
					0.06				
					0.17				0.17
			0.04						
									0.07
	0.2	0.2							
	0.31	0.15	0.15		0.15		0.15		
		0.26							
					0.09				
0.34		0.34		0.34		0.34	0.34	0.34	
			0.07						0.07
	0.07		0.15	0.32	0.23				0.15
	0.11	0.03	0.11	0.03	0.08	0.03	0.03		0.05
0.49	0.49	0.49	0.62	0.75	1.23	0.38	0.49	0.17	0.75
	0.04								
0.05	0.05		0.11	0.05	0.05		0.05	0.05	0.05
0.08	0.04	0.08	0.04	0.04	0.08		0.04		
0.37	0.61	0.61	3.18	1.6	3.18		0.61	0.61	1.21
					0.07				
					0.07				
				0.34	0.34				0.1
				0.08	0.08				
0.04	0.08	0.04	0.29	0.45	0.39	0.08	0.08		0.39
								0.02	
	0.07				0.02		0.02		0.02
	0.23	1.33	0.88	1.87	2.55		0.53	1.33	0.88
0.02	0.04	0.02							
0.77	0.77	1.58	0.94	0.94	1.35	0.46	1.14	0.77	0.61
			0.14	0.14					
			0.34						0.16
			0.12						

	0.05	0.05			0.05		0.05		0.05
					0.07				
	0.06	0.06	0.06				0.06		0.06
					0.04		0.04		
0.12	0.12	0.12	0.12		0.12		0.42	0.12	0.12
					0.08				
0.03	0.03	0.03		0.03			0.03		
	0.11								
			0.07	0.07	0.07				0.07
0.04		0.04			0.04		0.08	0.04	
0.06	0.32	0.17	0.1	0.06	0.21	0.06	0.65	0.37	0.1
				0.09	0.09		0.09		0.09
	0.1		0.1		0.1		0.1		
	0.08	0.04		0.08	0.04	0.04	0.04		
0.11	0.24	0.11	0.11	0.24	0.11			0.11	0.11
0.19	1.34	0.97	0.41	0.67	0.97	0.19	1.34	0.19	
							0.03		
		0.1	0.1	0.22	0.22				0.1
			0.19	0.3	0.3				0.3
				0.11					0.11
					0.07				
			0.06		0.06				
0.05	0.11	0.05	0.05		0.17	0.05			0.05
0.12	0.39	0.39	0.39	0.55	0.12	0.24	0.55		0.55
								0.39	
						0.16	0.16		0.16
0.04	0.04				0.04				0.04
	0.09				0.09				
0.72	0.86	0.51	0.26	0.23	0.3	0.26	0.36	0.17	0.23
0.04	0.08	0.08	0.08	0.22	0.27	0.13	0.22	0.13	0.22
0.06						0.06			
		0.09	0.09		0.09			0.19	
								0.02	
				0.06					
0.73	0.9	1.08	2.95	2.61	3.33	0.58	1.5	1.08	2.61
					0.03				
	0.09						0.09		
0.14	0.25	0.14			0.56	0.1	0.25	0.1	
			0.03			0.03			
0.28	0.42	0.58	0.31	0.31	0.26	0.34	0.68	0.75	0.34
0.06	0.13		0.13	0.06	0.13		0.13		0.13
0.11	0.14	0.14	0.02		0.09	0.04	0.11	0.04	0.07
			0.09	0.2					

		0.09	0.09		0.09				
				0.15	0.15				
					0.05	0.03			0.03
		0.11							
0.09	0.19	0.09		0.14			0.19		0.09
0.22	0.22	0.22	0.22	0.22	0.22	0.22	0.36	0.36	0.36
					0.08				
0.33	0.15		0.15	0.15	0.15		0.15		0.15
0.16	0.18	0.3	0.07	0.07	0.27	0.1	0.1	0.18	0.05
	0.15	0.33		0.15	0.15		0.15		0.15
					0.14				
0.04	0.18		0.13	0.13	0.28	0.04	0.23	0.09	0.23
0.68	0.23	0.68	0.36	0.86	0.86	0.36	0.23	0.11	0.51
0.13	0.23	0.28	0.39	0.63	0.5	0.39	0.33	0.23	0.44
0.31	0.35	0.31	0.4	0.4	0.4	0.14	0.45	0.14	0.35
0.35	0.29	0.22	0.25	0.46	0.46	0.22	0.29	0.08	0.25
0.43	0.43	0.43	0.43	0.43	0.43	0.43	0.43	0.43	0.43
									0.18
0.41	0.43	0.47	0.37	0.43	0.51	0.19	0.39	0.47	0.33
			0.09	0.09					0.09
					0.24				
	0.05		0.05		0.1				
		0.1		0.1	0.1				0.1
					0.1				
	0.18						0.18	0.18	
	0.19	0.31	0.31	0.43	0.86		0.31	0.43	0.56
0.23	0.23	0.23	0.15	0.15	0.31	0.15	0.23		0.15
	0.02	0.02					0.05		
							0.13	0.13	
0.38	0.18	0.62	1.24	2.1	1.63		0.18	0.38	1.24
						0.06			
				0.05	0.05				
		0.05	0.05		0.05		0.05		0.05
			0.11	0.23	0.11				0.23
			0.86	0.86	1.03				0.56
		0.12			0.25	0.12		0.06	0.12
				0.35	0.16				0.35
			0.09						0.09
		0.05		0.05		0.05			
0.06	0.06	0.03		0.06	0.06			0.03	0.03
					0.07		0.04		
				0.12					
						0.05	0.05		
				0.08	0.08				
				0.02	0.02				

			0.02						
					0.14				
									0.06
0.04	0.04	0.08	0.04	0.04	0.04		0.12	0.12	0.04
			0.54	0.75	0.75				0.98
			0.13						
	0.08	0.08	0.08	0.08			0.08	0.08	
				0.18	0.18				0.18
0.23	0.23	0.23	0.11	0.11	0.23		0.23	0.23	
0.04		0.04							
								0.09	
0.43	0.64	0.43	0.87	0.5	0.64	0.09	0.57	0.2	0.57
	0.03				0.03		0.03		
					0.19				
					0.24		0.24	0.24	
	0.1		0.1	0.48	0.22				0.1
			0.05	0.05	0.05				0.05
0.05	0.1	0.1	0.22	0.28	0.28		0.1		0.16
	0.05						0.05		
			0.35	0.11	0.22				0.11
	0.03								
			0.14	0.14	0.14				0.14
			0.73	0.98	0.73				0.73
			0.43	0.43	0.31				0.43
			0.2	0.2	0.2				0.57
		0.3							
								0.28	
			0.26						
				0.43					
		0.33				0.33			
			0.29	0.47					0.29
0.04	0.04	0.04	0.09	0.23	0.13	0.04	0.09	0.09	0.18
0.05	0.14		0.09	0.05	0.09		0.05		0.2
				0.1					
				0.12					
									0.03
0.25	0.25	0.33	1.2	3.09	2.86	0.86	1.08	1.92	2.45
								0.4	
0.08	0.08	0.16	0.36	0.16	0.26			0.16	0.08
1.64	0.56	2.06	1.84	2.3	3.12	0.82	0.96	1.45	0.96
1.17	0.99	1.17	2.95	2.33	2.63	1.57	1.57	1.8	2.63
3.89	6.15	11.66	64.91	60.86	50.14	9.46	11.66	14.31	53.49
			0.37	0.37	0.37				0.29

0.12	0.19	0.12	0.12	0.12	0.26	0.06	0.19	0.19	0.12
	0.07		0.14	0.07	0.14				0.14
	0.16		0.16		0.16				0.16
		0.1	0.1		0.35			0.1	
0.25	0.4	0.4	0.25	0.25	0.25		0.25	0.12	0.25
0.08	0.08	0.17	0.26	0.26	0.26		0.08		0.36
					0.14				0.14
		0.04							
	0.12	0.25	0.12	0.12	0.76	0.12	0.25		0.25
0.07	0.07		0.14	0.14	0.39	0.07	0.14		0.07
	0.08								
			0.02						
0.03	0.03								
0.05	0.02		0.02	0.02	0.02		0.05		0.02
									0.12
			0.62	1.07	0.62				0.62
0.12	0.08	0.08	0.16	0.12	0.2		0.25	0.04	0.04
0.41	0.54	1	0.83	0.68	0.83	0.3	0.83	0.3	1.18
0.09	0.31	0.09			0.31		0.31		0.09
	0.21		0.1		0.1				0.1
0.09	0.09		0.09	0.09	0.19		0.09		0.19
0.11	0.23	0.23	0.23	0.11	0.23	0.37	0.23	0.23	0.23
			0.37		1.55			0.17	0.26
							0.04		
								0.16	
					0.05				
	0.02				0.07		0.02	0.02	
	0.09		0.03		0.03		0.06		
	0.04		0.04		0.04		0.04	0.04	0.04
	0.07								0.07
					0.15				
			0.03		0.03				
0.11					0.11				
				0.24					
			0.16	0.16	0.16				0.25
				0.09					
				0.32					0.32
0.08	0.08	0.08	0.08	0.16	0.08				0.25
	0.1	0.34	0.1	0.1	0.1	0.1		0.48	0.22
				0.14	0.07				0.14
				0.05					
			0.18	0.06					0.12
			0.08						0.08

0.59	0.32	0.32	0.2	0.45	0.32		0.32		0.32
0.11	0.11		0.11	0.11	0.11				
	0.05	0.03	0.11	0.08	0.16	0.05	0.03	0.03	0.11
	0.13								
		0.1			0.1				0.1
				0.08			0.08		
0.05	0.05	0.05	0.11	0.11	0.05		0.05	0.05	0.05
	0.15		0.32	0.15	0.32	0.15			
0.35		0.06		0.06			0.06		
				0.08					0.08
			0.08	0.12	0.08				
0.14	0.14	0.31	0.31	0.31	0.49		0.14		0.14
				0.19					
0.08	0.14	0.03	0.03		0.03	0.05	0.17	0.03	0.08
0.11	0.11	0.11	0.23	0.23	0.23	0.11	0.23	0.11	0.36
0.04		0.04		0.04					
0.04	0.12	0.12	0.16	0.12	0.12	0.04	0.12	0.04	0.12
0.03	0.06		0.03	0.09	0.09		0.09	0.06	0.09
			0.14	0.14	0.14				0.14
	0.12		0.12				0.26		0.12
0.15	0.33	0.15	0.15	0.15	0.15		0.15	0.15	0.33
									0.1
				0.15					
		0.07							
				0.11	0.11				
									0.07
							0.13		
0.1	0.22	0.1	0.22	0.22	0.22		0.22		0.48
0.27	0.61	0.35	0.35	0.61	0.43	0.13	0.61	0.35	0.27
	0.14				0.14				0.14
			0.27						0.27
0.19		0.19			0.09		0.09		
4.88	6.73	4.88	6.73	9.15	12.34	5.74	9.15	5.74	5.74
0.11	0.11	0.11				0.11	0.11		0.11
				0.16					
0.09					0.09				
			0.03	0.03	0.03				0.06
0.07	0.15	0.24	0.15	0.15	0.24	0.07	0.07	0.07	0.15
			0.06	0.06	0.2			0.06	0.06
0.82	3.04	1.71	2	1.71	3.46	3.04	4.45	3.46	4.45
0.36	0.57	0.66	0.46	0.6	0.72	0.34	0.57	0.18	0.75
0.07	0.23	0.07	0.15	0.15	0.32	0.07	0.07	0.07	0.07
0.17				0.37					0.17
									0.2
0.13	0.13		0.13	0.13			0.13		0.27
0.23	0.41	0.07	1.13	1.13	1.13	0.15	0.32	0.23	1.13

	0.07	0.07	0.14	0.07	0.14		0.07		0.31
			0.04	0.04	0.09				0.04
		0.08							
	0.09				0.39	0.09	0.09	0.18	0.09
0.06									
	0.39	0.09	0.28	0.64	0.39	0.09	0.18	0.18	0.39
0.12									
			0.4	0.97	0.66				0.97
			0.64	0.34	0.34	0.1			0.48
				0.11					
	0.07	0.03	0.07	0.11	0.11	0.03	0.03		0.14
0.1	0.1	0.1	0.1		0.1		0.1		0.1
1.7	1.37	3.9	1.37	1.7	1.89	1.37	1.89	4.6	1.37
			0.21		0.38				
	0.06		0.06				0.06		
	0.06	0.03	0.03	0.03	0.03	0.03	0.06		0.03
0.15	0.22	0.12	0.09	0.15	0.29	0.06	0.32	0.18	0.12
0.02	0.02	0.02							
	0.05	0.05					0.05		0.05
0.08	0.04				0.04	0.04	0.04	0.04	0.04
				0.06	0.06				0.06
							0.04		
0.17			0.23				0.11	0.05	
0.02	0.06	0.02	0.02	0.04	0.04		0.02		
0.27	0.24	0.27	0.06	0.21	0.17	0.08	0.27	0.14	0.08
		0.12			0.12				
0.04	0.08	0.08	0.08	0.08	0.18	0.04	0.08	0.08	0.13
			0.03		0.03		0.03		
0.06	0.24	0.08	0.03	0.06	0.08	0.08	0.11	0.03	0.03
0.04	0.04	0.04					0.04		
		0.03	0.06		0.09		0.03	0.03	0.03
0.01					0.01		0.01	0.03	
				0.04					
0.08	0.12				0.16		0.04		0.08
			0.24	0.24	0.15				0.24
					0.04				
0.03	0.03	0.04		0.04	0.08			0.05	0.01
0.03	0.03	0.03	0.04	0.03	0.08	0.01	0.04	0.04	0.03
					0.02				
				0.05	0.05				
				0.1					
0.33	0.61	0.33	1.15	0.96	1.37	0.33	0.61	0.61	1.37
				0.08					
	0.09		0.09	0.05	0.09		0.14		0.09

	0.07	0.07	0.21	0.07	0.14		0.07	0.07	0.58
0.32	0.47	0.39	0.65	0.47	0.84	0.18	0.47	0.18	0.84
			0.22	0.5	0.5				0.5
					0.11	0.05			
			0.06	0.19					0.12
					0.05				
0.07	0.15	0.07	0.15	0.07	0.15	0.07			0.15
0.24		0.54	0.54	0.54			0.24		0.54
	0.02								
				0.17	0.17				0.37
				0.1					0.1
				0.37					
	0.23								
0.29	0.29	0.29	0.29	0.29	0.29			0.29	0.29
		0.34	0.34		0.34			0.34	0.34
	0.16						0.16		
0.18	0.18		0.4	0.18	0.4		0.18		0.18
	0.03								0.03
								0.03	
0.05	0.16	0.05	0.1	0.05	0.05		0.05		
	0.06						0.06		
	0.13	0.13			0.13		0.13		
				0.06					
0.2	0.43	0.2	0.43		0.2		0.43	0.43	0.2
			0.51	1.28	0.67				0.51
			0.05	0.05					0.05
		0.05							
	0.31	0.44	0.72	1.06	1.25	0.2	0.57	0.57	0.88
0.57	0.43	1.24	4.51	4.51	5.59	0.57	1.05	0.57	4.51
		0.05			0.05				
0.39	0.39	0.5	0.28	0.28	0.39	0.08	0.63	0.39	0.39
					0.07				
			0.05	0.05	0.05				
									0.06
0.09									
				0.08			0.08	0.08	0.17
	0.11								
0.03	0.03	0.03	0.05	0.08	0.08		0.03	0.03	0.05
			0.03		0.03				
0.05	0.05	0.02	0.08	0.02	0.08		0.08		0.08
0.02		0.02			0.02		0.04		
					0.03				
				0.08			0.08		0.08
	0.04		0.04		0.12		0.04		0.04

			0.22	0.22	0.22	0.05	0.1	0.05	0.22
			0.12	0.12	0.12	0.12			0.25
						0.19			
			0.07	0.14	0.07				0.14
			0.8	0.48	0.34			0.1	1.19
			0.08		0.08				0.25
			0.04	0.04		0.02			
0.23	0.23	0.23	0.23	0.53	0.53	0.23	0.53	0.23	0.23
			0.3	0.3	0.7	0.14	0.14	0.14	0.3
	0.03		0.07						
			0.09		0.03				0.03
0.16	0.04	0.08	0.04	0.04	0.2		0.08	0.04	
			0.04						0.04
0.18	0.29	0.18	0.29	0.29	0.18	0.09	0.29		0.29
0.12	0.58	0.26	0.58	0.12	0.98	0.26	0.41	0.26	0.26
		0.11	0.11	0.22	0.83			0.22	0.11
0.07	0.07	0.07	0.07	0.07	0.22		0.07	0.07	0.07
					0.03				
									0.09
									0.05
					0.13				
0.06	0.08	0.08	0.02	0.1	0.04		0.06	0.08	0.04
0.08	0.12	0.12	0.12	0.04	0.17		0.12	0.08	
	0.03				0.03		0.03		
0.08	0.08	0.08	0.08					0.08	
0.22	0.22	0.22	0.11	0.22	0.11		0.22	0.11	0.22
					0.02				
0.13			0.13	0.29	0.29				
				0.02	0.02				
0.13	0.13		0.27	0.13	0.2				0.35
0.13	0.27	0.13	0.13	0.2	0.2		0.27	0.35	0.27
	0.06		0.12	0.25					0.12
	0.06		0.12				0.12		0.06
0.18	0.32	0.12	0.32	0.4	0.4		0.25	0.06	0.57
	0.06			0.06					0.12
		0.03							
	0.02								
							0.05		
		0.05							
			0.22	0.22	0.49	0.11			0.49
					0.26				
			0.02		0.04				

					0.1				
0.54	1.14	0.72	1.26	1.52	1.38	0.31	0.92	0.63	1.14
			0.18	0.23	0.23	0.04	0.04		0.28
					0.07				0.07
				0.1					
							0.04	0.04	
			0.37	0.37	0.37				0.37
			0.45	0.91	2.03				0.45
		0.1	0.2	0.1	0.45			0.1	0.32
							0.08		
	0.48		0.22		0.64	0.1	0.48		0.34
0.27	0.31	0.23	0.09	0.13	0.23	0.06	0.31	0.06	0.2
							0.08		
			0.03	0.06					
			0.03						
			0.07	0.15	0.07				
					0.28				
	0.2	0.09			0.09		0.09	0.09	
			0.03	0.03	0.03			0.03	
				0.09					0.09
		0.08							
	0.06	0.13	0.13	0.13	0.06		0.06		0.2
			0.21	0.47					0.21
				0.02					
0.07	0.07	0.07					0.07		0.07
	0.15		0.23	0.07	0.15		0.07	0.07	0.15
			0.07	0.07	0.07				0.24
									0.07
				0.05					
0.05			0.05				0.05		
					0.06				0.06
									0.07
				0.11					
					0.08				
	0.02	0.01	0.01	0.01	0.02		0.02		
			0.56	0.82	0.35				0.82
	0.05		0.15	0.39	0.15				0.21
			0.2	0.26	0.52	0.05			0.15
			0.22	0.11	0.11				0.11
			0.08		0.08		0.18		0.18
			0.05						0.05
				0.05	0.05				
0.66	0.58	0.84	0.66	0.43	0.75	0.23	0.66	0.43	0.58
			0.94	0.39					
	0.18	0.18		0.18	0.18				0.18
0.16		0.16			0.16		0.16		

0.3	0.19	0.3	0.19	0.19	0.3		0.09	0.09	0.09
		0.58	0.58	1.51			0.58		0.58
		0.01			0.02				
0.2	0.43	0.2	1.05	1.05	1.46	0.2	0.72	0.72	1.46
	0.12		0.12		0.12				
				0.37					
				0.05					
0.02	0.02		0.02	0.02	0.02		0.02		0.02
	0.03								
			0.19		0.19				
0.17	0.17	0.17	0.17	0.36	0.17	0.17	0.17	0.17	0.17
						0.15			0.32
	0.11	0.24	0.24		0.24		0.11	0.11	0.11
			0.12		0.12				
				2.08			3.39		
		0.66		0.82					0.64
1.87	2.08				3.09		2.08		
				1.68					1.5
	0.92								
								0.75	
			2.54						
			1.21						
		6.21							
0.82			1.17				1.13	0.79	
		5.69							1.87
	1.29				1.45				
		1.17				0.92		0.99	
	0.75								
0.61			0.85		0.63	0.55	0.72		
									1.49
2.56	3.4		2.82		3.72	3.4	2.82	2.32	
		1.45		1.13					0.99
					1.17				
0.99	1.25						1.41	1.02	
			0.15	0.23					
		0.23		0.36	0.23	0.17			0.27
0.19	0.17						0.13	0.19	
			0.37						
	0.02								
			0.03	0.03					
		0.03	0.4	0.29	0.71	0.15	0.06	0.03	0.45
		0.03	0.23	0.23	0.61	0.03	0.03		0.27
0.05	0.05	0.05	0.05	0.03	0.08	0.03	0.03	0.03	

0.03	0.03	0.03	0.03	0.05	0.05		0.03		
0.15	0.28	0.18	0.18	0.15	0.3	0.06	0.25	0.18	0.15
								0.1	
0.14	0.67	0.29	1.77	1.44	1.44		0.29	0.14	1.77
									0.07
					0.07				
			0.3	0.48	0.3	0.14			0.3
0.04	0.04	0.04						0.04	
					0.14				0.14
				0.05	0.09				0.05
			0.25	0.57	0.31	0.09	0.05		0.31
0.07			0.23	0.15	0.32		0.07		0.42
0.07		0.07		0.07	0.32		0.15	0.15	
	0.07		0.15						0.15
0.07	0.07	0.07	0.15	0.23	0.23	0.07	0.15	0.07	0.23
	0.03								
0.06	0.18	0.12	0.12	0.12	0.18		0.12	0.18	0.12
					0.09				
	0.08		0.17	0.27	0.08				0.37
			0.06		0.06				
				0.03	0.1				0.03
0.17	0.36	0.36	0.36	0.17	0.36	0.17	0.36	0.17	0.36
0.11	0.11	0.23	0.11	0.23	0.23	0.11	0.11		0.11
0.07	0.15	0.09	0.13	0.15	0.13		0.11	0.05	0.15
	0.12	0.12					0.26		
	0.03				0.03				
0.04	0.04	0.08		0.12		0.04	0.04		0.04
				0.03				0.03	
0.13	0.13	0.2	0.2	0.2	0.2	0.2	0.06	0.2	0.13
0.11	0.05	0.05	0.05	0.05	0.05			0.05	0.05
	0.02				0.02				
	0.03	0.03		0.07	0.07	0.07		0.03	0.07
0.08	0.19	0.19	0.1	0.13	0.22	0.08	0.25	0.19	0.16
0.08		0.08	0.22	0.17	0.13		0.08		0.08
0.07	0.07	0.07	0.07		0.14		0.14	0.07	0.14
0.06	0.25	0.12	0.25	0.25	0.32	0.18	0.25		0.32
0.14	0.09	0.04	0.09	0.04	0.04	0.04	0.04	0.04	0.19
0.05	0.17		0.3	0.11	0.24		0.11	0.05	0.24
0.17	0.17	0.05	0.17	0.11	0.17		0.17	0.05	0.3
			0.34						0.34
			0.39	0.39	0.39				0.39
0.17			0.17	0.17			0.37		0.37
	0.37		0.37	0.37	0.87		0.37		0.37

0.41	0.99	0.41	2.97	0.99	0.41				0.99
0.29	0.29	0.29	0.29	0.29	0.29			0.29	0.29
		0.1							
			0.07						
	0.04								
				0.02					
0.23	0.31	0.23	0.19	0.23	0.27	0.07	0.19	0.15	0.03
				0.04					
0.03	0.03	0.03		0.03			0.03	0.03	0.03
			0.14	0.14					0.14
0.1	0.07		0.03		0.03		0.07		0.07
	0.1	0.03	0.1	0.07	0.03		0.03	0.03	0.1
0.46	1.13	2.1	2.1	3.53	3.53	5.61	2.1	8.64	5.61
	0.03			0.06	0.06				0.03
					0.2				0.2
0.15	0.15	0.15	0.15		0.15	0.15			0.15
	0.33		0.77	0.77	0.77				0.77
0.05		0.05							
0.06	0.2	0.06	0.06	0.06	0.35			0.06	
			0.08	0.08	0.08				0.08
			0.08	0.17	0.36				
					0.07				
							0.07		
			0.06	0.12	0.12				
				0.12	0.12		0.1		0.1
					0.02				
						0.03			
	0.04						0.04	0.04	
						0.02			
0.3	0.3	0.3	0.3	0.3	0.3	0.3			0.3
				0.06	0.06				
			0.2	0.2	0.13				0.2
0.37	0.6	0.6	4.15	5.02	4.15	0.48	1.36	0.87	5.51
			0.29	0.4	0.4				0.66
	0.08				0.08				
			0.07		0.07		0.07		
	0.06		0.06				0.06	0.06	0.06
									0.15
			0.13						0.13
			0.27	0.13	0.43		0.27		0.27
				0.13					
			0.16						
			0.14	0.68	0.58	0.14	0.14	0.07	0.39
									0.13
			0.24	0.37	0.7				0.37
				0.13					
			1.02	0.8	1.02				1.27

			0.06		0.06				0.06
0.04	0.13	0.04	0.04	0.04	0.13		0.08	0.08	0.08
			0.03		0.09				
			0.28	0.45	0.13				0.28
					0.11				0.05
			0.72	0.97	0.5				0.97
	0.03	0.03	0.03			0.03	0.03	0.03	
	0.07	0.07			0.07		0.07	0.07	
				0.12					
	0.03								
			1.49						
				0.04					
					0.08				
									0.07
		0.11							
	0.31			0.31	0.31		0.31		
		0.09	0.09	0.09				0.09	0.09
0.13	0.13	0.06	0.06	0.06	0.29		0.06		0.13
				0.14					0.3
						0.05			0.05
								0.03	
					0.22				
				0.04					
				0.05	0.1				0.05
	0.08	0.08	0.08	0.08	0.17				
				0.07					
			0.07						0.07
			0.1	0.21	0.1				0.1
		0.04	0.04						
		0.22		0.22	0.22				
					0.04				0.04
	0.2				0.09		0.31		0.09
					0.02			0.02	0.02
	0.18	0.29	0.29	0.29	0.29		0.18		0.29
0.13	0.66	0.46	0.88	0.88	0.88	0.29	1.13	0.66	0.88
	0.07	0.07		0.07	0.07				
			0.11	0.11	0.23				0.11
0.04	0.09	0.04			0.04	0.04	0.13		
									0.15
0.05	0.2	0.15			0.2		0.15	0.1	
	0.51	0.51	0.51	0.51	0.51		0.51	0.51	0.51
	0.08	0.17	0.08	0.08	0.08	0.17	0.08	0.17	0.08
			0.17						0.17
			0.05		0.05	0.05		0.05	

					0.11		0.11		
				0.09					0.09
0.09	0.04	0.04		0.04		0.04	0.04		
		0.19							
	0.08		0.16	0.08	0.08		0.08		0.08
			0.09		0.09				
	0.03	0.03		0.03	0.03		0.03		
				0.11	0.11		0.11		
			0.13						
				0.1	0.1				0.1
			0.05	0.03	0.08				0.05
			0.18	0.18	0.09				0.09
			0.06					0.06	
			0.25	0.56	0.12				0.25
0.09	0.09	0.09	0.09	0.09	0.19		0.09	0.09	0.09
	0.25		0.57	0.25	0.25				0.25
									0.04
						0.05			0.05
					0.17				
			1.38	2.05	0.86				0.45
0.35		0.35							
					0.06				
				0.09					0.18
									0.05
							0.1		
					0.16				
0.09	0.19	0.09	0.19					0.09	0.09
	0.35	0.16							0.16
0.04	0.16	0.12	0.16	0.08	0.21	0.04	0.16	0.08	0.21
0.03	0.07	0.07	0.07	0.07	0.1	0.07	0.1		0.07
			0.09	0.09	0.09				0.09
		0.12							
			0.12					0.12	0.12
				0.03	0.03		0.03		0.03
									0.31
					0.1				0.1
0.21	0.1	0.21	0.33	0.21	0.1		0.1		0.21
0.09	0.09	0.09	0.57	1.06	0.57	0.09	0.2	0.2	0.43
		0.03							
0.06	0.06		0.06				0.06		0.06
			0.25	0.25	0.12				
			0.18	0.29	0.18				0.29
									0.08
									0.06

				0.13	0.13	0.13		0.13	0.13
0.18	0.18	0.4	0.4	0.4	0.4	0.4	0.66	0.66	0.66
			0.03	0.03	0.11				0.03
			0.35	0.16	0.16				0.46
					0.08				
				0.36					
			0.16	0.16	0.16	0.16	0.16	0.08	0.34
		0.04							
	0.03	0.03	0.03		0.08	0.03	0.08	0.03	
			0.12		0.12				0.12
0.45					0.45				
0.5		0.5		0.5	0.5		0.5	0.5	0.5
				0.2					
	0.07		0.14				0.07		
			0.58						
			0.04	0.08	0.04	0.04	0.04		0.17
0.05			0.11	0.16	0.16				0.16
0.03		0.03	0.03		0.03	0.03			0.03
	0.05								
					0.03				
					0.05				
	0.11								
				0.09					
		0.11	0.11		0.24		0.11	0.11	
	0.11		0.11		0.11		0.11	0.11	0.23
			0.09						
0.12	0.3	0.12	0.12	0.12	0.16	0.09	0.23	0.16	0.23
			0.18	0.39	0.18				0.18
		0.37			0.37				
					0.21				
	0.1								
			0.18						
	0.31				0.31	0.31	0.31		0.31
					0.13				
				0.09					
			0.08	0.49					0.38
				0.07					
			0.13	0.13	0.13				0.06
	0.16		0.08	0.08	0.08		0.08		0.08
	0.03								
0.21	0.46	0.46	0.46	0.46	0.46	0.46	1.13	0.46	0.46
			0.32	0.74	0.32	0.15	0.15	0.15	0.15
				0.09					
			0.25	0.12					0.12

1.53	0.97	1.86	3.41	4.31	5.8	1.38	0.86	1.53	4.31
0.03	0.03	0.05	0.03			0.03	0.03		
	0.06		0.44	0.53	0.2		0.06	0.06	0.62
			0.17						
				0.03					0.07
					0.07				
0.03	0.03	0.06	0.13	0.06	0.16	0.03	0.06	0.03	0.09
				0.02	0.02			0.02	
0.1									
	0.18	0.25	0.06	0.06	0.25		0.12	0.18	0.06
0.42	0.55	0.62	1.64	1.03	2.01	0.42	1.03	0.85	0.94
				0.01	0.02				
		0.14		0.3					0.14
			0.16						
		0.08		0.08	0.08				
0.12	0.12	0.12	0.12	0.25	0.12				0.25
					0.03	0.03			
0.06									
	0.04		0.04	0.04			0.04		0.04
	0.03		0.03		0.07		0.03		0.03
0.03	0.03								
			0.05						
					0.03			0.03	
	0.16		0.16	0.16	0.16				0.16
	0.04		0.04	0.04		0.04		0.04	
	0.13		0.13	0.13	0.13	0.13	0.13	0.13	0.13
				0.13					
0.05	0.11	0.16	0.11	0.11		0.05	0.16	0.05	0.11
			0.03	0.03	0.06				0.03
0.04	0.04	0.04			0.04		0.04		
									0.05
0.14	0.29	0.29	0.14	0.29	0.66	0.29	0.29	0.14	0.14
0.39	0.58	0.64	0.18	0.23	0.64		0.45	0.51	0.13
0.23	0.16	0.19	0.75	0.51	0.8	0.19	0.16	0.12	0.65
0.08	0.04	0.04	0.12		0.24		0.04	0.08	0.04
0.13	0.35	0.27	2.74	2.32	4.36	0.82	1.18	0.82	3.22
			0.08		0.08				0.08
			0.54	0.54	0.68				0.41
	0.26	0.12	0.26	0.12	0.12			0.12	0.12
					0.3				
0.03			0.03				0.03	0.03	0.03
	0.04	0.04			0.08			0.04	0.04
					0.06				
				0.16					

	0.05						0.03		
		0.02						0.03	
				0.05					
0.8	0.22	0.8	0.48	1.2	2.96	0.22	0.8	0.22	0.48
				0.13	0.13				
			0.05				0.05		0.05
	0.1		0.1		0.1		0.1		
							0.03		
0.07	0.07	0.15		0.07	0.24		0.07	0.15	0.07

			Percent Increase Accumulat				
			Average			Error (average deviation frc	
KO-HS	**MT-HS**	**Protein**	**Wildtype**	**Knockout**	**Mutant**	**Wildtype**	**Knockout**
1.08	0.28	GPP1_YEAST	954%	508%	331%	223%	223%
0.85		GPP2_YEAST				n/a	n/a
	0.18	BDH1_YEAST	HS only		HS only	n/a	n/a
0.33	0.26	NEW1_YEAST	-8%	-42%	46%	51%	7%
0.38	0.28	RNQ1_YEAST	0%	174%	234%	n/a	201%
0.14	0.1	FKS1_YEAST	63%	17%	-47%	13%	n/a
		FKS2_YEAST				n/a	n/a
0.19	0.19	GAS1_YEAST	-12%	-39%	-49%	12%	16%
0.07	0.14	GAS5_YEAST	32%	-67%	-51%	68%	2%
0.24	0.14	GLGB_YEAST	HS only	HS only	1003%	n/a	n/a
0.34	0.79	CH10_YEAST	HS only	-28%	132%	n/a	28%
0.33		HSP12_YEAST		HS only		n/a	n/a
1.67	1.09	SNU13_YEAST	59%	109%	178%	14%	56%
		NOB1_YEAST	0%			n/a	n/a
		PRS4_YEAST				n/a	n/a
0.07		PRS6A_YEAST	HS only	-53%		n/a	n/a
		PRS6B_YEAST	HS only			n/a	n/a
0.39	0.14	PRS7_YEAST	118%	51%	HS only	61%	n/a
0.36	0.26	PRS8_YEAST	HS only	100%	HS only	n/a	n/a
0.23		PRS10_YEAST	HS only	HS only		n/a	n/a
0.03	0.03	RPN1_YEAST	0%	HS only	0%	n/a	n/a
0.65	0.22	RPN11_YEAST	HS only	HS only	HS only	n/a	n/a
0.21		RPN13_YEAST		HS only		n/a	n/a
		RPN2_YEAST		0%	0%	n/a	n/a
0.07		RPN7_YEAST				n/a	n/a
0.09		RPN8_YEAST	HS only	122%		n/a	n/a
0.08		PANE_YEAST	HS only	HS only		n/a	n/a
		DOG2_YEAST				n/a	n/a
0.11		LEU9_YEAST		HS only		n/a	n/a
		LEU1_YEAST	HS only			n/a	n/a
0.1	0.06	ODO1_YEAST		HS only	100%	n/a	n/a
0.16	0.16	RIB3_YEAST		HS only	HS only	n/a	n/a
0.18	0.18	PDE1_YEAST	0%	HS only	HS only	n/a	n/a
0.74	0.59	HSP30_YEAST	HS only	640%	HS only	n/a	n/a
0.21	0.1	RT01_YEAST	HS only	110%	110%	n/a	n/a
		RT13_YEAST				n/a	n/a
0.56	0.25	RT06_YEAST	62%	HS only	124%	62%	n/a
0.28		RT02_YEAST	HS only	HS only		n/a	n/a
0.17	0.17	RT04_YEAST	0%	113%	113%	n/a	n/a
		RT51_YEAST	HS only	111%	233%	n/a	n/a
0.06	0.06	NAM9_YEAST	HS only		HS only	n/a	n/a
0.1		RTPT_YEAST	HS only	HS only		n/a	n/a
		RSM28_YEAST				n/a	n/a

0.34		RT10_YEAST	HS only	HS only		n/a	n/a
		RT12_YEAST				n/a	n/a
0.28	0.13	RT17_YEAST	HS only	HS only	0%	n/a	n/a
0.15		RT18_YEAST	HS only	0%		n/a	n/a
0.37		RT19_YEAST		0%	0%	n/a	n/a
		RT23_YEAST		117%		n/a	n/a
		RT24_YEAST				n/a	n/a
0.12		RT25_YEAS7				n/a	n/a
0.12		RT26_YEAST	HS only	HS only		n/a	n/a
0.23		RT28_YEAST	HS only	0%		n/a	n/a
		RT35_YEAST				n/a	n/a
0.22		RT05_YEAST	HS only	HS only		n/a	n/a
		RT07_YEAST	HS only			n/a	n/a
0.47		RT08_YEAST	HS only	HS only		n/a	n/a
0.11		RT09_YEAST	HS only	0%		n/a	n/a
0.23		SWS2_YEAST	0%		0%	n/a	n/a
		HMDH1_YEAST				n/a	n/a
0.03		HMDH2_YEAST	0%			n/a	n/a
		3HAO_YEAST				n/a	n/a
		HIBCH_YEAST				n/a	n/a
		LEUC_YEAST	HS only			n/a	n/a
2.76	0.7	LEU3_YEAST		1676%	514%	n/a	324%
		MKAR_YEAST	0%		0%	n/a	n/a
		ERG27_YEAST	GR only	0%		n/a	n/a
	0.63	RSSA1_YEAS1			-25%	n/a	n/a
1.66		RSSA2_YEAS1	207%	152%		n/a	55%
9.35	6.98	RS10A_YEAST	575%	37%	5%	575%	112%
3.55	2.12	RS11_YEAST	-37%	-54%	-58%	1%	6%
1.38	0.92	RS12_YEAST	21%	119%	0%	21%	119%
2.99	2.99	RS13_YEAST	-38%	-22%	-56%	14%	1%
23.84	8.92	RS14A_YEAST	-51%	HS only	HS only	n/a	n/a
		RS14B_YEAST		GR only	GR only	n/a	n/a
3.34	4.35	RS15_YEAST	1%	-53%	-26%	40%	0%
7.25	5.68	RS16_YEAST	20%	0%	0%	42%	0%
11.8	5.77	RS17A_YEAST	-18%	29%	-50%	18%	66%
4.93	6.23	RS18_YEAST	34%	-28%	-13%	55%	9%
2.55	1.87	RS19A_YEAST	113%	-44%	-29%	77%	21%
8.57	4.28	RS3A1_YEAS1	-14%	-52%	-62%	46%	12%
8.57	3.16	RS3A2_YEAS1	-13%	-51%	-79%	47%	28%
0.86	0.86	RS2_YEAST	35%	-40%	-74%	64%	25%
10.01	5.82	RS20_YEAST	14%	75%	-33%	58%	44%
13.44	0.95	RS21A_YEAST	161%	102%	-85%	112%	n/a
13.44	0.95	RS21B_YEAST	273%	44%	-85%	n/a	n/a
11.25	14.39	RS22A_YEAST	-12%	-51%	-64%	41%	12%
0.88	0.23	RS23_YEAST	18%	69%	-77%	51%	0%
3.61	6.14	RS24_YEAST	3%	-43%	-6%	26%	21%
2.96	2.96	RS25A_YEAST	-5%	-26%	0%	44%	26%

3.36		RS26A_YEAST	165%	506%		n/a	594%
	3.41	RS26B_YEAST			39%	n/a	n/a
3.3	1.99	RS27A_YEAST	-17%	-47%	-58%	17%	11%
28.53	4.43	RS28A_YEAST	157%	98%	278%	157%	42%
28.53		RS28B_YEAST		HS only	278%	n/a	n/a
0.61		RS29A_YEAST	-89%	49%	-81%	n/a	110%
0.6	1.54	RS29B_YEAST		0%		n/a	n/a
2.18	2.62	RS3_YEAST	-26%	-43%	-44%	11%	13%
8.35	1.45	RS30_YEAST	0%	-69%	-78%	61%	7%
2.06	1.11	RS37_YEAST	881%	-73%	-20%	881%	11%
6.22	5.42	RS4_YEAST	28%	19%	-36%	58%	34%
1.6	0.15	RS5_YEAST	0%	74%	-54%	0%	45%
4.88	3.02	RS6_YEAST	-42%	-57%	-85%	7%	15%
5.55	3.79	RS7A_YEAST	-27%	-31%	2%	7%	14%
3.09	4.6	RS7B_YEAST	13%	-66%	-33%	13%	2%
1.89	0.83	RS8_YEAST	-20%	25%	-61%	20%	25%
		RS9A_YEAST	4%	-33%	0%	24%	n/a
2.93	1.49	RS9B_YEAST				n/a	n/a
0.92	0.22	GATA_YEAST	1214%	1214%	HS only	n/a	n/a
	0.1	PNPP_YEAST				n/a	n/a
0.24	0.27	XRN1_YEAST	116%	9%	162%	4%	32%
		XRN2_YEAST	100%	GR only		n/a	n/a
0.68	0.42	IMG1_YEAST	HS only	258%	42%	n/a	n/a
		RM01_YEAST	HS only			n/a	n/a
0.13		RM11_YEAST				n/a	n/a
0.18	0.18	MNP1_YEAST	0%	0%	0%	0%	0%
		RM13_YEAST				n/a	n/a
0.13		RM15_YEAST				n/a	n/a
		RM17_YEAST	0%			n/a	n/a
0.22	0.22	RM19_YEAST	HS only	HS only	HS only	n/a	n/a
0.38	0.08	RM02_YEAST		HS only	HS only	n/a	n/a
		RM23_YEAST				n/a	n/a
		RM24_YEAST				n/a	n/a
0.21		RM28_YEAST	HS only	0%	0%	n/a	n/a
		RM03_YEAST	HS only			n/a	n/a
0.41		RM33_YEAST	HS only	HS only	139%	n/a	n/a
		RM34_YEAST				n/a	n/a
0.17	0.08	RM35_YEAST	56%	HS only	HS only	56%	n/a
		RM36_YEAST				n/a	n/a
0.25		RM38_YEAST	0%	0%	GR only	n/a	0%
		RM04_YEAS7				n/a	n/a
		RM40_YEAST				n/a	n/a
0.33		RM44_YEAST	0%	68%	0%	n/a	68%
		RN49_YEAST				n/a	n/a
		RM51_YEAST				n/a	n/a
		RM06_YEAST				n/a	n/a
	0.13	RM08_YEAST	HS only		-28%	n/a	n/a

		RM09_YEAST				n/a	n/a
0.11		RL4P_YEAST				n/a	n/a
0.33		FTHC_YEAST				n/a	n/a
0.13	0.22	METE_YEAST	350%	HS only	1000%	n/a	n/a
0.44	0.2	RIB4_YEAST		120%	HS only	n/a	n/a
0.66	0.36	RLA0_YEAST	125%	-6%	17%	125%	30%
		RLA3_YEAST	GR only		0%	n/a	n/a
1.49	0.36	RLA2_YEAST	-58%	0%	22%	n/a	0%
		RLA4_YEAST		GR only		n/a	n/a
		NMD3_YEAST	100%			n/a	n/a
2.5	1.01	RL1_YEAST	18%	105%	181%	38%	42%
2.36	1.24	RL10_YEAST	-43%	131%	-56%	0%	15%
0.67	0.19	RL11A_YEAST	-48%	63%	HS only	3%	n/a
		RL11B_YEAST			GR only	n/a	n/a
2.77	2.12	RL12_YEAST	73%	43%	7%	14%	82%
	0.83	RL13A_YEAST	-26%	46%	0%	n/a	n/a
0.83	0.57	RL13B_YEAST	GR only	46%		n/a	n/a
	1.41	RL14A_YEAST	-10%	76%	-49%	39%	n/a
2.78		RL14B_YEAST				n/a	n/a
2.05	1.65	RL15A_YEAST	-26%	111%	13%	26%	9%
1.15	0.58	RL16A_YEAST	-13%	-40%	-43%	13%	16%
0.84		RL16B_YEAST	-46%	-34%	-21%	23%	10%
5.13	1.69	RL17A_YEAST	-55%	-11%	-65%	6%	33%
5.13	1.69	RL17B_YEAST	-61%	9%	-65%	n/a	41%
0.93	0.64	RL18_YEAST	31%	-14%	0%	69%	14%
0.87	1.19	RL19_YEAST	-71%	40%	-62%	1%	40%
2.07	1.71	RL2_YEAST	9%	55%	-21%	53%	6%
2.76	1.7	RL20_YEAST	-46%	-1%	-45%	3%	46%
2.65	0.2	RL21A_YEAST	55%	15%	-45%	55%	15%
2.02	0.2	RL21B_YEAST	74%	61%	-57%	n/a	61%
	0.28	RL22A_YEAST	-56%	125%	-28%	n/a	n/a
15.02	9.09	RL23_YEAST	-30%	-51%	-20%	9%	30%
2.14	1.59	RL24A_YEAST	-36%	-27%	-54%	15%	27%
2.83	1.15	RL24B_YEAST	-24%	30%	-59%	n/a	1%
2.58	1.89	RL25_YEAST	49%	-32%	24%	19%	10%
12.2	3.09	RL26A_YEAST	31%	40%	-80%	2%	81%
3.52	3.52	RL27A_YEAST	-23%	-23%	2%	n/a	n/a
		RL27B_YEAST				n/a	n/a
3.06	1.23	RL28_YEAST	-2%	16%	-46%	38%	16%
1.03	1.79	RL3_YEAST	47%	-24%	-32%	32%	11%
3.22	1.37	RL30_YEAST	62%	135%	339%	14%	0%
0.29	0.67	RL31A_YEAST	-75%	37%	-21%	0%	94%
2.1	0.97	RL32_YEAST	-23%	58%	-19%	23%	58%
4.15	1.27	RL33A_YEAST	0%	21%	-68%	0%	21%
		RL33B_YEAST	0%	0%		n/a	n/a
1.08	0.63	RL34A_YEAST	-42%	0%	-28%	8%	0%
		RL34B_YEAST				n/a	n/a

5.82	1.61	RL35_YEAST	28%	5%	-39%	53%	29%
3.4		RL36A_YEAST	78%	-31%	0%	38%	n/a
	2.27	RL36B_YEAST				n/a	n/a
18.11	3.37	RL38_YEAST	441%	-43%	-61%	473%	11%
		RL39_YEAST	GR only		-62%	n/a	n/a
		RL40_YEAST				n/a	n/a
0.31	0.72	RL44_YEAST	74%	29%	85%	0%	104%
0.91	0.91	RL43_YEAST	-57%	0%	-63%	19%	0%
2.14	1.21	RL4B_YEAST	-4%	-23%	-22%	39%	1%
0.23	0.11	RL5_YEAST	0%	20%	114%	0%	89%
1.33	1.33	RL6A_YEAST				n/a	n/a
		RL6B_YEAST	81%	25%	0%	53%	n/a
1.1		RL7A_YEAST	26%	31%	GR only	3%	31%
	2.04	RL7B_YEAST			HS only	n/a	n/a
2.37	0.44	RL8A_YEAST	-12%	-26%	-60%	31%	26%
2.81	1.34	RL8B_YEAST	-21%	-19%	-42%	21%	19%
2.01	1.2	RL9A_YEAST		24%	16%	n/a	44%
		RL9B_YEAST	14%		110%	14%	n/a
0.16		LOC1_YEAS7	HS only	HS only		n/a	n/a
0.65	0.65	NIP7_YEAST	192%	0%	261%	69%	0%
		NOP8_YEAST	0%	117%		n/a	n/a
0.34	0.14	K6PF1_YEAST	157%	429%	69%	14%	286%
0.65	0.22	K6PF2_YEAST	218%	342%	125%	n/a	149%
1.04	0.3	6PGD1_YEAST	HS only	1029%	1200%	n/a	n/a
		6PGD2_YEAST				n/a	n/a
0.43	0.43	SOL4_YEAST	HS only	HS only	HS only	n/a	n/a
0.1		SOL2_YEAST		HS only		n/a	n/a
0.45	0.39	GRP78_YEAST	380%	45%	206%	193%	4%
0.66	0.36	ARB1_YEAST	248%	179%	169%	121%	21%
		ADY4_YEAST				n/a	n/a
0.66	0.45	ILVB_YEAST	68%	0%	26%	32%	12%
0.66	0.5	ILV6_YEAST	43%	141%	189%	n/a	53%
0.94	0.28	THIL_YEAST	611%	339%	56%	n/a	83%
1.13	0.85	ACAC_YEAST	10%	-35%	-19%	29%	9%
	0.13	ACH1_YEAST			HS only	n/a	n/a
0.1	0.1	ACS2_YEAST	50%	75%	50%	50%	25%
		ARGD_YEAST				n/a	n/a
0.28	0.18	ACON_YEAST	350%	663%	72%	n/a	63%
		END3_YEAS7	GR only		0%	n/a	n/a
		END3_YEAST				n/a	n/a
	0.12	PAN1_YEAS7				n/a	n/a
		PAN1_YEAST	GR only	GR only	69%	n/a	n/a
0.03		SLA1_YEAS7	-38%	-63%	109%	n/a	23%
0.64	0.64	ACT_YEAST	-61%	-44%	414%	4%	26%
0.1		APD1_YEAST	HS only	0%	0%	n/a	n/a
0.05		ABP1_YEAST	0%	HS only		n/a	n/a
0.11		AIP1_YEAST	HS only	HS only		n/a	n/a

0.07		ARP9_YEAST	100%	0%		n/a	0%
	0.04	PRK1_YEAST			325%	n/a	n/a
0.73	0.48	ARP2_YEAST	561%	0%	99%	426%	0%
		ARPC1_YEAST				n/a	n/a
0.42	0.19	ARPC2_YEAST	172%	49%	333%	61%	9%
0.18	0.18	ARPC3_YEAST	-72%	0%	256%	n/a	0%
0.67	0.19	ARPC4_YEAST	91%	50%	22%	46%	50%
0.22	0.22	ARPC5_YEAST	-27%	0%	105%	27%	0%
0.07	0.32	ARP3_YEAST	171%	-54%	82%	58%	30%
		ARP5_YEAST				n/a	n/a
		ACK1_YEAST				n/a	n/a
0.27		ACPM_YEAST	HS only	HS only		n/a	n/a
		ACO1_YEAST				n/a	n/a
		AHC2_YEAST				n/a	n/a
0.18		APT1_YEAST				n/a	n/a
0.09		ADA_YEAST		HS only		n/a	n/a
0.1		ADK_YEAST	HS only			n/a	n/a
1.33	0.07	SAHH_YEAST	1800%	903%	177%	n/a	117%
		KAD1_YEAS1		-80%	0%	n/a	n/a
	0.14	KAD2_YEAST				n/a	n/a
0.37	0.07	PUR8_YEAST	200%	429%	0%	n/a	n/a
		PURA_YEAST	HS only			n/a	n/a
		CAP_YEAST		GR only		n/a	n/a
0.07		UBA4_YEAS1	HS only			n/a	n/a
		UBA4_YEAS7				n/a	n/a
0.04	0.04	SPB1_YEAST	HS only	HS only	HS only	n/a	n/a
1.22	0.82	ADT2_YEAST	89%	-51%	-30%	54%	3%
0.3		ADPP_YEAST	HS only	HS only		n/a	n/a
		ARF1_YEAST		0%		n/a	n/a
		AGE1_YEAST				n/a	n/a
		AGE2_YEAST	0%	0%	0%	n/a	n/a
		GCS1_YEAST				n/a	n/a
		GLO3_YEAST	0%	117%	0%	n/a	n/a
	0.06	GGA1_YEAST			HS only	n/a	n/a
0.06	0.11	GGA2_YEAST	73%	-82%	-51%	10%	2%
0.04		AAP1_YEAST				n/a	n/a
		SYAC_YEAST	HS only			n/a	n/a
8.38	3.45	ADH1_YEAST	328%	215%	273%	116%	99%
0.29	0.29	ADH3_YEAST	489%	433%	155%	0%	211%
		ADH4_YEAS7				n/a	n/a
		ADH5_YEAST	HS only			n/a	n/a
		ATF2_YEAST				n/a	n/a
0.99	0.65	ALDH2_YEAST	662%	1550%	HS only	n/a	n/a
2.49	2.28	ALDH3_YEAST	436%	453%	1654%	n/a	n/a
		ALDH5_YEAS7	HS only			n/a	n/a
		LEM3_YEAST	GR only	GR only	0%	n/a	n/a
0.54	0.28	TPS1_YEAST	125%	170%	624%	n/a	n/a

		KTR1_YEAST	-50%	-50%	0%	n/a	n/a
		ADD37_YEAST				n/a	n/a
	0.05	MPH3_YEAS8				n/a	n/a
0.03	0.09	MAN1_YEAST			200%	n/a	n/a
		AIM38_YEAST	0%	-55%	0%	n/a	n/a
0.08		GCST_YEAST	HS only	0%	350%	n/a	n/a
		APE2_YEAST				n/a	n/a
		ATO3_YEAST	0%	-54%	GR only	0%	n/a
	0.04	AMPD_YEAST			HS only	n/a	n/a
0.24	0.11	YNP5_YEAST	HS only	0%	0%	n/a	n/a
		YO052_YEAST	HS only			n/a	n/a
		CDC23_YEAST				n/a	n/a
0.15		YCU1_YEAST		HS only		n/a	n/a
		TRPD_YEAST				n/a	n/a
0.06		TRPE_YEAST	HS only	HS only		n/a	n/a
		TRPG_YEAST	HS only	0%		n/a	n/a
		SLH1_YEAST	0%	GR only	-33%	n/a	n/a
		AP1B1_YEAST				n/a	n/a
		AP1M1_YEAST				n/a	n/a
		AP1S1_YEAST	0%			n/a	n/a
0.03	0.03	AP2A_YEAST	HS only	-25%	50%	n/a	25%
		AP2M_YEAST	0%			n/a	n/a
0.21		AP2S_YEAST	0%	0%	0%	n/a	n/a
		AIF1_YEAST				n/a	n/a
		SYT1_YEAST				n/a	n/a
		GEA1_YEAST				n/a	n/a
		GEA2_YEAST				n/a	n/a
0.47	0.1	ARGI_YEAST	HS only	HS only	HS only	n/a	n/a
0.07		ARGJ_YEAST				n/a	n/a
0.16		RMT2_YEAST	HS only	HS only		n/a	n/a
0.14		ARLY_YEAST		HS only		n/a	n/a
0.08		ASSY_YEAST	HS only			n/a	n/a
		SYRC_YEAST	HS only			n/a	n/a
		SYRM_YEAST				n/a	n/a
0.54	0.06	ARO8_YEAST	HS only	HS only	HS only	n/a	n/a
0.17	0.17	ABF2_YEAST	126%	59%	0%	126%	59%
0.38	0.11	ASNS2_YEAST	HS only	533%	HS only	n/a	n/a
0.06		SYNC_YEAST		HS only		n/a	n/a
0.57	0.35	AATC_YEAST	HS only	613%	HS only	n/a	n/a
		AATM_YEAST	0%	0%	0%	n/a	n/a
0.42	0.09	DHAS_YEAST	HS only	833%	HS only	n/a	n/a
		MKC7_YEAST				n/a	n/a
0.06	0.12	SYDC_YEAST	HS only	0%	HS only	n/a	n/a
0.05	0.05	SYDM_YEAST		HS only		n/a	n/a
0.53	0.24	HIS1_YEAST	HS only	HS only	HS only	n/a	n/a
	0.13	ATPF_YEAST			HS only	n/a	n/a
0.16	0.35	ATPO_YEAST			119%	n/a	n/a

0.51	0.19	ATPA_YEAST	396%	85%	45%	127%	4%
3.28	1	ATPB_YEAST	985%	295%	144%	42%	107%
		ATP7_YEAST				n/a	n/a
		ATPD_YEAST	HS only			n/a	n/a
		ATPJ_YEAST				n/a	n/a
		ATPK_YEAST		GR only	0%	n/a	n/a
0.29		ATPN_YEAST	0%	0%	0%	0%	0%
0.49	0.22	ATPG_YEAST	345%	345%	295%	n/a	0%
		ATP14_YEAST	HS only			n/a	n/a
		ATP18_YEAST				n/a	n/a
	0.4	STF2_YEAST			HS only	n/a	n/a
0.04		HMI1_YEAST				n/a	n/a
	0.05	KU70_YEAST				n/a	n/a
0.14		NAM7_YEAST	0%	100%	133%	n/a	n/a
		ULS1_YEAST				n/a	n/a
1.08	0.6	HSC82_YEAST	1588%	162%	308%	388%	110%
1.07	0.67	HSP82_YEAST	HS only	346%	HS only	n/a	n/a
		MDL1_YEAST		GR only		n/a	n/a
0.39	0.23	PDR12_YEAST	29%	-39%	-24%	37%	1%
0.25	0.25	PDR15_YEAST	HS only	HS only	-14%	n/a	n/a
		CHL1_YEAS7				n/a	n/a
		DBP1_YEAS7				n/a	n/a
		DBP10_YEAS7				n/a	n/a
		DBP10_YEAST	0%	30%	0%	n/a	n/a
1.48	0.98	DBP2_YEAS7	30%	15%	18%	21%	15%
	0.51	DBP3_YEAS7	76%		55%	n/a	n/a
0.6		DBP3_YEAST		0%		n/a	n/a
0.13		DBP4_YEAS7	225%	0%		n/a	0%
0.07		DBP5_YEAS7	50%	-25%	236%	n/a	25%
		DBP6_YEAS7	0%	GR only		n/a	n/a
0.05		DBP6_YEAST		HS only		n/a	n/a
0.16	0.07	DBP8_YEAS7	11%	-26%	0%	39%	26%
0.05	0.23	DBP9_YEAS7	68%	-53%	204%	42%	33%
5.38	2.76	DED1_YEAS7	92%	43%	40%	53%	43%
0.2	0.27	DHH1_YEAS7	99%	-27%	3%	70%	27%
		MTR4_YEAST	0%	GR only	100%	n/a	n/a
0.09	0.04	DRS1_YEAS7	28%	-26%	38%	n/a	5%
0.26	0.26	IF4A_YEAS7	450%	-51%	-11%	350%	5%
		FAL1_YEAS7	0%	-69%	-50%	n/a	n/a
0.63	0.36	HAS1_YEAST	105%	-24%	35%	61%	1%
0.04	0.04	MAK5_YEAS7	0%	50%	0%	n/a	50%
		MAK5_YEAST				n/a	n/a
0.31	0.2	MS116_YEAST	42%	-34%	-6%	81%	5%
		ROK1_YEAS7				n/a	n/a
	0.07	SUB2_YEAS7	84%	-53%	87%	30%	n/a
0.09		SUV3_YEAST				n/a	n/a
0.36	0.13	RRP3_YEAS7				n/a	n/a

		RRP3_YEAST	64%	50%	0%	n/a	n/a
		SPB4_YEAS7	HS only			n/a	n/a
		ATG14_YEAST				n/a	n/a
		ATG16_YEAS7				n/a	n/a
0.08		ATG19_YEAS7				n/a	n/a
		ATG2_YEAS7				n/a	n/a
0.06		ATG21_YEAS7	HS only			n/a	n/a
		ATG29_YEAS7				n/a	n/a
0.15		ATG29_YEAST				n/a	n/a
		CIS1_YEAST				n/a	n/a
		BAR1_YEAST				n/a	n/a
0.38	0.45	PUR91_YEAST	154%	245%	800%	n/a	n/a
0.3	0.17	PUR92_YEAST	41%	173%	HS only	n/a	n/a
0.22		PUR2_YEAST	HS only	HS only		n/a	n/a
0.94	0.51	BCA2_YEAST	944%	422%	HS only	n/a	n/a
	0.27	BCA1_YEAST	500%		HS only	n/a	n/a
0.05		BDF2_YEAST	0%	0%	GR only	n/a	n/a
0.12		BEM1_YEAST	158%	-26%	200%	158%	26%
0.05		BEM4_YEAST	0%	0%	100%	n/a	0%
		BUD4_YEAS7		GR only		n/a	n/a
0.04		BUD6_YEAST				n/a	n/a
		RAX1_YEAST		GR only	GR only	n/a	n/a
0.07	0.07	C1TC_YEAST	190%	0%	48%	76%	0%
0.43	0.3	C1TM_YEAST	193%	10%	24%	193%	0%
		ERG2_YEAST				n/a	n/a
		CANB_YEAST		GR only		n/a	n/a
0.15		KCC2_YEAST	HS only	HS only		n/a	n/a
		NCS1_YEAST	HS only			n/a	n/a
		CALM_YEAST		GR only		n/a	n/a
0.44	0.25	KAPR_YEAST	243%	-10%	68%	207%	10%
0.08		KAPA_YEAST				n/a	n/a
		KAPB_YEAST				n/a	n/a
0.08		KAPC_YEAST				n/a	n/a
0.32	0.32	CAN_YEAST	113%	113%	113%	n/a	n/a
		CBPS_YEAST				n/a	n/a
1.32	2.06	CPYI_YEAST	121%	313%	HS only	n/a	n/a
	0.04	YPP1_YEAS7	0%			n/a	n/a
		YPP1_YEAST				n/a	n/a
		YAT2_YEAST				n/a	n/a
		YMC1_YEAST		GR only		n/a	n/a
		KC11_YEAST				n/a	n/a
0.12	0.06	KC12_YEAST	25%	-25%	-33%	75%	25%
		KC13_YEAST		GR only		n/a	n/a
0.06		HRR25_YEAST	58%	-27%	0%	58%	27%
0.11		CSK2B_YEAST	HS only	HS only		n/a	n/a
0.12	0.12	CSK2C_YEAST	HS only	HS only	HS only	n/a	n/a
1.4	1.2	STDH_YEAST	204%	151%	79%	34%	134%

		CAT5_YEAST				n/a	n/a
1.12	1.63	CATT_YEAST	1136%	918%	1382%	n/a	n/a
		CHAC_YEAST	HS only			n/a	n/a
0.11	0.11	MOB2_YEAST	109%	-52%	114%	n/a	0%
0.23	0.05	DBF2_YEAST	360%	76%	30%	n/a	41%
0.59	0.92	CDC10_YEAST	14%	49%	0%	14%	85%
0.79	0.54	CDC11_YEAST	98%	27%	17%	27%	27%
1.26	0.81	CDC12_YEAST	91%	10%	-27%	47%	32%
0.04		CDC24_YEAST	HS only			n/a	n/a
0.5	0.11	CDC28_YEAST	59%	355%	0%	n/a	n/a
0.78	0.68	CDC3_YEAST	76%	11%	27%	6%	48%
0.17	0.17	CDC42_YEAST				n/a	n/a
0.3	0.08	CDC48_YEAST	850%	216%	190%	75%	59%
		CDC53_YEAST	HS only	0%	50%	n/a	n/a
0.07		CDC54_YEAST				n/a	n/a
		CDC7_YEAST				n/a	n/a
0.05		YL413_YEAST	-50%	-60%	-85%	17%	16%
0.01		TAO3_YEAST	0%	0%	0%	n/a	0%
		WSC2_YEAST				n/a	n/a
	0.12	HS150_YEAS6	HS only		HS only	n/a	n/a
	0.16	PST1_YEAS7			HS only	n/a	n/a
		CWP1_YEAST				n/a	n/a
0.37	0.27	ECM33_YEAS2	-28%	-39%	-44%	11%	25%
		CHL4_YEAST				n/a	n/a
		CBF3A_YEAST				n/a	n/a
0.16	0.05	PRTB_YEAST	HS only	HS only	HS only	n/a	n/a
		CNM67_YEAST				n/a	n/a
		CHS5_YEAST				n/a	n/a
		CHS3_YEAST		0%	0%	n/a	n/a
0.4	0.52	AROC_YEAST	217%	-57%	53%	217%	7%
	0.05	RLF2_YEAST				n/a	n/a
0.08		EAF3_YEAST		HS only		n/a	n/a
		EAF7_YEAST				n/a	n/a
0.07		RSC30_YEAST	0%	133%	133%	n/a	n/a
0.06		RSC58_YEAST		HS only		n/a	n/a
		RSC8_YEAST				n/a	n/a
		RSC4_YEAST				n/a	n/a
0.15	0.07	RSC7_YEAST	HS only	HS only	HS only	n/a	n/a
		RSC9_YEAST	HS only			n/a	n/a
0.07		SFH1_YEAST	HS only	HS only		n/a	n/a
0.02	0.04	CHD1_YEAST	HS only	175%	HS only	n/a	175%
		CSM3_YEAST				n/a	n/a
		CST9_YEAST				n/a	n/a
		CTF8_YEAST				n/a	n/a
0.48	0.58	CISY1_YEAST	174%	77%	346%	140%	51%
		AP18B_YEAST				n/a	n/a
0.37	0.14	CLH_YEAST	546%	367%	442%	229%	158%

		CLC1_YEAST		0%		n/a	n/a
0.14	0.03	COPA_YEAST	517%	373%	44%	50%	193%
0.07	0.03	COPB_YEAST	HS only	467%	HS only	n/a	n/a
		COPB2_YEAST	HS only	-64%	75%	n/a	n/a
0.06		COPD_YEAST		HS only		n/a	n/a
0.36	0.66	COPE_YEAST	HS only	227%	HS only	n/a	n/a
		COPG_YEAST				n/a	n/a
		COPZ_YEAST	HS only			n/a	n/a
	0.23	COFI_YEAST		GR only	HS only	n/a	n/a
		SWD2_YEAST	HS only	100%		n/a	n/a
		COG4_YEAST				n/a	n/a
		COG5_YEAST				n/a	n/a
		COG7_YEAST	HS only			n/a	n/a
		CSN10_YEAST				n/a	n/a
		CSN9_YEAST				n/a	n/a
0.03	0.03	SEC16_YEAST	800%	150%	1000%	n/a	150%
		CTR1_YEAST			GR only	n/a	n/a
	0.1	CORO_YEAST	GR only	GR only	540%	n/a	n/a
0.29	0.29	CCW12_YEAST			HS only	n/a	n/a
0.1		YKJ1_YEAST	HS only	HS only		n/a	n/a
		CTK1_YEAST				n/a	n/a
		CTK3_YEAST		0%	0%	n/a	n/a
0.62	0.45	URA7_YEAST	58%	61%	198%	n/a	39%
0.11	0.06	URA8_YEAS7	HS only	HS only	HS only	n/a	n/a
		PHO85_YEAST	GR only			n/a	n/a
0.92	0.3	DUG1_YEAST	471%	1214%	HS only	n/a	n/a
		STR3_YEAST				n/a	n/a
0.28		CBS_YEAST	HS only	210%		n/a	156%
0.28		CYS3_YEAST	HS only	111%		n/a	n/a
0.14	0.07	NFS1_YEAST	100%	75%	HS only	n/a	25%
0.06		BLH1_YEAST		HS only		n/a	n/a
	0.08	SYC_YEAST				n/a	n/a
2.64	4.6	CDD_YEAST	-3%	-52%	-11%	45%	26%
	0.07	MBI2_YEAST				n/a	n/a
		CBP2_YEAST				n/a	n/a
		CBP6_YEAST			0%	n/a	n/a
0.23	0.15	QCR1_YEAST	HS only	HS only	HS only	n/a	n/a
0.67	0.29	QCR2_YEAST	HS only	HS only	HS only	n/a	n/a
0.22		QCR6_YEAST				n/a	n/a
0.26	0.58	QCR7_YEAST	HS only	HS only	HS only	n/a	n/a
0.34	0.16	UCRI_YEAST	HS only	113%	56%	n/a	n/a
		CCHL_YEAST	HS only			n/a	n/a
32.79	13.99	CYC1_YEAST	5%	-55%	-18%	72%	31%
		COX5A_YEAST	HS only			n/a	n/a
0.44		COX8_YEAST				n/a	n/a
		COX4_YEAST				n/a	n/a
1.17	0.21	COX6_YEAST	HS only	HS only	HS only	n/a	n/a

		COX9_YEAST				n/a	n/a
0.11	0.22	CY1_YEAST	HS only	HS only	HS only	n/a	n/a
0.06		ERG5_YEAST				n/a	n/a
		CYK2_YEAST	100%			n/a	n/a
		CYK3_YEAST				n/a	n/a
		CTU1_YEAS1				n/a	n/a
		NAR1_YEAS7				n/a	n/a
		NBP35_YEAST				n/a	n/a
0.07		SER33_YEAST		HS only		n/a	n/a
		ARA2_YEAST	0%	0%	0%	0%	n/a
0.3	0.09	ARA1_YEAST	HS only	HS only	HS only	n/a	n/a
		DAD3_YEAST	HS only	137%		n/a	n/a
0.1	0.1	MOB1_YEAST		HS only	0%	n/a	n/a
		ERG4_YEAST				n/a	n/a
		PUT2_YEAST				n/a	n/a
0.2		HEM2_YEAST	HS only	HS only		n/a	n/a
		DCTD_YEAST	-71%	-71%	0%	n/a	n/a
0.46	0.1	DOHH_YEAST	HS only	HS only	HS only	n/a	n/a
0.27		DHYS_YEAST	HS only	HS only		n/a	n/a
		DFM1_YEAST	0%		0%	n/a	n/a
		DIP5_YEAST				n/a	n/a
0.9	0.38	DLDH_YEAST	270%	34%	30%	116%	0%
0.7	0.31	ODP2_YEAST	29%	19%	6%	10%	19%
0.15	0.07	ODO2_YEAST	229%	HS only	HS only	n/a	n/a
0.1		PYRD_YEAST		HS only		n/a	n/a
		DAK1_YEAST	HS only			n/a	n/a
		DAK2_YEAST				n/a	n/a
0.25	0.18	ILV3_YEAST	468%	-47%	138%	348%	0%
0.1		DIM1_YEAST	HS only	0%	0%	n/a	n/a
	0.08	ERG19_YEAST				n/a	n/a
		DLD1_YEAST				n/a	n/a
0.06		DLD2_YEAST	HS only	HS only		n/a	n/a
0.13		DLD3_YEAST	HS only	117%		n/a	n/a
		RAD17_YEAST		GR only		n/a	n/a
		LCD1_YEAST				n/a	n/a
		DUN1_YEAST				n/a	n/a
		RPH1_YEAST				n/a	n/a
		MSH1_YEAST				n/a	n/a
		DPOA_YEAST				n/a	n/a
		HCS1_YEAST				n/a	n/a
		DPOD2_YEAST				n/a	n/a
		DPOE_YEAST				n/a	n/a
		DPO5_YEAST				n/a	n/a
		DPOZ_YEAST				n/a	n/a
0.08		PRI1_YEAST	HS only	100%		n/a	n/a
		RAD52_YEAST			0%	n/a	n/a
		RDH54_YEAST	67%	-73%		67%	n/a

		RAD16_YEAST				n/a	n/a
	0.03	RAD2_YEAST				n/a	n/a
		RAD50_YEAST				n/a	n/a
0.17		RAD51_YEAST	HS only	HS only		n/a	n/a
		RAD9_YEAST				n/a	n/a
		DNA2_YEAST	GR only			n/a	n/a
		CDC47_YEAST				n/a	n/a
		MCM2_YEAST				n/a	n/a
0.03		MCM6_YEAST	HS only	HS only		n/a	n/a
		TOP1_YEAST	HS only			n/a	n/a
0.04		TOP2_YEAST	0%	100%		n/a	n/a
		PAT1_YEAST		0%		n/a	n/a
0.09		APN1_YEAST				n/a	n/a
		MAG_YEAST				n/a	n/a
		RAP1_YEAST				n/a	n/a
0.06	0.1	RPA1_YEAST	144%	-36%	0%	156%	21%
		RPA12_YEAST		GR only		n/a	n/a
0.2	0.03	RPA2_YEAST	271%	38%	233%	196%	38%
		RPA34_YEAST	GR only	GR only		n/a	n/a
		RPA43_YEAST		GR only		n/a	n/a
0.16	0.16	RPA49_YEAST	-25%	0%	213%	25%	n/a
0.2	0.06	RPB1_YEAST	650%	467%	1000%	50%	233%
		RPB11_YEAST	HS only			n/a	n/a
0.08		RPB2_YEAST	HS only	250%	167%	n/a	83%
		RPB3_YEAST				n/a	n/a
		RPB4_YEAST				n/a	n/a
		RPC10_YEAST				n/a	n/a
0.06	0.03	RPC2_YEAST	0%	100%	HS only	n/a	n/a
0.1	0.1	RPC6_YEAST	HS only			n/a	n/a
		RPC9_YEAST				n/a	n/a
1.49	0.58	RPAC1_YEAST	263%	54%	94%	177%	12%
	0.23	RPAC2_YEAST	0%	-56%	-28%	0%	n/a
0.31		RPAB1_YEAST	0%	53%		0%	53%
0.22		RPAB3_YEAST		HS only		n/a	n/a
	0.52	RPAB4_YEAST	152%	152%	0%	n/a	n/a
1.17	0.47	RPAB5_YEAST	HS only	118%		n/a	31%
0.75	0.37	MDJ1_YEAST	516%	255%	646%	145%	2%
		XDJ1_YEAST				n/a	n/a
		JEM1_YEAST				n/a	n/a
0.65	0.39	SCJ1_YEAST	28%	-9%	15%	28%	36%
		DID4_YEAST			GR only	n/a	n/a
0.02		YL422_YEAST	HS only	0%		n/a	n/a
0.12		DPM1_YEAST		-26%		n/a	26%
		OST3_YEAST				n/a	n/a
		OST2_YEAST	HS only	0%	0%	n/a	n/a
0.07	0.07	OSTB_YEAST		0%	-53%	n/a	n/a
0.04		PMT2_YEAST				n/a	n/a

		PMT4_YEAST				n/a	n/a
		MRE11_YEAST				n/a	n/a
		MGM1_YEAST	HS only			n/a	n/a
0.09		BRE1_YEAST	-26%	-48%	-69%	n/a	14%
		DMA1_YEAST				n/a	n/a
0.21	0.08	RSP5_YEAST	83%	-15%	8%	67%	15%
0.17		EMI1_YEAST		HS only		n/a	n/a
	0.02	EDE1_YEAST		GR only	400%	n/a	n/a
54.21	71.8	EF1A_YEAST	8%	14%	22%	55%	38%
0.35	0.16	EF1B_YEAST	0%	0%	-27%	0%	0%
0.08	0.25	EF1G1_YEAST	-13%	56%	220%	13%	56%
0.35	0.45	EF1G2_YEAST	27%	119%	86%	2%	n/a
1.54	1.54	EF2_YEAST	-32%	21%	1%	16%	33%
0.77	0.82	EF3A_YEAST	-27%	18%	35%	6%	30%
0.15	0.24	EFTU_YEAST	243%	19%	123%	n/a	19%
0.09		ELO2_YEAST		0%		n/a	0%
		ELP1_YEAST	HS only	0%		n/a	n/a
0.06		ELP3_YEAST	HS only			n/a	n/a
	0.07	ELP4_YEAST				n/a	n/a
		ELP5_YEAST	0%	0%	0%	n/a	n/a
		ELP6_YEAST	HS only			n/a	n/a
	0.05	PPN1_YEAST				n/a	n/a
0.25	0.06	EDC3_YEAST	183%	171%	117%	133%	63%
16.82	3.07	ENO1_YEAST	588%	1443%	182%	n/a	n/a
24.58	4.06	ENO2_YEAST	2058%	1753%	1723%	1065%	495%
		ERR1_YEAST				n/a	n/a
	0.08	ERR3_YEAST				n/a	n/a
		TSC13_YEAST				n/a	n/a
0.51	0.51	ETR1_YEAST	600%	HS only	HS only	n/a	n/a
	0.14	ENT1_YEAST			HS only	n/a	n/a
0.05		ENT2_YEAST	-69%	-50%	-63%	n/a	0%
		ENT3_YEAST				n/a	n/a
		ENT4_YEAST		0%		n/a	n/a
0.08	0.08	ENT5_YEAST	0%	0%	50%	n/a	n/a
	0.1	ERV29_YEAST		0%	-27%	n/a	n/a
		ERV46_YEAST	HS only		0%	n/a	n/a
		ERG28_YEAST				n/a	n/a
0.22	0.11	ERJ5_YEAST		59%		n/a	n/a
0.44	0.28	EMG1_YEAST	238%	221%	119%	n/a	17%
0.06		ENP1_YEAST		0%		n/a	0%
		IF4F2_YEAST		0%		n/a	n/a
0.03		IF4F1_YEAST	0%	-57%	233%	n/a	n/a
0.25	0.31	ERF3_YEAST	73%	-38%	-13%	73%	5%
1.68	0.42	ERF1_YEAST	114%	51%	18%	65%	38%
0.47		IF1A_YEAST	HS only	124%		n/a	n/a
	0.1	IF2A_YEAST	GR only	120%	0%	n/a	n/a
0.39	0.39	IF2B_YEAST	485%	-33%	79%	452%	33%

0.52	0.13	IF2G_YEAST	222%	0%	-17%	147%	0%
0.1		EIF2A_YEAST	HS only	220%		n/a	n/a
0.1	0.07	EIF3A_YEAST	11%	-70%	-34%	59%	0%
0.04	0.08	EIF3B_YEAS7	190%	-71%	69%	260%	11%
0.04		EIF3C_YEAS7		-50%	-50%	n/a	n/a
	0.04	EIF3C_YEAST				n/a	n/a
0.57		EIF3G_YEAS7	233%	209%	GR only	0%	166%
		EIF3G_YEAST				n/a	n/a
0.19	0.19	EIF3I_YEAS7	0%	56%	111%	n/a	56%
		EIF3J_YEAST		GR only		n/a	n/a
0.15		IF4B_YEAST	HS only	114%	0%	n/a	n/a
0.52		IF4E_YEAST	-80%	79%	-43%	n/a	17%
0.08		IF5_YEAST	0%	-19%	225%	0%	19%
1.67	1.2	IF5A2_YEAST	3%	0%	-14%	31%	0%
0.1	0.13	IF2P_YEAST	33%	-25%	283%	33%	25%
0.29		IF6_YEAST	107%	0%		n/a	n/a
1.93	0.71	SUI1_YEAST	187%	86%	300%	113%	86%
		EXO70_YEAST				n/a	n/a
0.04		SEC10_YEAST		HS only		n/a	n/a
		SEC15_YEAST	HS only			n/a	n/a
0.02	0.02	SEC3_YEAST			HS only	n/a	n/a
		SEC5_YEAST				n/a	n/a
0.04		SEC6_YEAST			0%	n/a	n/a
0.03		SEC8_YEAST	-50%	25%		n/a	75%
		EXO1_YEAST				n/a	n/a
		CSL4_YEAST				n/a	n/a
0.29	0.14	RRP40_YEAST			HS only	n/a	n/a
0.17		RRP43_YEAST				n/a	n/a
		RRP45_YEAST				n/a	n/a
		RRP46_YEAST				n/a	n/a
0.03	0.03	RRP44_YEAST				n/a	n/a
0.06	0.06	POB3_YEAST	HS only	HS only	HS only	n/a	n/a
0.23	0.03	SPT16_YEAST	800%	142%	211%	n/a	142%
0.11		CAPZB_YEAST		HS only		n/a	n/a
0.13		FSH1_YEAST	HS only	HS only		n/a	n/a
		FSH3_YEAST	HS only			n/a	n/a
		FPPS_YEAST				n/a	n/a
0.16	0.05	FAS2_YEAST	579%	53%	55%	321%	75%
0.17	0.1	FAS1_YEAST	169%	36%	33%	131%	18%
		YL352_YEAST				n/a	n/a
		FRE1_YEAST				n/a	n/a
0.26	0.17	HEMH_YEAST		HS only	113%	n/a	n/a
		FIMB_YEAST				n/a	n/a
0.45	0.45	FKBP3_YEAST	487%	261%	126%	263%	79%
		FKBP_YEAST				n/a	n/a
0.37	0.37	FKBP4_YEAST	182%	87%	170%	n/a	50%
		FLC1_YEAST		GR only		n/a	n/a

0.26		FHP_YEAST	HS only	HS only		n/a	n/a
	0.14	YCP4_YEAST		GR only	0%	n/a	n/a
0.07		F26_YEAST				n/a	n/a
3.77	2.09	ALF_YEAST	464%	443%	854%	n/a	95%
0.48	0.48	FUMH_YEAST	329%	HS only	586%	114%	n/a
0.72	0.07	FRDS_YEAST	53%	380%	HS only	n/a	n/a
0.04	0.03	NOT1_YEAST	HS only	-63%	HS only	n/a	n/a
		NOT2_YEAST				n/a	n/a
		NOT4_YEAST				n/a	n/a
		NOT5_YEAST				n/a	n/a
	0.06	GIP2_YEAST				n/a	n/a
		GIP4_YEAST	0%			n/a	n/a
0.07		EXG1_YEAST	107%	-25%	343%	107%	25%
		BGL2_YEAST				n/a	n/a
1.25	0.65	HXKG_YEAST	567%	862%	132%	n/a	n/a
0.09	0.04	GFA1_YEAST	HS only	0%	250%	n/a	n/a
0.13	0.06	G6PD_YEAST	HS only	HS only	HS only	n/a	n/a
0.22		YMY9_YEAST		100%		n/a	n/a
0.66	0.12	G6PI_YEAST	HS only	308%	HS only	n/a	n/a
0.07		GID8_YEAST		HS only		n/a	n/a
		CCR4_YEAST	0%			n/a	n/a
0.16		PROB_YEAST	120%	-38%	175%	n/a	15%
0.23	0.05	DCE_YEAST	HS only	HS only	HS only	n/a	n/a
		GLT1_YEAST	100%	400%	267%	n/a	n/a
0.05		GSH1_YEAST		0%		n/a	n/a
1.28	0.39	GLNA_YEAST	HS only	HS only	HS only	n/a	n/a
		SYEC_YEAST	125%	0%	250%	n/a	n/a
0.88	0.23	GLRX2_YEAST	130%	207%	65%	n/a	76%
		GPX2_YEAST		120%		n/a	n/a
0.57	0.14	GSHR_YEAST	200%	443%	150%	n/a	n/a
0.29	0.14	GST1_YEAST	HS only	HS only	0%	n/a	n/a
		GST2_YEAST				n/a	n/a
		GSHB_YEAST				n/a	n/a
2.49	0.78	G3P1_YEAST	HS only	HS only	76%	n/a	n/a
		G3P2_YEAST	147%		32%	n/a	n/a
5.21	2.84	G3P3_YEAST	141%	68%	9%	69%	26%
0.17		GPD1_YEAST	HS only	HS only	0%	n/a	n/a
0.07		GPD2_YEAST		-27%	0%	n/a	27%
		GPT1_YEAST				n/a	n/a
0.03		GDE1_YEAST	HS only	-40%	0%	n/a	n/a
0.2		GCSH_YEAST				n/a	n/a
		GCSP_YEAST				n/a	n/a
0.19	0.14	GYS1_YEAST	HS only	HS only	56%	n/a	n/a
0.54	0.76	GYS2_YEAST	154%	1163%	173%	n/a	1038%
0.04	0.2	GDE_YEAST	HS only		213%	n/a	n/a
0.4	0.31	PHSG_YEAST	843%	471%	HS only	n/a	n/a
		KRE2_YEAST				n/a	n/a

0.51	0.1	SYG_YEAST	HS only	HS only	HS only	n/a	n/a
		SYG2_YEAST				n/a	n/a
0.13		GUAA_YEAST	HS only	467%		n/a	n/a
		IMH1_YEAST				n/a	n/a
		YSP2_YEAST	GR only	0%	GR only	n/a	n/a
		GRH1_YEAST				n/a	n/a
		WHI2_YEAST	HS only			n/a	n/a
0.28	0.13	GCH1_YEAST		HS only	HS only	n/a	n/a
		RIB1_YEAST				n/a	n/a
0.06		MTG2_YEAST	HS only	HS only		n/a	n/a
0.14	0.01	BEM2_YEAST	161%	-40%	7%	89%	1%
		GYP1_YEAST				n/a	n/a
		GYP3_YEAST				n/a	n/a
		GYP8_YEAST				n/a	n/a
		SAC7_YEAST				n/a	n/a
0.32		GSP1_YEAST				n/a	n/a
		GSP2_YEAST	HS only			n/a	n/a
		GTR2_YEAST				n/a	n/a
0.97	0.53	RBG1_YEAST	151%	23%	116%	n/a	23%
0.55	0.34	RHO1_YEAST	-16%	23%	-66%	16%	23%
0.14		RHO3_YEAST	HS only	HS only		n/a	n/a
0.1		RHO5_YEAST	55%	29%	-34%	55%	81%
0.16		YPT1_YEAST	HS only	HS only		n/a	n/a
0.34		YPT7_YEAST		HS only		n/a	n/a
		G4P1_YEAST	HS only	0%		n/a	n/a
		LTE1_YEAST				n/a	n/a
0.04		GPB1_YEAST	HS only	0%		n/a	n/a
1.2	1.2	GBLP_YEAST	-34%	305%	3%	3%	62%
		GBG_YEAST	HS only			n/a	n/a
		KGUA_YEAST				n/a	n/a
0.61	0.37	GAR1_YEAST	129%	91%	39%	129%	26%
1.2	1.2	NHP2_YEAST	74%	-49%	50%	35%	3%
1.58	3.15	NOP10_YEAST	464%	-25%	258%	364%	25%
1	0.56	CBF5_YEAST	50%	-1%	59%	23%	28%
		YB92_YEAST				n/a	n/a
0.31		YGK1_YEAST	HS only	HS only		n/a	n/a
0.85	0.23	HS104_YEAST	1300%	3183%	3031%	n/a	450%
6.35	2.61	HSP26_YEAST	1527%	4133%	1640%	n/a	n/a
1.63	0.76	HSP42_YEAST	347%	859%	850%	n/a	n/a
3.16	1.35	HSP60_YEAST	596%	807%	706%	n/a	136%
0.16	0.08	HSP78_YEAST	1050%	HS only	HS only	n/a	n/a
0.79	0.71	HSP7F_YEAST	680%	177%	468%	360%	119%
0.56	0.5	HSP79_YEAST	357%	HS only	900%	n/a	n/a
5.98	3.93	HSP71_YEAST	260%	163%	246%	108%	37%
5.36	3.71	HSP72_YEAST	202%	164%	241%	62%	4%
		HSP73_YEAST				n/a	n/a
2.48	1.22	HSP74_YEAST	560%	HS only	HS only	n/a	n/a

	2.31	HSP75_YEAST	21%	-40%	-5%	n/a	n/a
4.87	2.14	HSP76_YEAST	47%	-23%	-7%	26%	17%
1.54	0.99	HSP77_YEAST	1526%	148%	130%	964%	34%
0.17	0.17	STI1_YEAST	HS only	120%	HS only	n/a	n/a
	0.01	SEN1_YEAST	-38%	-25%	500%	38%	n/a
		HOT13_YEAST				n/a	n/a
0.04		HAP1W_YEAST	HS only	HS only		n/a	n/a
0.25		GPG1_YEAST				n/a	n/a
		COQ1_YEAST	0%			n/a	n/a
		COQ3_YEAST				n/a	n/a
0.78	0.29	HXKA_YEAST	HS only	HS only	HS only	n/a	n/a
0.29		HXKB_YEAST	HS only	314%		n/a	n/a
0.13	0.13	HMO1_YEAST	HS only	0%	0%	n/a	0%
	0.05	GNP1_YEAST		GR only	-67%	n/a	n/a
0.12	0.25	HXT7_YEAST	HS only	208%	44%	n/a	108%
0.03	0.03	TRK1_YEAST		0%	HS only	n/a	n/a
		HOT1_YEAST				n/a	n/a
0.04		HIS2_YEAST	HS only	HS only		n/a	n/a
		SYH_YEAST	HS only			n/a	n/a
		GCN5_YEAST			-50%	n/a	n/a
		SAS3_YEAST				n/a	n/a
		ASF1_YEAST				n/a	n/a
		CTI6_YEAST				n/a	n/a
0.04		HDA1_YEAST				n/a	n/a
0.09	0.09	HOS3_YEAST	1%	-26%	-22%	54%	26%
0.15	0.07	RPD3_YEAST		HS only	HS only	n/a	n/a
0.85	0.28	H1_YEAST	64%	-28%	102%	64%	28%
1.59	1.59	H2A1_YEAST	80%	26%	11%	80%	26%
1.54	1.01	H2AZ_YEAST	85%	26%	4%	33%	26%
	4.17	H2B1_YEAST	33%			n/a	n/a
5.53		H2B2_YEAST	33%	37%	71%	n/a	37%
0.93	0.55	H3_YEAST	-41%	178%	-56%	0%	109%
77.31	42.78	H4_YEAST	130%	-29%	210%	96%	29%
		SET1_YEAST				n/a	n/a
	0.21	HNT1_YEAST				n/a	n/a
	0.09	HMT1_YEAST				n/a	n/a
0.05		LYS4_YEAST		HS only		n/a	n/a
0.25	0.25	HOSC_YEAST	38%	-22%	-22%	38%	22%
0.09		DHOM_YEAST		HS only		n/a	n/a
0.09		KHSE_YEAST	HS only	HS only		n/a	n/a
		SNL1_YEAST		GR only		n/a	n/a
		AHA1_YEAST	0%	0%		n/a	n/a
0.06	0.13	HMCS_YEAST	117%	192%	117%	n/a	192%
0.14		HPRT_YEAST		HS only		n/a	n/a
0.06	0.12	IMA1_YEAST		83%	0%	n/a	133%
		IMB1_YEAST	HS only	0%		n/a	n/a
		IMB4_YEAST		0%		n/a	n/a

		ISN1_YEAST				n/a	n/a
0.03		IST2_YEAST	HS only	77%	133%	n/a	156%
		I23O_YEAST				n/a	n/a
		BUD2_YEAST				n/a	n/a
		IRA1_YEAST				n/a	n/a
		SLI15_YEAST	HS only	-36%		n/a	n/a
0.26		IES5_YEAST				n/a	n/a
0.17		PHO88_YEAST	0%	-55%	0%	n/a	0%
0.1		PHO86_YEAST		0%	0%	n/a	n/a
0.11	0.11	IPYR_YEAST	118%	118%	118%	n/a	118%
0.1		IPYR2_YEAST				n/a	n/a
1.83		IMDH2_YEAST	HS only	598%		n/a	218%
		VIP1_YEAST				n/a	n/a
		ISC1_YEAST	100%	100%	100%	n/a	n/a
0.03		INP52_YEAST				n/a	n/a
		INP53_YEAST	13%	-80%	50%	88%	n/a
		INV1_YEAST	HS only			n/a	n/a
		ISU1_YEAST			0%	n/a	n/a
		ISU2_YEAST				n/a	n/a
		AFT1_YEAST				n/a	n/a
		IAH1_YEAST	HS only			n/a	n/a
0.42	0.3	IDH1_YEAST	111%	137%	95%	0%	97%
1.83	1.83	IDH2_YEAST	457%	144%	191%	169%	25%
		IDHH_YEAST		50%		n/a	n/a
0.91	0.43	IDHP_YEAST	0%	-36%	-53%	0%	12%
		SYIC_YEAST	HS only			n/a	n/a
0.23		IDI1_YEAST	HS only	HS only		n/a	n/a
		ISW1_YEAST				n/a	n/a
	0.03	ISW2_YEAST				n/a	n/a
		IOC3_YEAST	HS only			n/a	n/a
		IOC4_YEAST	HS only			n/a	n/a
0.27		APJ1_YEAST	HS only	HS only		n/a	n/a
0.09		KAR4_YEAST				n/a	n/a
		KEL1_YEAST	0%	-40%	120%	n/a	n/a
0.37	0.08	ILV5_YEAST	131%	-39%	8%	n/a	9%
		YBD2_YEAST	3%	100%	0%	53%	n/a
		YL032_YEAST				n/a	n/a
		KRE5_YEAST				n/a	n/a
		CIN8_YEAST		GR only		n/a	n/a
		KAR3_YEAST				n/a	n/a
		KIP2_YEAST	0%			n/a	n/a
		SMY1_YEAST				n/a	n/a
		NUF2_YEAST				n/a	n/a
0.07		KYNU_YEAST	HS only	HS only		n/a	n/a
		LAH1_YEAST				n/a	n/a
0.59	0.59	LGUL_YEAST	HS only	490%	490%	n/a	n/a
		LRE1_YEAST				n/a	n/a

		LYS5_YEAST				n/a	n/a
		CP51_YEAST	HS only			n/a	n/a
0.1		LSG1_YEAST	-50%	25%	110%	n/a	75%
		LSB1_YEAST				n/a	n/a
0.32	0.23	LSB3_YEAS7	-23%	-26%	-2%	23%	2%
		ASPG1_YEAST				n/a	n/a
		LCMT2_YEAST	HS only			n/a	n/a
	0.08	SOG2_YEAST				n/a	n/a
0.12	0.03	SYLC_YEAST	HS only	0%	HS only	n/a	n/a
0.05	0.05	YD266_YEAST		0%	160%	n/a	n/a
		TGL3_YEAST				n/a	n/a
0.04		TGL5_YEAST				n/a	n/a
		LIP5_YEAST		0%		n/a	n/a
0.14	0.2	LCF1_YEAST	240%	90%	275%	60%	90%
		LCF3_YEAST				n/a	n/a
0.5		LCF4_YEAST	HS only	970%		n/a	70%
	0.2	PPAL_YEAST				n/a	n/a
0.18	0.5	GLY1_YEAST	244%	125%	525%	n/a	n/a
0.18	0.06	HXT1_YEAST	-33%	-58%	-70%	8%	17%
0.18	0.12	HXT3_YEAST	-57%	-59%	-66%	5%	15%
		PLB1_YEAST				n/a	n/a
0.02		NTE1_YEAST	HS only	-67%		n/a	n/a
0.11		SYKC_YEAST		0%		n/a	n/a
		SYKM_YEAST				n/a	n/a
		YO111_YEAST				n/a	n/a
		ALR1_YEAST				n/a	n/a
	0.04	ALR2_YEAST				n/a	n/a
2.14	0.46	ALDH6_YEAST	662%	1704%	2186%	n/a	1253%
0.34	0.62	MDHM_YEAST	HS only	HS only	HS only	n/a	n/a
1.52	2.03	MDHP_YEAST	132%	-20%	18%	57%	20%
		MASY_YEAST				n/a	n/a
		FABD_YEAST				n/a	n/a
		MNR2_YEAST				n/a	n/a
0.07	0.07	DCW1_YEAST	0%	0%	0%	n/a	0%
0.08		MNN9_YEAST	0%	0%	0%	n/a	0%
		VAN1_YEAST				n/a	n/a
0.55	0.69	MPG1_YEAST	68%	-34%	25%	48%	19%
		MPI_YEAST	HS only	114%		n/a	n/a
		MKK2_YEAST				n/a	n/a
0.05		PBS2_YEAST		0%		n/a	n/a
	0.05	MHP1_YEAST	0%	GR only	500%	n/a	n/a
0.25		MATA1_YEAST		HS only		n/a	n/a
0.06		MRC1_YEAST	HS only			n/a	n/a
		MED11_YEAST				n/a	n/a
		MED15_YEAST				n/a	n/a
0.35		MED20_YEAST	HS only	HS only		n/a	n/a
0.27		MED22_YEAST	130%	HS only		n/a	n/a

	0.03	MED5_YEAST				n/a	n/a
0.14		MED8_YEAST				n/a	n/a
		RIM4_YEAST				n/a	n/a
	0.14	MSC3_YEAST	125%	0%	56%	0%	n/a
		MSC6_YEAST				n/a	n/a
		MCA1_YEAS7	HS only			n/a	n/a
2.05	1.4	AMPM1_YEAST	1187%	1838%	1775%	463%	625%
0.08	0.08	AMPM2_YEAST	100%	0%	0%	n/a	n/a
0.08	0.04	SYMC_YEAST	288%	163%	0%	188%	63%
0.02		MMS1_YEAST				n/a	n/a
0.14		YB9H_YEAST		HS only		n/a	n/a
		MDN1_YEAST				n/a	n/a
		MCM10_YEAST				n/a	n/a
0.08		MCM5_YEAST	HS only	HS only		n/a	n/a
0.21	0.21	FIS1_YEAST	60%	-27%	36%	60%	27%
		ACEB_YEAST				n/a	n/a
		ODC2_YEAST		GR only	GR only	n/a	n/a
		MAM33_YEAST				n/a	n/a
		ATP10_YEAST	GR only			n/a	n/a
		RIM2_YEAST	0%	GR only	0%	n/a	n/a
		TCM62_YEAST				n/a	n/a
0.06	0.06	MCX1_YEAST			HS only	n/a	n/a
		NTG1_YEAST				n/a	n/a
0.22	0.11	YHM2_YEAST	-25%	50%	-28%	25%	50%
	0.04	YME2_YEAS7				n/a	n/a
0.17		ERV1_YEAST				n/a	n/a
		MG101_YEAST	-37%		383%	n/a	n/a
		MTG1_YEAST	HS only			n/a	n/a
		TIM10_YEAST				n/a	n/a
		TIM14_YEAST				n/a	n/a
		TIM16_YEAST	HS only		0%	n/a	n/a
		TIM21_YEAST				n/a	n/a
0.33	0.15	TIM44_YEAST	122%	-15%	-38%	95%	41%
	0.18	TOM20_YEAST	0%		0%	n/a	n/a
		TOM40_YEAST				n/a	n/a
		TOM6_YEAST				n/a	n/a
		TOM70_YEAS7	50%		-38%	50%	n/a
		PMIP_YEAST				n/a	n/a
	0.06	MMT1_YEAST				n/a	n/a
		NUC1_YEAST			0%	n/a	n/a
0.04		IML2_YEAS7	HS only			n/a	n/a
0.08	0.17	OM45_YEAST	113%	0%	488%	n/a	n/a
4.41	2.08	VDAC1_YEAST	570%	327%	293%	432%	175%
		YKR18_YEAS7				n/a	n/a
		OAC1_YEAST	-55%			n/a	n/a
		MPM1_YEAS7	HS only			n/a	n/a
0.42	0.42	PRX1_YEAST	250%	321%	306%	n/a	71%

1.57	0.37	MPCP_YEAST	67%	-14%	-4%	41%	34%
		FMP38_YEAST				n/a	n/a
1.73	1.73	MAS5_YEAST	126%	13%	135%	59%	34%
		AFG3_YEAST				n/a	n/a
		RCA1_YEAST	0%	GR only	0%	n/a	n/a
0.05		GEM1_YEAST				n/a	n/a
	0.07	MPPA_YEAST		0%		n/a	n/a
0.07	0.07	MPPB_YEAST	HS only	HS only	0%	n/a	n/a
		FUS3_YEAST	-25%	100%	0%	25%	n/a
0.07		HOG1_YEAST	HS only	HS only		n/a	n/a
		KSS1_YEAST				n/a	n/a
		SLT2_YEAST				n/a	n/a
	0.17	CSM1_YEAST				n/a	n/a
0.49		GLRX5_YEAST	HS only	HS only		n/a	n/a
		MSB1_YEAST			GR only	n/a	n/a
		RNA15_YEAST				n/a	n/a
		YTH1_YEAST	HS only			n/a	n/a
0.1		CTH1_YEAST	HS only	HS only		n/a	n/a
0.11	0.05	MEX67_YEAST	240%	-38%	-10%	240%	3%
		GFD1_YEAST				n/a	n/a
		MTR2_YEAST			0%	n/a	n/a
0.66	0.13	MRT4_YEAST	91%	349%	254%	n/a	59%
		PUF2_YEAST				n/a	n/a
		PUF3_YEAST	GR only			n/a	n/a
		DCP1_YEAST	0%	243%	0%	n/a	n/a
0.03		DCP2_YEAS7		HS only		n/a	n/a
0.72	0.2	MEU1_YEAST	HS only	HS only	0%	n/a	n/a
0.25		TR112_YEAST		HS only		n/a	n/a
0.07		MRD1_YEAST		-43%		n/a	n/a
2.41	3.18	MBF1_YEAST	143%	129%	138%	77%	170%
0.5		MLC1_YEAST	-27%	-1%	117%	27%	71%
0.28	0.5	BBC1_YEAST	4%	-53%	-21%	21%	5%
		MYO1_YEAST				n/a	n/a
		MYO2_YEAST	100%	0%		n/a	n/a
0.13	0.05	MYO3_YEAST	19%	-20%	121%	4%	20%
0.14	0.03	MYO5_YEAS7	-56%	-53%	113%	4%	8%
		TRM1_YEAST				n/a	n/a
0.33		TRPF_YEAST	HS only	HS only		n/a	n/a
		AML1_YEAST				n/a	n/a
		NAH1_YEAST		GR only	GR only	n/a	n/a
		HPA3_YEAST				n/a	n/a
0.09	0.09	HST2_YEAST	HS only	HS only	HS only	n/a	n/a
		SIR2_YEAST		GR only	100%	n/a	n/a
	0.1	MAOM_YEAST	100%		100%	n/a	n/a
		NPY1_YEAST	HS only			n/a	n/a
0.12		NCB5R_YEAS7	0%	-72%		n/a	6%
		NCB5R_YEAST			-28%	n/a	n/a

	0.22	MCR1_YEAS7		100%	80%	n/a	n/a
0.09	0.09	ADH6_YEAST	HS only	0%	HS only	n/a	n/a
1.51	0.26	OYE2_YEAST	576%	735%	53%	n/a	53%
0.26		OYE3_YEAST				n/a	n/a
		NCPR_YEAST				n/a	n/a
1.3	0.45	GRE3_YEAST	550%	550%	350%	n/a	n/a
1.39	0.62	KAR_YEAST	805%	562%	520%	n/a	n/a
		GRE2_YEAST				n/a	n/a
0.52		DHE4_YEAST	HS only	HS only		n/a	n/a
	0.07	DHE5_YEAST				n/a	n/a
		NBP1_YEAST				n/a	n/a
0.2		NACA_YEAST	130%	-47%	0%	130%	8%
0.22	0.22	NACB1_YEAS7		0%	HS only	n/a	n/a
		RPI1_YEAST				n/a	n/a
		PMD1_YEAST				n/a	n/a
0.07	0.04	UTP17_YEAST	238%	-58%	114%	238%	5%
0.63	0.5	TREA_YEAST	850%	688%	1150%	n/a	n/a
0.54		NIF3_YEAST	HS only	HS only		n/a	n/a
0.73	0.31	PNC1_YEAST	HS only	HS only	240%	n/a	n/a
0.13	0.13	NRK1_YEAST	HS only		HS only	n/a	n/a
		NMA1_YEAST				n/a	n/a
0.07		NPT1_YEAST	HS only	HS only		n/a	n/a
0.11		NADC_YEAST	HS only	HS only		n/a	n/a
0.26		NFU1_YEAST	HS only	HS only		n/a	n/a
	0.04	NPR1_YEAST	GR only	GR only		n/a	n/a
		SNG1_YEAST				n/a	n/a
		NCE1_YEAST				n/a	n/a
0.7	0.43	NCE2_YEAST	-29%	63%	-19%	29%	0%
		NHP6B_YEAST	HS only			n/a	n/a
		UPF3_YEAST				n/a	n/a
0.64	0.13	ARD1_YEAST	HS only	HS only	HS only	n/a	n/a
		NAT1_YEAST				n/a	n/a
	0.04	MDM20_YEAST	GR only		100%	n/a	n/a
		MAK3_YEAST				n/a	n/a
0.43	0.27	NUG1_YEAST	87%	-9%	119%	43%	9%
0.08		NSR1_YEAST	0%	-53%		n/a	n/a
0.02	0.02	NUM1_YEAST	0%	-25%	-63%	n/a	25%
		NAB2_YEAST				n/a	n/a
		SNF4_YEAST				n/a	n/a
		STH1_YEAST	HS only			n/a	n/a
0.46	0.21	BFR1_YEAST	47%	-58%	-50%	47%	18%
	0.26	NTF2_YEAST				n/a	n/a
0.04	0.04	NOP14_YEAST	50%	-58%	0%	50%	8%
0.04	0.09	NOC2_YEAST	0%	0%	0%	n/a	n/a
		NOC4_YEAST				n/a	n/a
0.05		NOC3_YEAST	100%	100%		n/a	n/a
0.21	0.05	NOG1_YEAST	233%	57%	0%	13%	17%

0.45	0.21	NOG2_YEAST	27%	-9%	-34%	6%	9%
		URB1_YEAST	0%	114%	200%	0%	n/a
		URB2_YEAST				n/a	n/a
0.22	0.14	NOP12_YEAST	289%	17%	89%	39%	60%
0.08		NOP13_YEAST		-50%		n/a	n/a
	0.16	NOP3_YEAST	50%	-69%	144%	50%	n/a
0.14	0.09	NOP4_YEAST	79%	-15%	0%	1%	15%
3.87	1.35	NOP56_YEAST	124%	13%	12%	11%	4%
2.58	1.34	NOP58_YEAS7	139%	31%	-1%	24%	12%
0.72	0.14	NOP6_YEAST	HS only	66%	0%	n/a	66%
0.11	0.08	NET1_YEAST	170%	-38%	75%	130%	23%
	0.06	NUP59_YEAST	HS only			n/a	n/a
0.19	0.09	GLE2_YEAST	HS only	0%	HS only	n/a	0%
		NDC1_YEAST				n/a	n/a
0.04		NIC96_YEAST	-20%	-6%	0%	n/a	44%
0.08	0.04	NSP1_YEAST	50%	0%	100%	50%	n/a
		NU100_YEAST		GR only	0%	n/a	n/a
	0.03	NU116_YEAST	158%	-54%	14%	42%	n/a
0.03		NU133_YEAST				n/a	n/a
0.02		NU145_YEAST	0%	-60%	150%	n/a	0%
		NU157_YEAST	0%	GR only	150%	n/a	n/a
0.02	0.04	NU159_YEAST	11%	-57%	0%	89%	14%
0.04	0.04	NU170_YEAST	HS only	-50%	100%	n/a	17%
		NU188_YEAST		0%	200%	n/a	n/a
		NU192_YEAST	HS only	100%	100%	n/a	n/a
		NUP2_YEAST				n/a	n/a
		NUP49_YEAST				n/a	n/a
0.13		NUP57_YEAST	0%	58%	117%	0%	58%
		NUP60_YEAST	0%	0%		n/a	n/a
0.04		NUP82_YEAST	-36%	-28%	71%	36%	28%
0.15	0.02	PO152_YEAST	210%	-13%	-43%	190%	13%
		POM34_YEAST	25%	-50%	-69%	75%	n/a
0.3		SEH1_YEAST	56%	300%	0%	56%	67%
0.8	0.48	NDK_YEAST	0%	51%	38%	n/a	16%
0.07		NAP1_YEAST				n/a	n/a
		MALX3_YEAST				n/a	n/a
0.21	0.06	YOR1_YEAST	63%	-44%	-49%	28%	20%
0.12		ORN_YEAST	HS only	HS only		n/a	n/a
0.35		OAT_YEAST	HS only	HS only		n/a	n/a
		OSM1_YEAST				n/a	n/a
0.05	0.13	OSH2_YEAST	41%	-32%	40%	1%	18%
		OSH3_YEAST	50%	-54%	0%	50%	n/a
0.14	0.07	OSH6_YEAST	0%	-34%	50%	n/a	34%
	0.05	PBP1_YEAST	111%	20%	36%	n/a	n/a
		PBP2_YEAST	HS only			n/a	n/a
		PAN3_YEAST				n/a	n/a
		REP1_YEAST	HS only			n/a	n/a

		REP2_YEAST	109%			n/a	n/a
0.13	0.02	ARO1_YEAST	-50%	650%	HS only	n/a	n/a
0.17		MSRA_YEAST		HS only		n/a	n/a
		PTR2_YEAST			GR only	n/a	n/a
0.28	0.39	PPID_YEAST	258%	167%	121%	75%	167%
		ESS1_YEAST	0%		121%	n/a	n/a
2.86	2.18	CYPH_YEAST	1168%	242%	509%	485%	25%
		PTH2_YEAST				n/a	n/a
		PWP1_YEAST				n/a	n/a
0.03		PWP2_YEAST	57%	-36%	57%	n/a	36%
0.15	0.15	DOT5_YEAST			0%	n/a	n/a
		GPX3_YEAST				n/a	n/a
1.57	1.2	TSA1_YEAST	0%	63%	606%	0%	16%
		TSA2_YEAST	HS only		412%	n/a	n/a
0.19	0.42	AHP1_YEAST	67%	221%	121%	n/a	221%
		SPS19_YEAST				n/a	n/a
0.09	0.09	PTE1_YEAST			56%	n/a	n/a
		PEX8_YEAST				n/a	n/a
		FOX2_YEAST				n/a	n/a
		PEX17_YEAST				n/a	n/a
		PEX11_YEAST				n/a	n/a
		PEX5_YEAST				n/a	n/a
0.26	0.26	FAT2_YEAST	208%	-18%	-20%	33%	18%
		PIP2_YEAST				n/a	n/a
0.1	0.05	PESC_YEAST	30%	-27%	340%	30%	27%
		PAD1_YEAST	0%	-52%		n/a	n/a
	0.06	SYFA_YEAST			HS only	n/a	n/a
0.59		SYFB_YEAST	360%	780%		n/a	300%
0.07		STE2_YEAST	GR only	-71%	GR only	n/a	n/a
		PHM7_YEAST				n/a	n/a
		PEM1_YEAST				n/a	n/a
5.99	3.91	NPC2_YEAST	5%	-28%	26%	25%	9%
	0.04	VPS34_YEAST				n/a	n/a
0.09	0.05	SLM1_YEAST	10%	-50%	100%	46%	14%
		SLM2_YEAST		GR only		n/a	n/a
0.03		PIK1_YEAST				n/a	n/a
		STT4_YEAST		50%		n/a	n/a
		CSR1_YEAST	HS only			n/a	n/a
0.09		PDR16_YEAST				n/a	n/a
0.09		PDR17_YEAST				n/a	n/a
		AROF_YEAST				n/a	n/a
0.09		AROG_YEAST		HS only		n/a	n/a
		PGM3_YEAST				n/a	n/a
0.25		PGM1_YEAST				n/a	n/a
0.73	0.18	PGM2_YEAST	683%	508%	200%	n/a	n/a
5.36	10.79	PGK_YEAST	25%	-44%	36%	16%	2%
39.69	8.24	PMG1_YEAST	1125%	2782%	573%	721%	1255%

0.1		PMG2_YEAST		HS only		n/a	n/a
		SAC1_YEAST		GR only	0%	n/a	n/a
		SPO14_YEAST			0%	n/a	n/a
4.83	2.24	PMM_YEAST	1504%	1332%	2985%	456%	627%
0.06		PUR6_YEAST		50%		n/a	50%
		PUR4_YEAST	HS only			n/a	n/a
0.05		PALA_YEAST	HS only	HS only		n/a	n/a
0.05	0.1	TPA1_YEAST	200%	0%	100%	n/a	n/a
10.55	7.14	PMA1_YEAST	43%	48%	-25%	5%	11%
		FTR1_YEAST				n/a	n/a
1.73	1.13	PDR5_YEAST	-2%	-4%	-47%	9%	23%
		SNI1_YEAST				n/a	n/a
0.39		PCC1_YEAST	HS only	HS only		n/a	n/a
		PAP_YEAST				n/a	n/a
0.07		POP2_YEAST	114%	0%		n/a	0%
0.05		PAP2_YEAST	-71%	0%	-71%	n/a	0%
1.13	0.71	PABP_YEAST	209%	-20%	-15%	175%	20%
0.59	0.85	PAA1_YEAST	314%	247%	136%	n/a	n/a
		FMS1_YEAST				n/a	n/a
0.06		TPO1_YEAST	42%	-2%	-25%	42%	65%
0.11	0.11	TPO2_YEAST	HS only		HS only	n/a	n/a
0.11		TPO3_YEAST	HS only	0%	120%	n/a	n/a
		TPO4_YEAST				n/a	n/a
		TPP1_YEAST				n/a	n/a
0.1		HEM3_YEAST	HS only	HS only		n/a	n/a
1.82	1.82	ALDH4_YEAST	810%	550%	653%	n/a	n/a
		PFD3_YEAST				n/a	n/a
0.25		PFD4_YEAST				n/a	n/a
		PFD5_YEAST	HS only			n/a	n/a
		PML1_YEAST				n/a	n/a
		PML39_YEAST				n/a	n/a
		PRP19_YEAST				n/a	n/a
		PRP16_YEAST				n/a	n/a
		PRP22_YEAST				n/a	n/a
0.37	0.13	PRP43_YEAST	2%	-20%	4%	16%	20%
		PRP2_YEAST				n/a	n/a
		ISY1_YEAST				n/a	n/a
		RDS3_YEAST				n/a	n/a
		URN1_YEAST				n/a	n/a
0.05		ESF1_YEAST	HS only	0%		n/a	0%
0.12		PNO1_YEAST		-52%	0%	n/a	n/a
0.04		RIX1_YEAS7		0%		n/a	n/a
0.16	0.16	BDH2_YEAST	HS only	HS only	HS only	n/a	n/a
0.13		GAS3_YEAST	-64%	-64%	-64%	0%	n/a
	0.11	PLSC_YEAST	0%	100%	15%	n/a	n/a
0.15		PSMD9_YEAST				n/a	n/a
		PSD10_YEAST	HS only			n/a	n/a

	0.06	PRPD_YEAST				n/a	n/a
0.08		ACON2_YEAST	HS only	HS only		n/a	n/a
		YMX7_YEAST	HS only			n/a	n/a
0.06		ALAT_YEAST	HS only			n/a	n/a
0.05		ALAM_YEAST				n/a	n/a
		MNN10_YEAST	0%	0%	0%	n/a	n/a
0.08		MNN11_YEAST				n/a	n/a
	0.02	DHR1_YEAST	175%	0%	-30%	225%	n/a
0.04		DHR2_YEAST	GR only	-56%		n/a	n/a
0.09		DPP3_YEAST		HS only		n/a	n/a
		SNT1_YEAST				n/a	n/a
0.1	0.1	ETFA_YEAST	HS only	HS only	HS only	n/a	n/a
		ETFB_YEAST	59%			n/a	n/a
	0.05	ETFD_YEAST			100%	n/a	n/a
		SCW4_YEAST	HS only			n/a	n/a
		CRH2_YEAST		GR only		n/a	n/a
0.22		HOS2_YEAST				n/a	n/a
		NIT3_YEAST				n/a	n/a
2.62	0.54	IMDH3_YEAST	923%	277%	399%	523%	n/a
0.45		IMDH4_YEAST		61%		n/a	n/a
		ALG9_YEAST				n/a	n/a
		KTR3_YEAST	GR only		-50%	n/a	n/a
	0.05	ARX1_YEAST	0%	-55%	HS only	n/a	n/a
		FSF1_YEAST		GR only	0%	n/a	n/a
	0.06	ADRO_YEAST				n/a	n/a
		MSS4_YEAST				n/a	n/a
		ATC5_YEAST		0%		n/a	n/a
		ATC4_YEAST	100%	GR only	-75%	n/a	n/a
		SYPM_YEAST	HS only			n/a	n/a
		QOR_YEAST	HS only			n/a	n/a
		HSL1_YEAST				n/a	n/a
		KKQ8_YEAST				n/a	n/a
0.06		KBN8_YEAST				n/a	n/a
		KD025_YEAST				n/a	n/a
		KN8R_YEAST				n/a	n/a
0.03		KOE5_YEAST	HS only	HS only		n/a	n/a
		KOK0_YEAST				n/a	n/a
		BIT2_YEAST				n/a	n/a
		HMS1_YEAST				n/a	n/a
	0.03	STB4_YEAST	0%	GR only	0%	n/a	n/a
		AQR1_YEAST		GR only	GR only	n/a	n/a
0.39	0.12	PHB1_YEAST	294%	-12%	15%	185%	12%
0.22	0.1	PHB2_YEAST	458%	60%	27%	262%	60%
		LAS17_YEAST	GR only	GR only	-55%	n/a	n/a
		ADY1_YEAST				n/a	n/a
		POC1_YEAST	HS only			n/a	n/a
		POC2_YEAST				n/a	n/a

1.14	0.24	PSA3_YEAST	HS only	936%	HS only	n/a	n/a
0.35	0.16	PSB2_YEAST		HS only	HS only	n/a	n/a
0.29	0.29	PSB1_YEAST	HS only	HS only	HS only	n/a	n/a
2	0.28	PSA6_YEAST	546%	1308%	HS only	n/a	131%
0.92	0.11	PSB5_YEAST	588%	736%	HS only	n/a	n/a
0.16	0.16	PSB6_YEAST	HS only	HS only	HS only	n/a	n/a
		PSB4_YEAST	0%			n/a	n/a
1.54	1.54	PSA1_YEAST	460%	607%	493%	311%	393%
0.62	0.13	PSA7_YEAST	0%	94%	115%	n/a	35%
		PSB7_YEAST				n/a	n/a
0.82	0.13	PSA5_YEAST	HS only	HS only	HS only	n/a	n/a
0.82	0.82	PSB3_YEAST	63%	134%	134%	n/a	n/a
0.61	0.13	PSA4_YEAST	231%	369%	HS only	n/a	n/a
1.12	0.29	PSA2_YEAST	HS only	HS only	HS only	n/a	n/a
0.08		CIC1_YEAST		-56%		n/a	n/a
		AFR1_YEAST	0%	0%	0%	n/a	n/a
		AIM2_YEAST				n/a	n/a
		AIR2_YEAST				n/a	n/a
0.1	0.21	APA1_YEAST	0%	0%	HS only	n/a	n/a
	0.04	ARG56_YEAST	-50%		HS only	n/a	n/a
		ASK10_YEAST	0%	GR only	400%	n/a	n/a
0.15		AST1_YEAST	114%	30%	0%	n/a	30%
		AST2_YEAST				n/a	n/a
		ATP11_YEAST				n/a	n/a
		ATP13_YEAST				n/a	n/a
		BCH2_YEAST				n/a	n/a
0.37		BCP1_YEAST	HS only	HS only		n/a	n/a
0.06		BFR2_YEAST	0%	0%	0%	n/a	0%
0.2		BIM1_YEAST				n/a	n/a
0.12	0.41	BMH1_YEAST	717%	-54%	73%	n/a	n/a
	0.25	BMH2_YEAST	508%	-29%	HS only	n/a	n/a
		BNI1_YEAST		GR only	50%	n/a	n/a
0.03	0.03	BOB1_YEAST	133%	-14%	20%	n/a	56%
		BOI2_YEAST	HS only			n/a	n/a
	0.06	BSP1_YEAST	42%	GR only	183%	42%	n/a
0.93	0.44	BTN2_YEAST	HS only	HS only	HS only	n/a	n/a
		BUR2_YEAST				n/a	n/a
		BZZ1_YEAST			100%	n/a	n/a
	0.03	CF130_YEAST				n/a	n/a
		CAJ1_YEAST				n/a	n/a
0.09		CBP3_YEAST	-53%		-53%	n/a	n/a
0.18		CG121_YEAST	HS only	HS only		n/a	n/a
0.11	0.36	CMS1_YEAST	142%	0%	28%	85%	0%
		CSF1_YEAST				n/a	n/a
		CWH43_YEAST				n/a	n/a
0.52	0.4	DCS2_YEAST	344%	HS only	HS only	n/a	n/a
0.21	0.1	MPD1_YEAST	242%	219%	93%	n/a	219%

0.04	0.02	DOP1_YEAST	200%	25%	175%	n/a	25%
		DSE1_YEAST				n/a	n/a
		EAP1_YEAST			0%	n/a	n/a
		EBS1_YEAST		GR only		n/a	n/a
	0.02	ECM30_YEAST				n/a	n/a
0.04	0.04	EFR3_YEAST	25%	50%	100%	75%	50%
		FAF1_YEAST				n/a	n/a
0.1		FNTA_YEAST	HS only			n/a	n/a
		FMP27_YEAST		GR only		n/a	n/a
0.15	0.15	FMP52_YEAST	HS only	HS only	HS only	n/a	n/a
	0.06	FYV10_YEAST				n/a	n/a
0.04		GCN20_YEAST	125%	0%	125%	n/a	0%
0.1	0.22	GCY_YEAST	55%	0%	0%	n/a	n/a
	0.06	GDS1_YEAST				n/a	n/a
0.93	0.33	GVP36_YEAST	HS only	HS only	HS only	n/a	n/a
0.17		HAM1_YEAST	HS only	HS only		n/a	n/a
		HBT1_YEAST				n/a	n/a
		HGH1_YEAST				n/a	n/a
		HIR1_YEAST				n/a	n/a
		HIR2_YEAST				n/a	n/a
		HIT1_YEAST				n/a	n/a
		HLJ1_YEAST		GR only	0%	n/a	n/a
		IGO2_YEAST				n/a	n/a
		PIH1_YEAST				n/a	n/a
	0.34	ISD11_YEAST	GR only		0%	n/a	n/a
		IVY1_YEAST	HS only			n/a	n/a
0.15		KES1_YEAST	HS only	357%		n/a	n/a
		KPC1_YEAST	67%	-73%	167%	n/a	n/a
0.27	0.17	MCK1_YEAST	62%	4%	76%	35%	49%
	0.04	SCY1_YEAST				n/a	n/a
	0.05	KRI1_YEAST	120%	0%	0%	n/a	n/a
	0.13	LDB16_YEAST				n/a	n/a
		LDB19_YEAST	-50%	0%	0%	n/a	n/a
1.21	0.61	LSM12_YEAST	759%	130%	211%	n/a	32%
		LTV1_YEAST				n/a	n/a
		MAK11_YEAST				n/a	n/a
0.34		MAK16_YEAST		HS only		n/a	n/a
		MIDA_YEAST				n/a	n/a
0.5	0.25	MKT1_YEAST	506%	494%	875%	119%	31%
		MLP1_YEAST				n/a	n/a
	0.02	MLP2_YEAST		GR only	HS only	n/a	n/a
0.88	0.88	MMF1_YEAST	HS only	390%	29%	n/a	324%
		MON2_YEAST				n/a	n/a
0.61	0.21	MRH1_YEAST	27%	-12%	-44%	5%	34%
		MSF1_YEAST				n/a	n/a
		MSO1_YEAST	HS only			n/a	n/a
		MSS18_YEAST				n/a	n/a

		MUK1_YEAST		GR only	0%	n/a	n/a
		NAM1_YEAST				n/a	n/a
	0.06	NAM8_YEAST				n/a	n/a
		NBA1_YEAST	HS only	GR only		n/a	n/a
0.04		NIP80_YEAST		0%		n/a	n/a
0.12	0.26	NIP29_YEAST	0%	-71%	58%	n/a	n/a
		NIS1_YEAST				n/a	n/a
		NNF2_YEAST		0%		n/a	n/a
		NSG1_YEAST				n/a	n/a
0.07		NTA1_YEAST	HS only	HS only		n/a	n/a
		NUD1_YEAST			0%	n/a	n/a
0.06		NUF1_YEAST	67%	-86%	24%	0%	5%
0.18		OCA4_YEAST		100%		n/a	n/a
		OPY1_YEAST		GR only		n/a	n/a
		PAM1_YEAST		0%	0%	n/a	n/a
0.11		PAR32_YEAST	0%	0%	0%	n/a	n/a
		PBP4_YEAST	116%	-50%	0%	n/a	n/a
	0.05	PCF11_YEAST				n/a	n/a
		PDC2_YEAST				n/a	n/a
		PET54_YEAST	HS only		120%	n/a	n/a
0.3	0.09	SDS22_YEAST	HS only	HS only	HS only	n/a	n/a
		PP2C1_YEAST				n/a	n/a
		PP2C2_YEAST				n/a	n/a
0.06		2ABA_YEAST				n/a	n/a
		PSP2_YEAST	0%		240%	0%	n/a
		PXR1_YEAS7	177%	41%	-69%	48%	n/a
0.24	0.12	PXR1_YEAST			-69%	n/a	n/a
		RFS1_YEAST	0%			n/a	n/a
0.04		ROD1_YEAST				n/a	n/a
		SCD6_YEAST				n/a	n/a
0.11	0.03	SC160_YEAST	-38%	-71%	-62%	26%	2%
0.13	0.13	SDA1_YEAST	85%	67%	119%	15%	108%
		SDS23_YEAS7	GR only			n/a	n/a
0.06		SDS23_YEAST				n/a	n/a
		SFK1_YEAST			0%	n/a	n/a
		SIP3_YEAST				n/a	n/a
		SIP5_YEAST				n/a	n/a
2.29	1.74	SIS1_YEAST	327%	121%	135%	23%	69%
		SKG3_YEAST				n/a	n/a
0.09		SKT5_YEAST		0%		n/a	n/a
0.03	0.21	SLA2_YEAST	GR only	-88%	205%	n/a	n/a
0.2		SLM4_YEAST				n/a	n/a
		SNI2_YEAST				n/a	n/a
0.26	0.06	SNQ2_YEAST	5%	-44%	-74%	5%	18%
0.13		DCA13_YEAST	117%	-27%		n/a	27%
0.02	0.02	SPA2_YEAST	-3%	-82%	-43%	78%	n/a
0.2	0.09	SPT2_YEAST		HS only		n/a	n/a

		SPT3_YEAST			0%	n/a	n/a
		SRN2_YEAST				n/a	n/a
		SSD1_YEAST	0%			n/a	n/a
		SSO1_YEAST				n/a	n/a
	0.11	SSO2_YEAST				n/a	n/a
0.09		SST2_YEAST		-39%		n/a	13%
	0.04	STB6_YEAST				n/a	n/a
0.11	0.11	SUR7_YEAST	32%	-35%	-35%	32%	35%
		TEX1_YEAST				n/a	n/a
		THO1_YEAST	-55%	0%		n/a	n/a
0.02	0.05	TIF31_YEAST	-53%	-71%	-41%	3%	9%
		TMA23_YEAST		0%	-55%	n/a	n/a
0.14		GOS1_YEAST				n/a	n/a
0.04	0.04	SEC1_YEAST	350%	-55%	-56%	125%	27%
0.51	0.36	SEC13_YEAST	-3%	198%	127%	44%	76%
0.56	0.23	SEC23_YEAST	106%	122%	39%	94%	52%
0.31	0.14	SEC24_YEAST	90%	-8%	15%	60%	23%
0.32	0.16	SEC31_YEAST	-7%	34%	105%	21%	24%
0.43		SC61G_YEAST	0%	0%	0%	0%	0%
		UPS1_YEAST				n/a	n/a
0.24	0.19	PYR1_YEAST	32%	-19%	-26%	42%	19%
		URE2_YEAST	HS only			n/a	n/a
		VAB2_YEAS7				n/a	n/a
0.1		WHI3_YEAST				n/a	n/a
0.1	0.05	WHI4_YEAST		HS only	0%	n/a	n/a
		YGP1_YEAST				n/a	n/a
0.18	0.18	YOP1_YEAST		0%	0%	n/a	n/a
0.43	0.43	YRO2_YEAST	HS only	83%	89%	n/a	44%
		YSC84_YEAST	-17%	-35%	35%	17%	n/a
		YSP1_YEAST		GR only		n/a	n/a
		ZPS1_YEAST				n/a	n/a
1.24	0.62	PST2_YEAST	226%	828%	113%	n/a	239%
		PPOX_YEAST				n/a	n/a
		YJB0_YEAST				n/a	n/a
	0.05	PUF6_YEAST	HS only		0%	n/a	n/a
0.11		PNPH_YEAST	HS only	HS only		n/a	n/a
0.56	0.43	YN14_YEAST	HS only	HS only	HS only	n/a	n/a
	0.12	YEC0_YEAST	0%		104%	n/a	n/a
		KAD6_YEAST				n/a	n/a
		YP088_YEAST	HS only			n/a	n/a
		IRC3_YEAST				n/a	n/a
0.03		ECM32_YEAST		0%	100%	n/a	n/a
0.07	0.04	YL419_YEAST		75%	HS only	n/a	n/a
0.12		DLHH_YEAST		HS only		n/a	n/a
		METX_YEAST				n/a	n/a
	0.08	CYSK_YEAST			HS only	n/a	n/a
		INO80_YEAS7				n/a	n/a

0.02		INO80_YEAST				n/a	n/a
		YG4D_YEAST				n/a	n/a
		HFD1_YEAST				n/a	n/a
0.04	0.04	FLC3_YEAST	0%	-33%	-58%	n/a	33%
0.64	0.36	EMI2_YEAST	HS only	HS only	HS only	n/a	n/a
0.13		YL126_YEAST				n/a	n/a
		HOC1_YEAST		0%	GR only	n/a	n/a
	0.08	YLF2_YEAST				n/a	n/a
		MGDP1_YEAST				n/a	n/a
0.23	0.23	YHM1_YEAST	-52%	-26%	0%	n/a	26%
		PT127_YEAST				n/a	n/a
		DET1_YEAST				n/a	n/a
0.57	0.14	YHI0_YEAST	318%	-11%	9%	216%	11%
		AXL1_YEAST		GR only		n/a	n/a
	0.27	PHS_YEAST				n/a	n/a
0.1		BUD16_YEAST				n/a	n/a
		PLR1_YEAST				n/a	n/a
		FMP46_YEAST				n/a	n/a
	0.1	YPR1_YEAST	HS only	380%	HS only	n/a	n/a
	0.05	YL143_YEAST	HS only		HS only	n/a	n/a
0.22	0.1	NOP2_YEAST	340%	150%	180%	n/a	30%
		THIX_YEAST		GR only		n/a	n/a
0.35		THTR_YEAST	HS only	HS only		n/a	n/a
		SEF1_YEAST				n/a	n/a
0.14		YKD3A_YEAST	HS only	HS only		n/a	n/a
0.98	0.15	YOR31_YEAST	HS only	HS only	HS only	n/a	n/a
0.43	0.2	YGD9_YEAST	HS only	HS only	HS only	n/a	n/a
0.57	0.09	YGP7_YEAST	HS only	HS only	HS only	n/a	n/a
0.3	0.3	API2_YEAST				n/a	n/a
		YCE2_YEAST				n/a	n/a
		YG3E_YEAST				n/a	n/a
		YI20A_YEAST				n/a	n/a
		YO318_YEAST				n/a	n/a
		YD020_YEAST	HS only			n/a	n/a
0.09	0.18	XPP_YEAST	238%	238%	163%	113%	238%
0.14	0.09	YIK8_YEAST	80%	58%	HS only	n/a	122%
		YL455_YEAST				n/a	n/a
0.14		PDX3_YEAST				n/a	n/a
		P5CR_YEAST				n/a	n/a
		PYC1_YEAST				n/a	n/a
2.86	2.09	PDC1_YEAST	282%	650%	388%	98%	486%
		PDC6_YEAST				n/a	n/a
0.16	0.26	ODPX_YEAST	350%	100%	63%	n/a	n/a
0.82	0.56	ODPA_YEAST	15%	148%	-5%	2%	163%
2.05	0.82	ODPB_YEAST	110%	83%	35%	42%	52%
44.04	13.37	KPYK1_YEAST	1017%	584%	162%	552%	306%
0.29		KPYK2_YEAST	HS only	HS only		n/a	n/a

0.06	0.06	QDR2_YEAST	50%	-53%	24%	50%	16%
0.14	0.14	GDI1_YEAST	HS only	0%	HS only	n/a	n/a
	0.16	YRB1_YEAST	HS only		HS only	n/a	n/a
	0.35	RAS2_YEAST			250%	n/a	n/a
0.12	0.12	RSR1_YEAST	0%	-45%	-19%	n/a	7%
		DOM3Z_YEAST	225%	225%	53%	n/a	n/a
		RMI1_YEAST				n/a	n/a
		RCY1_YEAST				n/a	n/a
0.4	0.12	RV161_YEAST	108%	30%	204%	n/a	30%
0.07	0.07	RV167_YEAST	50%	25%	HS only	50%	75%
0.07		RCC1_YEAST				n/a	n/a
		RT103_YEAST				n/a	n/a
		ADR1_YEAST				n/a	n/a
	0.06	PHO2_YEAST				n/a	n/a
		SIR3_YEAST				n/a	n/a
		SIR4_YEAST	-60%	0%		n/a	n/a
		RFA2_YEAST				n/a	n/a
0.62		RFA3_YEAST	HS only	HS only		n/a	n/a
0.08	0.04	RFC1_YEAST	33%	-9%	75%	n/a	59%
0.3	0.09	RFC2_YEAST	198%	-19%	-44%	95%	45%
		RFC3_YEAST		GR only	244%	n/a	n/a
0.1		RFC4_YEAST	HS only			n/a	n/a
0.09	0.19	RFC5_YEAST	0%	0%	HS only	n/a	0%
0.11	0.23	RTN1_YEAST	36%	-52%	0%	73%	0%
	0.48	RTN2_YEAST	HS only		182%	n/a	n/a
		RFX1_YEAST				n/a	n/a
		RHEB_YEAST				n/a	n/a
		RGD1_YEAST				n/a	n/a
0.05		ROM2_YEAST		150%		n/a	n/a
		LRG1_YEAST		GR only		n/a	n/a
0.04		RGD2_YEAST	HS only	0%		n/a	n/a
		RNT1_YEAST				n/a	n/a
		RMP1_YEAST				n/a	n/a
		RPM2_YEAST				n/a	n/a
		RPP1_YEAST				n/a	n/a
	0.07	RNY1_YEAST				n/a	n/a
		POP8_YEAST				n/a	n/a
0.04		RIR1_YEAST				n/a	n/a
0.25	0.16	RIR2_YEAST	HS only	HS only	HS only	n/a	n/a
		RIR4_YEAST				n/a	n/a
		SML1_YEAST				n/a	n/a
0.16		KPR1_YEAST	0%	100%	0%	n/a	n/a
0.34	0.1	KPR3_YEAST	120%	0%	-75%	n/a	n/a
0.07		KPR5_YEAST		HS only		n/a	n/a
		RKM1_YEAST				n/a	n/a
		RKM3_YEAST	HS only			n/a	n/a
		RMAR_YEAST	HS only			n/a	n/a

		KRR1_YEAST	-66%	41%	0%	n/a	n/a
		RRP1_YEAST	0%	0%		n/a	n/a
0.03	0.03	RRP12_YEAST	120%	30%	217%	n/a	30%
	0.13	RRP15_YEAST				n/a	n/a
0.1		RRP7_YEAST			0%	n/a	n/a
		RRP8_YEAST				n/a	n/a
0.05	0.05	RRP9_YEAST	120%	60%	0%	n/a	60%
		RSA3_YEAST		0%		n/a	n/a
0.06		RRB1_YEAST		0%		n/a	n/a
0.08		SQT1_YEAST		HS only		n/a	n/a
0.12		RIX7_YEAST		HS only		n/a	n/a
0.14	0.14	NOP15_YEAST	121%	61%	58%	n/a	61%
		ALB1_YEAS7				n/a	n/a
0.05		BMS1_YEAST	-1%	-71%	0%	61%	n/a
0.36	0.36	BRX1_YEAST	168%	83%	168%	59%	26%
0.09		NOL10_YEAST		HS only		n/a	n/a
0.04		ERB1_YEAS7	250%	-33%	0%	50%	33%
0.09	0.03	MAK21_YEAST	0%	25%	-50%	n/a	25%
0.14	0.07	NOP53_YEAST	HS only	HS only	HS only	n/a	n/a
		NSA2_YEAS7	HS only	GR only		n/a	n/a
		RLP24_YEAST	0%	-55%	0%	n/a	n/a
0.1		RLP7_YEAST				n/a	n/a
0.15		SLX9_YEAST		HS only		n/a	n/a
		SSF2_YEAST				n/a	n/a
		RL1D1_YEAST				n/a	n/a
0.07		YTM1_YEAS7				n/a	n/a
		SDO1_YEAST				n/a	n/a
0.1		RPF1_YEAST	120%	-27%	120%	n/a	27%
0.2	0.13	SSZ1_YEAST	69%	-34%	-20%	39%	34%
0.14		RRF1_YEAST				n/a	n/a
		RBX1_YEAST	HS only			n/a	n/a
0.29	0.09	RCL1_YEAST		222%	-53%	n/a	n/a
7.86	6.73	YRA1_YEAST	19%	11%	85%	19%	25%
0.11	0.11	REXO4_YEAST	0%	0%		n/a	n/a
0.06		NGL2_YEAST				n/a	n/a
		SSU72_YEAST				n/a	n/a
		TFB3_YEAST				n/a	n/a
		NAB6_YEAST	HS only			n/a	n/a
0.07	0.15	SRO9_YEAST	114%	0%	57%	0%	0%
	0.2	NDI1_YEAST	HS only		233%	n/a	n/a
3.04	3.46	FBRL_YEAST	95%	-38%	51%	49%	6%
0.57	0.24	RRP5_YEAST	74%	3%	21%	46%	3%
0.07	0.15	EBP2_YEAST	57%	-17%	236%	57%	17%
		FCF1_YEAST				n/a	n/a
0.2		FYV7_YEAST				n/a	n/a
		UTP23_YEAST	0%	0%		n/a	n/a
1.28	0.51	RUVB1_YEAST	522%	238%	818%	131%	62%

0.07		RUVB2_YEAST	HS only	0%	100%	n/a	0%
0.04		PRTD_YEAST	HS only	HS only		n/a	n/a
		CARP_YEAST				n/a	n/a
0.09	0.09	LYS1_YEAST	0%	0%	-50%	n/a	n/a
		SAM3_YEAST				n/a	n/a
0.28	0.09	METK1_YEAST	333%	60%	142%	n/a	4%
0.26		SGF29_YEAST				n/a	n/a
1.14	0.4	DCPS_YEAST	HS only	HS only	HS only	n/a	n/a
0.22	0.22	SEC14_YEAST	380%	HS only	HS only	n/a	n/a
0.04		SFB2_YEAST		HS only		n/a	n/a
	0.03	SFB3_YEAST	367%	57%	267%	n/a	n/a
0.02		ESP1_YEAST				n/a	n/a
0.1		YJU3_YEAST	0%	0%	0%	n/a	n/a
1.37	0.94	GLYC_YEAST	-10%	-2%	-66%	10%	26%
		GLYM_YEAST				n/a	n/a
		LCB1_YEAST		GR only		n/a	n/a
		KIN1_YEAST	0%	-50%	0%	n/a	n/a
0.09	0.03	AKL1_YEAST	30%	-52%	29%	70%	20%
		BCK1_YEAST				n/a	n/a
		BUR1_YEAST		GR only		n/a	n/a
		CBK1_YEAST	0%	GR only		n/a	n/a
		CHK1_YEAST				n/a	n/a
0.04		CLA4_YEAST		0%		n/a	n/a
		DBF20_YEAST	35%			n/a	n/a
0.02		GCN2_YEAST	0%	-17%	100%	n/a	17%
0.06	0.03	GIN4_YEAST	-39%	-45%	-58%	39%	33%
		HAL5_YEAST			0%	n/a	n/a
0.08	0.04	HRK1_YEAST	163%	0%	38%	63%	0%
		KIC1_YEAST				n/a	n/a
0.03		KIN2_YEAST	-56%	-74%	0%	6%	1%
		KIN4_YEAST		GR only		n/a	n/a
		KSP1_YEAST	HS only		200%	n/a	n/a
0.01		ATR_YEAST		0%		n/a	n/a
	0.04	PKH1_YEAST				n/a	n/a
		PKH3_YEAST				n/a	n/a
0.08	0.08	PTK2_YEAST		100%	HS only	n/a	n/a
0.33	0.07	RIO2_YEAST	HS only	HS only	HS only	n/a	n/a
		SCH9_YEAST				n/a	n/a
		TOR1_YEAST		33%	100%	n/a	n/a
0.04		TOR2_YEAST	117%	0%	167%	83%	0%
		VPS15_YEAST				n/a	n/a
		YPK1_YEAST				n/a	n/a
		PP11_YEAST				n/a	n/a
0.61	0.33	PP12_YEAST	282%	29%	135%	33%	29%
0.09		PP2A1_YEAST				n/a	n/a
		PP2A2_YEAST				n/a	n/a
	0.14	PPZ1_YEAST	HS only	-44%	HS only	n/a	n/a

0.11		TYE7_YEAST				n/a	n/a
0.21	0.14	SYSC_YEAST	HS only	100%	100%	n/a	100%
0.56	0.12	SHS1_YEAST	235%	10%	41%	132%	10%
0.35		SFGH_YEAST	HS only	HS only		n/a	n/a
		SRPR_YEAST				n/a	n/a
		SRP54_YEAST	HS only			n/a	n/a
0.05		SRP68_YEAST				n/a	n/a
		SRP72_YEAST				n/a	n/a
0.07	0.07	GBP2_YEAST	114%	-53%	114%	0%	n/a
0.54	0.92	RIM1_YEAST	125%	125%		n/a	n/a
		PDS5_YEAST				n/a	n/a
0.17		SAR1_YEAST		HS only		n/a	n/a
		SGT2_YEAST				n/a	n/a
		RUXE_YEAST				n/a	n/a
		SMD1_YEAST				n/a	n/a
		SMD2_YEAST	0%	0%	0%	n/a	n/a
		SMD3_YEAST	HS only		0%	n/a	n/a
		RSMB_YEAST		GR only		n/a	n/a
		LSM1_YEAST	122%	0%		n/a	n/a
		ATN1_YEAST				n/a	n/a
		ATN2_YEAST				n/a	n/a
0.1		SAS10_YEAST	100%	16%	0%	n/a	84%
		SAS4_YEAST		GR only		n/a	n/a
		SAS5_YEAST		GR only	0%	n/a	n/a
		MVP1_YEAST				n/a	n/a
0.2		SNX3_YEAST	115%	-53%	0%	n/a	n/a
0.67	0.36	SPEE_YEAST	HS only	HS only	HS only	n/a	n/a
0.05		LCB4_YEAST	HS only	HS only		n/a	n/a
		LCB5_YEAST				n/a	n/a
0.57	0.88	LSP1_YEAST	340%	121%	119%	n/a	121%
3.6	2.85	PIL1_YEAST	691%	596%	375%	0%	353%
		SGPL_YEAST			0%	n/a	n/a
0.18	0.08	SPC42_YEAST	180%	-50%	-51%	208%	22%
		RMD1_YEAST				n/a	n/a
		RMD8_YEAST				n/a	n/a
0.22		SPO73_YEAST				n/a	n/a
		SPO77_YEAST				n/a	n/a
		SPG5_YEAST				n/a	n/a
0.08	0.08	ERG6_YEAST		0%	0%	n/a	n/a
0.11	0.11	SUT1_YEAST				n/a	n/a
0.08	0.05	SMC1_YEAST	67%	167%	117%	n/a	0%
		SMC2_YEAST				n/a	n/a
0.02		SMC3_YEAST	60%	-68%	300%	n/a	8%
		SMC4_YEAST			0%	n/a	n/a
		SMC6_YEAST				n/a	n/a
		RAD27_YEAST				n/a	n/a
0.08	0.04	SVL3_YEAST	HS only	100%	HS only	n/a	n/a

	0.05	DHSX_YEAST				n/a	n/a
0.16		DHSA_YEAST	340%	60%		n/a	n/a
		DHSB_YEAST	108%			n/a	n/a
	0.42	SDHF1_YEAS7				n/a	n/a
		SDHF2_YEAS1				n/a	n/a
0.07		UGA2_YEAST	HS only	HS only		n/a	n/a
0.48	0.22	SUCA_YEAST	HS only	HS only	120%	n/a	n/a
		SUCB_YEAST	HS only			n/a	n/a
0.06		MET3_YEAST				n/a	n/a
	0.02	SKI3_YEAST				n/a	n/a
		SODC_YEAST	0%	130%	130%	0%	n/a
0.14	0.7	SODM_YEAST	114%	0%	400%	n/a	n/a
		SGD1_YEAST				n/a	n/a
0.03		SUM1_YEAST	HS only			n/a	n/a
	0.16	SYP1_YEAST	-75%	0%	225%	n/a	n/a
		MPT5_YEAST	HS only			n/a	n/a
0.18	0.09	SRP40_YEAST	142%	-19%	0%	81%	19%
0.41	0.26	STM1_YEAST	192%	-40%	138%	192%	40%
	0.35	FMP45_YEAST	HS only		357%	n/a	n/a
0.07	0.07	HSV2_YEAST	0%	0%	107%	n/a	0%
		SNF5_YEAST				n/a	n/a
		YO338_YEAST				n/a	n/a
		SWC3_YEAST				n/a	n/a
	0.06	SWC4_YEAST			HS only	n/a	n/a
0.06		KOG1_YEAST	-67%	13%	-50%	n/a	13%
0.08	0.04	TCO89_YEAST	50%	-50%	-4%	n/a	17%
		AVO1_YEAST		GR only		n/a	n/a
	0.08	AVO2_YEAST	0%		0%	n/a	n/a
0.11	0.11	LST8_YEAST	-50%	-25%	-25%	n/a	25%
	0.02	MOT1_YEAST			HS only	n/a	n/a
		TBP_YEAST	0%			n/a	n/a
		TBP7_YEAST				n/a	n/a
0.06		TCPB_YEAST	108%	0%		n/a	n/a
0.13	0.13	TCPD_YEAST	0%	-39%	-5%	n/a	13%
0.06		TCPE_YEAST	HS only	317%		n/a	n/a
		TCPG_YEAST	HS only	GR only		n/a	n/a
0.18	0.12	TCPQ_YEAST	78%	-2%	167%	n/a	27%
0.12		TCPZ_YEAST		0%		n/a	n/a
	0.03	TERT_YEAST				n/a	n/a
		RIF1_YEAST				n/a	n/a
0.18		TIP1_YEAST				n/a	n/a
	0.06	THI6_YEAST				n/a	n/a
		THI7_YEAST				n/a	n/a
		THI72_YEAST				n/a	n/a
0.49	0.35	TRXB1_YEAST	345%	HS only	HS only	n/a	n/a
	0.26	TRX3_YEAST			HS only	n/a	n/a
		THO2_YEAST				n/a	n/a

		SRY1_YEAST				n/a	n/a
1.52	0.39	THDH_YEAST	201%	49%	27%	67%	16%
0.18	0.09	SYTC_YEAST	600%	350%	HS only	n/a	n/a
		SYTM_YEAST				n/a	n/a
0.1		TYSY_YEAST		HS only		n/a	n/a
		TOF2_YEAST				n/a	n/a
0.17		RAF_YEAST	HS only	HS only		n/a	n/a
0.45	0.74	TAL2_YEAST	HS only	HS only	HS only	n/a	n/a
0.1	0.1	TAL1_YEAST	HS only	HS only	175%	n/a	n/a
		MIG3_YEAST				n/a	n/a
0.1		TFS2_YEAST	240%	-79%		n/a	n/a
0.09	0.06	SPT5_YEAST	83%	-65%	0%	150%	6%
		IWS1_YEAST				n/a	n/a
		PDR1_YEAST				n/a	n/a
		TFC3_YEAST				n/a	n/a
		TFC7_YEAST				n/a	n/a
0.28	0.28	TOA2_YEAST			HS only	n/a	n/a
		TF2B_YEAST		GR only	0%	n/a	n/a
		TAF1_YEAST				n/a	n/a
		TAF11_YEAST				n/a	n/a
		TAF4_YEAS7				n/a	n/a
0.2		TAF6_YEAST	HS only	175%	-54%	n/a	58%
		TAF9_YEAST	HS only			n/a	n/a
		SNF2_YEAST				n/a	n/a
		MOT3_YEAST		GR only		n/a	n/a
0.07		ADA2_YEAST	HS only	-27%		n/a	27%
0.15	0.07	WTM1_YEAST	HS only	HS only	HS only	n/a	n/a
		WTM2_YEAST				n/a	n/a
		ASH1_YEAST				n/a	n/a
		DOT6_YEAST	0%			n/a	n/a
		GAT1_YEAST				n/a	n/a
		RXT2_YEAST				n/a	n/a
		RXT3_YEAST				n/a	n/a
0.07		UME1_YEAST				n/a	n/a
		OPI1_YEAST				n/a	n/a
		TRA1_YEAST		-50%	100%	n/a	n/a
0.35	0.16	SCP1_YEAST	HS only	HS only	HS only	n/a	n/a
0.39	0.05	TKT1_YEAST	HS only	680%	HS only	n/a	n/a
0.2	0.45	TKT2_YEAST	200%	HS only	HS only	n/a	n/a
0.11		EI2BA_YEAST	HS only	HS only		n/a	n/a
0.08		EI2BB_YEAST	HS only	-56%		n/a	n/a
		EI2BD_YEAST	HS only			n/a	n/a
		EI2BG_YEAST				n/a	n/a
0.11		RLI1_YEAST	76%	-55%	-11%	76%	29%
		TMA10_YEAST				n/a	n/a
0.18		TMA20_YEAST		0%	0%	n/a	n/a
		DENR_YEAST			0%	n/a	n/a

		TMA46_YEAST	-37%	0%	0%	n/a	n/a
		TMA7_YEAST	HS only			n/a	n/a
		GCN1_YEAST			100%	n/a	n/a
0.72	0.72	TCTP_YEAST	528%	72%	315%	103%	72%
		SEC62_YEAST				n/a	n/a
		SEC72_YEAST				n/a	n/a
		TMN2_YEAST				n/a	n/a
		TR120_YEAST	0%	0%		n/a	n/a
		TR130_YEAST				n/a	n/a
		TRS20_YEAST				n/a	n/a
0.17		BET3_YEAST	0%	56%	0%	0%	56%
	0.15	TRS23_YEAST	113%			n/a	n/a
0.11		TRS31_YEAST	HS only	0%	0%	n/a	n/a
		TRS33_YEAST				n/a	n/a
		YA11A_YEAST				n/a	n/a
0.58		YB11B_YEAST		HS only		n/a	n/a
		YB12A_YEAST		GR only		n/a	n/a
2.55		YD11A_YEAST		HS only		n/a	n/a
		YD11B_YEAST				n/a	n/a
		YD17A_YEAST				n/a	n/a
		YD12A_YEAST				n/a	n/a
	0.55	YD12B_YEAST				n/a	n/a
		YD15A_YEAST				n/a	n/a
		YG12B_YEAST	43%			n/a	n/a
	1.87	YJ12A_YEAST				n/a	n/a
		YJ12B_YEAST				n/a	n/a
	0.64	YM11B_YEAST				n/a	n/a
		YM14B_YEAST			GR only	n/a	n/a
	0.52	YN11A_YEAST				n/a	n/a
		YN11B_YEAST	39%			n/a	n/a
2.08		YN12A_YEAST				n/a	n/a
	2.09	YO11A_YEAST	10%	GR only	-10%	n/a	n/a
0.92		YO11B_YEAST		HS only		n/a	n/a
		YP13B_YEAST				n/a	n/a
		YP14B_YEAST		GR only		n/a	n/a
0.32		YB21A_YEAST		HS only		n/a	n/a
		YB21B_YEAST	59%		0%	n/a	n/a
	0.07	YD21A_YEAST				n/a	n/a
		YD23B_YEAST		GR only		n/a	n/a
		YF21B_YEAST				n/a	n/a
0.32		YG21B_YEAST				n/a	n/a
		YI31B_YEAST				n/a	n/a
0.02		YJ41B_YEAST				n/a	n/a
0.03		TPS3_YEAST		HS only		n/a	n/a
0.49	0.45	TSL1_YEAST	200%	717%	1833%	n/a	n/a
0.23	0.18	TPS2_YEAST	800%	667%	1933%	n/a	n/a
	0.05	TCB1_YEAST	0%	-40%	63%	n/a	n/a

		TCB2_YEAST	0%	67%	67%	n/a	n/a
0.13	0.18	TCB3_YEAST	85%	-47%	33%	65%	1%
		TGS1_YEAST				n/a	n/a
2.15	0.89	TPIS_YEAST	1164%	378%	466%	n/a	263%
		TRM82_YEAS1				n/a	n/a
		TRM82_YEAS7				n/a	n/a
0.14		TPT1_YEAST	114%	HS only		n/a	n/a
	0.06	RIT1_YEAST				n/a	n/a
		TYW1_YEAST			GR only	n/a	n/a
		TYW2_YEAST				n/a	n/a
0.05		DUS3_YEAS7		HS only		n/a	n/a
	0.08	TAD1_YEAST				n/a	n/a
0.25	0.09	TRP_YEAST	244%	400%	HS only	n/a	n/a
		SYWC_YEAST	229%			n/a	n/a
0.17		SYWM_YEAST				n/a	n/a
0.07	0.15	TBA1_YEAST		-53%	179%	n/a	n/a
		TBA3_YEAST	HS only			n/a	n/a
0.07		TBB_YEAST	171%	88%	229%	57%	141%
0.03		PTP3_YEAST				n/a	n/a
0.06	0.06	CDC14_YEAST	100%	-42%	-8%	n/a	8%
0.09	0.09	PVH1_YEAST			HS only	n/a	n/a
0.08		SYYC_YEAST	HS only	238%		n/a	n/a
		SYYM_YEAST				n/a	n/a
		SF3B1_YEAST				n/a	n/a
0.17		IMP3_YEAST	112%	-53%	0%	0%	0%
0.11	0.11	IMP4_YEAST	0%	55%	0%	0%	55%
0.07	0.02	UTP10_YEAST	86%	-18%	-8%	n/a	18%
		UTP11_YEAS6		GR only		n/a	n/a
		UTP12_YEAST				n/a	n/a
		UTP13_YEAST	0%	200%		n/a	n/a
		UTP14_YEAST				n/a	n/a
0.13	0.13	UTP15_YEAST	9%	85%	-18%	44%	31%
	0.05	UTP18_YEAST	-55%	0%	0%	n/a	n/a
		UTP20_YEAST				n/a	n/a
0.03		UTP21_YEAST	0%	133%	133%	n/a	n/a
0.13	0.03	UTP22_YEAST	63%	-40%	-34%	38%	8%
0.08	0.08	UTP4_YEAST	175%	0%	63%	n/a	n/a
0.05		UTP5_YEAST				n/a	n/a
0.07		UTP6_YEAST	0%	-50%	100%	n/a	n/a
0.06	0.06	UTP7_YEAST	197%	-38%	167%	119%	38%
0.04		UTP8_YEAST	170%	-28%	0%	205%	28%
		UTP9_YEAST	500%	-35%		n/a	n/a
0.11	0.05	MPP10_YEAST	0%	-35%	120%	n/a	0%
		LSM2_YEAST	HS only			n/a	n/a
		LSM3_YEAST	HS only			n/a	n/a
0.17		LSM4_YEAST	0%	-54%		n/a	n/a
0.37	0.37	LSM5_YEAST	HS only	0%	HS only	n/a	0%

		LSM6_YEAS7	624%	0%	0%	n/a	n/a
		LSM7_YEAST	0%	0%	0%	n/a	n/a
		COQ5_YEAST				n/a	n/a
0.07		COQ6_YEAST				n/a	n/a
		UBP10_YEAST				n/a	n/a
		UBP15_YEAST				n/a	n/a
0.07	0.11	UBP3_YEAST	-37%	-44%	-5%	20%	19%
		UBP5_YEAST				n/a	n/a
0.03		UBP7_YEAST		0%	GR only	n/a	0%
0.14		UBL1_YEAST	HS only	HS only		n/a	n/a
	0.03	BUL1_YEAST	-70%	GR only	HS only	n/a	n/a
0.03		BUL2_YEAST	HS only	-15%	0%	n/a	15%
2.1	2.1	UBIQ_YEAST	178%	106%	-4%	178%	106%
	0.03	UBA1_YEAST		100%	HS only	n/a	n/a
		UBC7_YEAST				n/a	n/a
		MDY2_YEAST	0%		0%	0%	n/a
0.33	0.77	SMT3_YEAST	HS only	133%	HS only	n/a	n/a
		ULP1_YEAST				n/a	n/a
0.06		BRE5_YEAST	0%	-70%	483%	n/a	n/a
		UBX4_YEAST	HS only			n/a	n/a
		UBX6_YEAST				n/a	n/a
		UAP1_YEAST				n/a	n/a
		GPT_YEAST				n/a	n/a
0.06		YD061_YEAST		HS only		n/a	n/a
	0.07	YN99_YEAST			HS only	n/a	n/a
	0.02	YO075_YEAST			HS only	n/a	n/a
		FUN30_YEAST				n/a	n/a
		YHJ1_YEAST		GR only		n/a	n/a
		YL247_YEAST				n/a	n/a
0.3	0.3	YA044_YEAST	0%	0%	0%	0%	n/a
		YJY5_YEAST				n/a	n/a
		YBQ6_YEAST	HS only			n/a	n/a
5.02	1.55	OLA1_YEAST	1035%	503%	335%	13%	234%
0.66		YG3Y_YEAST	HS only	HS only		n/a	n/a
		YG4I_YEAST				n/a	n/a
		YD133_YEAST				n/a	n/a
		YOL19_YEAST	HS only	GR only		n/a	n/a
		YP041_YEAST				n/a	n/a
0.13	0.13	YIG4_YEAST	HS only			n/a	n/a
0.13		FMP41_YEAST	HS only	-52%		n/a	n/a
		YMRF1_YEAST				n/a	n/a
		YN00_YEAST				n/a	n/a
0.14	0.3	YHC1_YEAST	179%	0%	329%	n/a	n/a
		YIV6_YEAST				n/a	n/a
0.37	0.53	YJ66_YEAST	HS only	HS only	HS only	n/a	n/a
		YKH1_YEAST				n/a	n/a
1.02	0.6	YM71_YEAST	HS only	HS only	HS only	n/a	n/a

0.18		YFH6_YEAST	HS only			n/a	n/a
	0.04	YP091_YEAST	0%	-69%	88%	n/a	n/a
		YP115_YEAST				n/a	n/a
0.13	0.13	YNB0_YEAST	HS only	HS only	HS only	n/a	n/a
0.11	0.22	YNT4_YEAST				n/a	n/a
		IRC10_YEAST				n/a	n/a
	0.04	JIP4_YEAST				n/a	n/a
0.31		MRP8_YEAST	HS only	HS only		n/a	n/a
		RSN1_YEAST		GR only	GR only	n/a	n/a
		YBI6_YEAST		GR only	0%	n/a	n/a
		YBJ5_YEAST				n/a	n/a
		YBV8_YEAST				n/a	n/a
		YB191_YEAST				n/a	n/a
		YB75_YEAST				n/a	n/a
		YB96_YEAST				n/a	n/a
0.04		YB9F_YEAST				n/a	n/a
0.07		YB9P_YEAST				n/a	n/a
0.11		YCQ6_YEAST				n/a	n/a
		YD012_YEAST		0%		n/a	n/a
0.09		YD144_YEAST	HS only	HS only	GR only	n/a	n/a
		PAL1_YEAST	-54%	-54%	383%	n/a	n/a
0.3	0.14	YD391_YEAST		HS only		n/a	n/a
		YEA7_YEAST	0%			n/a	n/a
		YEF3_YEAST				n/a	n/a
		YEW7_YEAST				n/a	n/a
		YEN1_YEAST				n/a	n/a
		YER0_YEAST				n/a	n/a
		YGI2_YEAST		0%	113%	n/a	n/a
		YG2V_YEAST				n/a	n/a
0.07		YG32_YEAST	HS only			n/a	n/a
		YG37_YEAST	HS only			n/a	n/a
		YG3A_YEAST				n/a	n/a
0.22		YG4E_YEAST		HS only	0%	n/a	n/a
		YG5L_YEAST				n/a	n/a
		YG5X_YEAST		GR only		n/a	n/a
		YHO0_YEAST				n/a	n/a
	0.09	YHP7_YEAST	HS only	61%	0%	n/a	n/a
0.66		YHS7_YEAST	390%	-4%	91%	187%	37%
		YHU6_YEAST		0%	0%	n/a	n/a
		YH09_YEAST	HS only			n/a	n/a
0.04		YIJ1_YEAST	GR only	-69%	0%	n/a	n/a
		YIM7_YEAST				n/a	n/a
		YIS3_YEAST		GR only	33%	n/a	n/a
0.51	0.51	YJ133_YEAST	HS only	0%	0%	n/a	0%
0.17	0.08	YJR1_YEAST	-53%	56%	-53%	n/a	56%
		YJV7_YEAST	HS only			n/a	n/a
0.05	0.05	YJ16_YEAST			0%	n/a	n/a

		YJ81_YEAST				n/a	n/a
0.19		YJ9J_YEAST		HS only		n/a	n/a
		YKF4_YEAST	GR only	0%		n/a	n/a
		YKH0_YEAST				n/a	n/a
	0.08	YKH7_YEAST	HS only	0%	HS only	n/a	n/a
		YKJ8_YEAST				n/a	n/a
		YKK5_YEAST		0%	0%	n/a	n/a
0.23		YKM8_YEAST		109%		n/a	n/a
		YKN0_YEAST				n/a	n/a
		YKP1_YEAST				n/a	n/a
		YKV5_YEAST	HS only			n/a	n/a
		YKZ1_YEAST	HS only			n/a	n/a
		YK03_YEAST				n/a	n/a
0.56		YK23_YEAST	HS only	HS only		n/a	n/a
		YK50_YEAST	0%	0%	111%	n/a	n/a
0.25		YL104_YEAST	HS only	0%		n/a	n/a
		YL149_YEAST				n/a	n/a
		YL177_YEAST	0%			n/a	n/a
		YL179_YEAST				n/a	n/a
1.1	0.28	YL301_YEAST	HS only	HS only	HS only	n/a	n/a
	0.35	YL361_YEAST				n/a	n/a
		YL392_YEAST				n/a	n/a
0.09		YL460_YEAST		HS only		n/a	n/a
		YMC0_YEAST				n/a	n/a
		YMF0_YEAST				n/a	n/a
		YMH9_YEAST				n/a	n/a
		YML9_YEAST	111%		GR only	n/a	n/a
0.16		YMO3_YEAST				n/a	n/a
0.12	0.16	YMS1_YEAST	363%	-38%	88%	63%	13%
	0.03	YMX6_YEAST	67%	0%	43%	67%	n/a
	0.05	YMY8_YEAST				n/a	n/a
	0.03	YM11_YEAST				n/a	n/a
0.09		YM27_YEAST	HS only	HS only		n/a	n/a
		YM32_YEAST				n/a	n/a
0.12	0.12	YM44_YEAST	HS only		0%	n/a	n/a
0.03		YM54_YEAST		0%		n/a	n/a
		YM244_YEAST				n/a	n/a
	0.06	YM8A_YEAST				n/a	n/a
		YM8C_YEAST				n/a	n/a
0.1		YM91_YEAST	57%	55%	-52%	n/a	55%
0.57	0.09	YM94_YEAST	456%	631%	239%	78%	446%
		YM96_YEAST				n/a	n/a
		YNC2_YEAST	0%	GR only		n/a	n/a
0.4		YNK8_YEAST		HS only		n/a	n/a
0.09	0.09	YNN4_YEAST	HS only	HS only	HS only	n/a	n/a
		YNS1_YEAST				n/a	n/a
		YNT3_YEAST				n/a	n/a

	0.13	YNU0_YEAST	0%		0%	n/a	n/a
0.4	0.18	YNU8_YEAST	94%	41%	-36%	29%	81%
0.07		YN53_YEAST	HS only	HS only		n/a	n/a
0.46		YO022_YEAST	HS only	HS only		n/a	n/a
		YO083_YEAST				n/a	n/a
		YO086_YEAST				n/a	n/a
0.44	0.08	YO051_YEAST	113%	175%	0%	n/a	n/a
		YO112_YEAST				n/a	n/a
	0.03	YO227_YEAST		GR only	83%	n/a	n/a
0.12		YO289_YEAST	HS only			n/a	n/a
		YO304_YEAST				n/a	n/a
		YO316_YEAST			0%	n/a	n/a
		YP034_YEAST				n/a	n/a
		YP245_YEAST		GR only		n/a	n/a
		YP074_YEAST				n/a	n/a
0.17		YG5B_YEAST	325%	325%		n/a	n/a
0.16		YP184_YEAST	120%	HS only		n/a	n/a
	0.03	TBS1_YEAST				n/a	n/a
		YK44_YEAST	0%		0%	0%	n/a
		ESBP6_YEAST				n/a	n/a
		YO087_YEAST				n/a	n/a
		FMP40_YEAST				n/a	n/a
0.19		YKG9_YEAST				n/a	n/a
		YG1D_YEAST				n/a	n/a
		YJX8_YEAST				n/a	n/a
	0.11	YL023_YEAST			59%	n/a	n/a
0.11		YL064_YEAST	HS only	0%		n/a	n/a
		YEY6_YEAST				n/a	n/a
0.06	0.03	KRE33_YEAST	78%	-67%	-24%	78%	7%
0.18	0.39	YBY7_YEAST	HS only	HS only	HS only	n/a	n/a
		YCF7_YEAST			0%	n/a	n/a
0.47		YP225_YEAST				n/a	n/a
		YO287_YEAST				n/a	n/a
		YCY0_YEAST				n/a	n/a
		YBC8_YEAST	0%	GR only		n/a	n/a
		YGZA_YEAST				n/a	n/a
0.12		YCE7_YEAST				n/a	n/a
		YBZ1_YEAST				n/a	n/a
		YD161_YEAST	HS only			n/a	n/a
		YP045_YEAST				n/a	n/a
0.2		YHG9_YEAST	HS only	HS only		n/a	n/a
		YN8B_YEAST	HS only	-50%		n/a	n/a
		YK01_YEAST				n/a	n/a
0.21	0.21	YC16_YEAST	60%	-41%	-27%	60%	41%
0.15	0.15	UPP_YEAST	0%	0%	0%	n/a	n/a
		DCUP_YEAST				n/a	n/a
0.39	0.12	HEM4_YEAST	HS only	HS only		n/a	n/a

3.69	2.24	UGPA1_YEAST	168%	337%	129%	45%	8%
	0.03	ATH1_YEAST	0%	GR only		n/a	n/a
0.27		AMPL_YEAST	HS only	567%		n/a	217%
		VMA22_YEAST				n/a	n/a
0.03		VID30_YEAST		HS only		n/a	n/a
		PEP3_YEAST				n/a	n/a
0.03		PEP5_YEAST	267%	25%	167%	67%	75%
0.02		IML1_YEAST		HS only		n/a	n/a
		VAM7_YEAST				n/a	n/a
		VAC8_YEAST	HS only	-67%	0%	n/a	n/a
0.62	0.49	VPS1_YEAST	207%	24%	91%	83%	64%
		VPS13_YEAST				n/a	n/a
		VPS20_YEAST				n/a	n/a
		VPS21_YEAST				n/a	n/a
		VPS26_YEAST			0%	n/a	n/a
0.12	0.12	PEP11_YEAST	0%	108%	0%	n/a	n/a
		VPS3_YEAST				n/a	n/a
		VPS30_YEAST				n/a	n/a
		VPS33_YEAST	HS only	0%		n/a	n/a
0.07	0.03	VPS35_YEAST	HS only	133%	HS only	n/a	n/a
		VPS41_YEAST				n/a	n/a
		VPS5_YEAST				n/a	n/a
	0.03	VPS54_YEAST			0%	n/a	n/a
0.11		VPS66_YEAST				n/a	n/a
0.16		DID2_YEAST	HS only	0%		n/a	n/a
		VTC2_YEAST		0%		n/a	n/a
0.13	0.13	SNF7_YEAST	0%	0%	0%	n/a	0%
		SNF8_YEAST				n/a	n/a
0.05		VAL1_YEAST	120%	-34%	GR only	0%	34%
0.06		SYV_YEAST	HS only	HS only		n/a	n/a
		VRP1_YEAST		GR only	0%	n/a	n/a
		FAT1_YEAST				n/a	n/a
0.14	0.14	SCS2_YEAST	-26%	-26%	64%	26%	26%
0.09	0.04	SEC18_YEAST	-54%	-70%	-46%	n/a	10%
0.6	0.47	VATA_YEAST	234%	247%	306%	8%	28%
		VPH1_YEAST	50%	GR only	500%	n/a	n/a
4.36	2.74	VATB_YEAST	1150%	416%	874%	858%	147%
0.08		VATC_YEAST	HS only			n/a	n/a
0.41	0.09	VA0D_YEAST	HS only	HS only	HS only	n/a	n/a
		VATD_YEAST	HS only	-54%	0%	n/a	n/a
0.14		VATE_YEAST				n/a	n/a
		VATG_YEAST				n/a	n/a
0.03		YBK4_YEAST	0%	0%		n/a	n/a
	0.06	YCW2_YEAST				n/a	n/a
0.04	0.04	YMZ2_YEAST			50%	n/a	n/a
0.06		YP247_YEAST				n/a	n/a
		YFB0_YEAST				n/a	n/a

		YRF11_YEAST		GR only		n/a	n/a
		YRF13_YEAST			GR only	n/a	n/a
		YBP2_YEAST				n/a	n/a
0.48	0.48	GIS2_YEAST	39%	203%	194%	79%	243%
0.11		RME1_YEAST				n/a	n/a
		RTS2_YEAST				n/a	n/a
		SFP1_YEAST	HS only			n/a	n/a
	0.1	STP3_YEAST		GR only	HS only	n/a	n/a
		YP022_YEAST				n/a	n/a
0.07		ZUO1_YEAST		0%	60%	n/a	0%

tion in Insoluble Fraction Upon Heat Shock (HS)							
om the mean)	Replicate A			Replicate B			
Mutant	**Wildtype**	**Knockout**	**Mutant**	**Wildtype**	**Knockout**	**Mutant**	**Gene Name**
215%	731%	731%	546%	1177%	286%	115%	GPP1
n/a				HS only	HS only		GPP2
n/a	HS only	HS only	HS only	HS only		HS only	BDH1
6%	-59%	-35%	40%	42%	-48%	53%	NEW1
260%	0%	-26%	494%	HS only	375%	-26%	RNQ1
22%	75%	GR only	-25%	50%	17%	-69%	FKS1
n/a		HS only					GSC2
6%	0%	-24%	-42%	-24%	-55%	-55%	GAS1
14%	-36%	-65%	-65%	100%	-68%	-36%	GAS5
947%	HS only	HS only	1950%	HS only	HS only	56%	GLC3
n/a	HS only	-57%	HS only	HS only	0%	132%	HSP10
n/a		HS only	HS only		HS only	GR only	HSP12
105%	73%	53%	283%	44%	165%	73%	SNU13
n/a	0%		HS only	HS only			NOB1
n/a			HS only	HS only			RPT2
n/a	HS only	HS only	HS only	HS only	-53%	GR only	RPT5
n/a	HS only	HS only	HS only	HS only			RPT3
n/a	179%	51%	HS only	57%	HS only	HS only	RPT1
n/a	HS only	100%	HS only	HS only	HS only	HS only	RPT6
n/a	HS only	HS only	HS only	HS only	HS only		RPT4
n/a	0%	HS only	0%		HS only	HS only	RPN1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	RPN11
n/a		HS only			HS only		RPN13
n/a	HS only	0%	0%	GR only			RPN2
n/a					HS only		RPN7
n/a	HS only	122%	HS only	HS only	HS only		RPN8
n/a	HS only	HS only	HS only	HS only	HS only		PAN5
n/a	HS only	HS only					DOG2
n/a		HS only	HS only		HS only		LEU9
n/a	HS only			HS only			LEU4
n/a	HS only	HS only	HS only	GR only	HS only	100%	KGD1
n/a		HS only	HS only	HS only	HS only	HS only	RIB3
n/a	HS only	HS only	HS only	0%	HS only	HS only	PDE1
n/a	HS only	HS only	HS only	HS only	640%	HS only	HSP30
110%	HS only	HS only	220%	HS only	110%	0%	MRP1
n/a	HS only		HS only				MRP13
n/a	124%	HS only	124%	0%	HS only	HS only	MRP17
n/a	HS only	HS only	HS only	HS only	HS only		MRP2
n/a	HS only	HS only	HS only	0%	113%	113%	MRP4
n/a	HS only	111%	233%	HS only	GR only		MRP51
n/a	HS only		HS only	HS only	HS only	HS only	NAM9
n/a	HS only	HS only	HS only	HS only	HS only		PET123
n/a				GR only			RSM28

n/a	HS only	HS only	HS only	HS only	HS only		RSM10
n/a	GR only	HS only	GR only		GR only		MRPS12
n/a	HS only	HS only	HS only	HS only	HS only	0%	MRPS17
n/a	HS only	HS only	HS only	HS only	0%		MRPS18
n/a	HS only	HS only	0%		0%		RSM19
n/a		117%	HS only	HS only	GR only		RSM23
n/a		HS only					RSM24
n/a			HS only		HS only		RSM25
n/a	HS only	HS only	HS only	HS only	HS only		RSM26
n/a	HS only	0%	HS only	HS only	HS only		MRPS28
n/a			HS only	HS only	GR only		MRPS35
n/a	HS only	HS only	HS only	HS only	HS only		MRPS5
n/a	HS only	HS only		HS only			RSM7
n/a	HS only	HS only	HS only	HS only	HS only		MRPS8
n/a	HS only	HS only	HS only	HS only	0%		MRPS9
n/a	HS only	GR only	0%	0%	HS only		SWS2
n/a	HS only						HMG1
n/a			GR only	0%	HS only		HMG2
n/a		HS only					BNA1
n/a		HS only					EHD3
n/a	HS only	HS only		HS only			LEU1
381%		2000%	895%		1353%	133%	LEU2
n/a	0%	HS only	0%				IFA38
n/a	GR only	0%		GR only	GR only	GR only	ERG27
n/a			GR only	GR only		-25%	RPS0A
n/a	207%	207%	HS only	HS only	98%		RPS0B
30%	1150%	-74%	35%	0%	149%	-25%	RPS10A
12%	-36%	-48%	-46%	-39%	-59%	-70%	RPS11A
33%	0%	238%	33%	42%	0%	-33%	RPS12
6%	-24%	-22%	-50%	-52%	-23%	-62%	RPS13
n/a	-51%	HS only	HS only	HS only	HS only	HS only	RPS14A
n/a		GR only	GR only	GR only	GR only	GR only	RPS14B
26%	41%	-52%	0%	-39%	-53%	-52%	RPS15
0%	-22%	0%	0%	62%	0%	0%	RPS16A
30%	0%	95%	-20%	-36%	-36%	-80%	RPS17A
36%	89%	-19%	23%	-21%	-37%	-48%	RPS18A
29%	36%	-23%	0%	190%	-65%	-58%	RPS19A
22%	-60%	-64%	-39%	32%	-40%	-84%	RPS1A
11%	-60%	-79%	-67%	33%	-23%	-90%	RPS1B
13%	-29%	-16%	-61%	99%	-65%	-86%	RPS2
9%	-43%	119%	-41%	72%	31%	-24%	RPS20
n/a	49%	102%	GR only	273%	HS only	-85%	RPS21A
n/a		HS only	HS only	273%	44%	-85%	RPS21B
26%	28%	-63%	-37%	-53%	-39%	-90%	RPS22A
5%	-33%	69%	-72%	69%	69%	-82%	RPS23A
33%	28%	-22%	27%	-23%	-64%	-39%	RPS24A
0%	39%	-52%	0%	-50%	0%	0%	RPS25A

n/a	165%	-88%	GR only	HS only	1100%		RPS26A
n/a			HS only	GR only		39%	RPS26B
25%	-33%	-36%	-33%	0%	-58%	-83%	RPS27A
n/a	314%	140%	278%	0%	56%	HS only	RPS28A
n/a	HS only	HS only	278%	GR only	HS only	GR only	RPS28B
n/a	-89%	159%	-81%	GR only	-61%	GR only	RPS29A
n/a		GR only	GR only	GR only	0%	HS only	RPS29B
18%	-37%	-55%	-27%	-15%	-30%	-62%	RPS3
18%	-61%	-75%	-60%	60%	-62%	-96%	RPS30A
20%	0%	-84%	-40%	1762%	-62%	0%	UBI3
23%	-30%	-15%	-13%	86%	52%	-60%	RPS4A
34%	0%	30%	-21%	0%	119%	-88%	RPS5
9%	-49%	-41%	-76%	-35%	-72%	-94%	RPS6A
45%	-34%	-46%	46%	-19%	-17%	-43%	RPS7A
33%	26%	-64%	0%	0%	-67%	-65%	RPS7B
20%	0%	50%	-41%	-40%	0%	-81%	RPS8A
n/a	-20%	-33%	0%	28%	GR only	GR only	RPS9A
n/a					HS only	HS only	RPS9B
n/a	HS only	HS only	HS only	1214%	1214%	HS only	UGA1
n/a		HS only				HS only	PHO13
8%	113%	-23%	153%	120%	41%	170%	KEM1
n/a	100%	GR only	GR only		GR only		RAT1
42%	HS only	HS only	84%	HS only	258%	0%	IMG1
n/a	HS only	HS only	HS only	HS only			MRPL1
n/a			HS only		HS only		MRPL11
0%	0%	0%	0%	0%	0%	0%	MNP1
n/a			GR only				MRPL13
n/a			HS only		HS only		MRPL15
n/a	0%			HS only			MRPL17
n/a	HS only	HS only	HS only	HS only	HS only	HS only	MRPL19
n/a	HS only	HS only	HS only		HS only	HS only	MRP7
n/a	HS only	HS only	HS only			GR only	MRPL23
n/a					GR only		MRPL24
n/a	HS only	HS only	0%	HS only	0%		MRPL28
n/a	HS only	HS only	HS only	HS only			MRPL3
n/a	HS only	HS only	139%	HS only	HS only	GR only	MRPL33
n/a		HS only	HS only		GR only		YDR115W
n/a	113%	HS only	HS only	0%	HS only	HS only	MRPL35
n/a	HS only					GR only	MRPL36
n/a	GR only	0%	GR only	0%	0%	GR only	MRPL38
n/a		HS only		HS only			MRPL4
n/a		HS only		HS only			MRPL40
n/a	0%	136%	0%		0%	GR only	MRPL44
n/a	HS only	HS only	HS only				MRPL49
n/a	HS only						MRPL51
n/a	HS only		HS only				MRPL6
28%	HS only	HS only	0%	HS only	GR only	-55%	MRPL8

n/a				HS only			MRPL9
n/a					HS only		YML6
n/a	HS only		HS only		HS only		FAU1
n/a	350%	HS only	1000%	HS only	HS only	HS only	MET6
n/a	HS only		HS only		120%	HS only	RIB4
93%	250%	24%	110%	0%	-37%	-76%	RPP0
n/a	GR only	HS only	0%	GR only		GR only	RPP1B
112%	HS only	0%	133%	-58%	0%	-90%	RPP2A
n/a		GR only	HS only		GR only	GR only	RPP2B
n/a	100%	HS only		HS only			NMD3
203%	56%	63%	384%	-20%	148%	-23%	RPL1A
7%	-43%	117%	-49%	-43%	146%	-64%	RPL10
n/a	-45%	GR only	HS only	-50%	63%	HS only	RPL11A
n/a		HS only	GR only			GR only	RPL11B
60%	88%	125%	67%	59%	-39%	-53%	RPL12A
n/a	HS only	46%	HS only	-26%	GR only	0%	RPL13A
n/a	GR only	HS only	GR only	GR only	46%	HS only	RPL13B
n/a	30%	76%	HS only	-49%	GR only	-49%	RPL14A
n/a			GR only		HS only		RPL14B
13%	-53%	120%	0%	0%	103%	26%	RPL15A
13%	-27%	-56%	-56%	0%	-23%	-31%	RPL16A
n/a	-23%	-23%	-21%	-69%	-44%	GR only	RPL16B
22%	-61%	-44%	-43%	-48%	22%	-87%	RPL17A
22%	-61%	-32%	-43%	HS only	50%	-87%	RPL17B
0%	-38%	0%	0%	100%	-27%	0%	RPL18A
7%	-72%	79%	-55%	-70%	0%	-69%	RPL19A
21%	62%	62%	0%	-44%	49%	-42%	RPL2A
15%	-43%	46%	-31%	-48%	-47%	-60%	RPL20A
45%	110%	0%	0%	0%	30%	-90%	RPL21A
33%	74%	123%	-23%	HS only	0%	-90%	RPL21B
28%	HS only	125%	0%	-56%	GR only	-56%	RPL22A
79%	-21%	-21%	59%	-38%	-81%	-98%	RPL23A
18%	-21%	0%	-35%	-51%	-53%	-72%	RPL24A
21%	-24%	29%	-37%	GR only	31%	-80%	RPL24B
91%	30%	-23%	115%	68%	-42%	-67%	RPL25
13%	29%	-40%	-67%	33%	121%	-93%	RPL26A
26%	HS only	HS only	28%	-23%	-23%	-23%	RPL27A
n/a	GR only	GR only					RPL27B
23%	-40%	0%	-23%	35%	31%	-69%	RPL28
11%	80%	-13%	-21%	15%	-35%	-43%	RPL3
396%	48%	135%	735%	76%	135%	-57%	RPL30
21%	-75%	131%	-42%	-75%	-57%	0%	RPL31A
56%	0%	116%	37%	-46%	0%	-75%	RPL32
2%	0%	0%	-66%	0%	42%	-69%	RPL33A
n/a	0%	0%	HS only		GR only		RPL33B
n/a	-50%	0%	-28%	-35%	0%	HS only	RPL34A
n/a						GR only	RPL34B

39%	-25%	-24%	0%	81%	33%	-79%	RPL35A
n/a	39%	HS only	0%	116%	-31%	GR only	RPL36A
n/a		GR only				HS only	RPL36B
30%	914%	-32%	-31%	-32%	-54%	-91%	RPL38
n/a	GR only	HS only	-62%	GR only		GR only	RPL39
n/a				HS only			UBI1
85%	74%	132%	171%	74%	-75%	0%	RPL42A
3%	-38%	0%	-59%	-77%	0%	-66%	RPL43A
22%	-43%	-24%	0%	35%	-22%	-43%	RPL4B
114%	0%	-69%	227%	0%	109%	0%	RPL5
n/a	HS only				HS only	HS only	RPL6A
n/a	29%	25%	0%	134%	GR only	GR only	RPL6B
n/a	23%	61%	GR only	29%	0%	GR only	RPL7A
n/a			HS only			HS only	RPL7B
21%	19%	-52%	-39%	-43%	0%	-81%	RPL8A
28%	0%	-39%	-14%	-41%	0%	-70%	RPL8B
94%	HS only	68%	110%	GR only	-20%	-79%	RPL9A
n/a	0%	HS only	110%	28%	GR only	GR only	RPL9B
n/a	HS only	HS only	HS only	HS only	HS only		LOC1
n/a	122%	0%	HS only	261%	0%	261%	NIP7
n/a	0%	117%		HS only			NOP8
69%	143%	714%	139%	171%	143%	0%	PFK1
68%	218%	192%	192%	HS only	491%	57%	PFK2
n/a	HS only	1029%	1200%	HS only	HS only	HS only	GND1
n/a			HS only	HS only			GND2
n/a	HS only	HS only	HS only	HS only	HS only	HS only	SOL4
n/a		HS only			HS only		SOL2
121%	188%	49%	327%	573%	41%	86%	KAR2
44%	128%	159%	213%	369%	200%	125%	ARB1
n/a	GR only						ADY4
58%	37%	-12%	84%	100%	12%	-32%	ILV2
61%	43%	194%	250%	HS only	89%	127%	ILV6
n/a	HS only	256%	HS only	611%	422%	56%	ERG10
29%	-20%	-26%	10%	39%	-44%	-48%	FAS3
n/a		HS only	HS only			HS only	ACH1
50%	0%	50%	100%	100%	100%	0%	ACS2
n/a		HS only	HS only				ARG8
72%	350%	725%	144%	HS only	600%	0%	ACO1
n/a	GR only	GR only	0%	GR only		GR only	END3
n/a					GR only		END3
n/a						HS only	PAN1
n/a	GR only	GR only	69%	GR only	GR only	GR only	PAN1
n/a	-38%	-40%	109%	GR only	-85%	GR only	SLA1
158%	-57%	-18%	573%	-66%	-71%	256%	ACT1
n/a	HS only	0%	0%	HS only	HS only		APD1
n/a	0%	HS only	HS only	HS only	HS only	GR only	ABP1
n/a	HS only	HS only	HS only	HS only	HS only		AIP1

n/a	100%	0%	HS only	HS only	0%		ARP9
n/a			325%			HS only	PRK1
14%	135%	0%	113%	988%	0%	85%	ARP2
n/a	GR only		HS only		GR only		ARC40
333%	111%	58%	667%	233%	40%	0%	ARC35
n/a	-72%	0%	256%	HS only	0%	HS only	ARC18
22%	45%	100%	45%	137%	0%	0%	ARC19
159%	0%	0%	264%	-54%	0%	-54%	ARC15
32%	229%	-24%	50%	113%	-83%	113%	ARP3
n/a			HS only	HS only			ARP5
n/a					GR only		ACK1
n/a	HS only	HS only		HS only	HS only		ACP1
n/a		GR only				GR only	OLE1
n/a	HS only	HS only					AHC2
n/a					HS only		APT1
n/a		HS only	HS only		HS only		AAH1
n/a	HS only	GR only		HS only	HS only		ADO1
230%	1800%	1020%	407%	HS only	787%	-53%	SAH1
n/a	GR only	-80%	0%	HS only	GR only		ADK1
n/a				HS only		HS only	ADK2
n/a	HS only	HS only	HS only	200%	429%	0%	ADE13
n/a	HS only			HS only			ADE12
n/a		GR only			GR only		SRV2
n/a	HS only			HS only	HS only		UBA4
n/a		HS only					UBA4
n/a	HS only	HS only	HS only	HS only	HS only	HS only	SPB1
57%	35%	-54%	28%	144%	-47%	-87%	AAC2
n/a	HS only	HS only	HS only	HS only	HS only		YSA1
n/a		0%	GR only	HS only	GR only		ARF1
n/a	GR only						AGE1
n/a	HS only	0%	0%	0%	GR only	GR only	AGE2
n/a	GR only	GR only	GR only	HS only			GCS1
n/a	HS only	117%	0%	0%	GR only		GLO3
n/a			HS only	GR only		HS only	GGA1
3%	83%	-80%	-48%	64%	-84%	-54%	GGA2
n/a					HS only		AAP1
n/a	HS only			HS only			ALA1
180%	444%	314%	453%	212%	116%	93%	ADH1
200%	489%	644%	356%	489%	222%	-45%	ADH3
n/a		HS only					ADH4
n/a	HS only	HS only		HS only			ADH5
n/a	HS only		HS only		GR only		ATF2
n/a	HS only	HS only	HS only	662%	1550%	HS only	ALD2
n/a	HS only	HS only	HS only	436%	453%	1654%	ALD3
n/a	HS only			HS only			ALD5
n/a	GR only	GR only	0%	GR only	GR only	GR only	LEM3
509%	HS only	HS only	1133%	125%	170%	115%	TPS1

n/a	-50%	-50%	0%	HS only	GR only	GR only	KTR1
n/a	GR only		HS only	HS only			ADD37
n/a						HS only	MPH3
n/a			HS only	HS only	HS only	200%	AMS1
n/a	0%	-55%	0%		GR only		AIM38
n/a	HS only	HS only	350%	HS only	0%		GCV1
n/a			HS only				APE2
n/a	0%	-54%	GR only	0%	GR only	GR only	ATO3
n/a		GR only	HS only			HS only	AMD1
n/a	HS only	0%	HS only	HS only	HS only	0%	YNL155W
n/a	HS only	HS only	HS only	HS only			YOR052C
n/a		HS only					CDC23
n/a		HS only			HS only		YCR051W
n/a	HS only						TRP4
n/a	HS only	HS only		HS only	HS only		TRP2
n/a	HS only	0%	HS only	HS only			TRP3
n/a	0%	GR only	-33%	HS only	GR only		SLH1
n/a			HS only				APL2
n/a	GR only						APM1
n/a	0%						APS1
50%	HS only	-50%	100%	HS only	0%	0%	APL3
n/a	0%	GR only					APM4
n/a	0%	HS only	0%	HS only	0%	GR only	APS2
n/a	HS only	HS only					AIF1
n/a					GR only		SYT1
n/a	GR only						GEA1
n/a		GR only				GR only	GEA2
n/a	HS only	HS only	HS only	HS only	HS only	HS only	CAR1
n/a					HS only		ARG7
n/a	HS only	HS only		HS only	HS only		RMT2
n/a	HS only	HS only			HS only		ARG4
n/a	HS only		HS only	HS only	HS only		ARG1
n/a	HS only	HS only	HS only	HS only			YDR341C
n/a				HS only		GR only	MSR1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	ARO8
0%	253%	118%	0%	0%	0%	0%	ABF2
n/a	HS only	HS only	HS only	HS only	533%	HS only	ASN2
n/a		HS only		HS only	HS only		DED81
n/a	HS only	613%	HS only	HS only	HS only	HS only	AAT2
n/a	0%	0%	0%	HS only	GR only		AAT1
n/a	HS only	833%	HS only	HS only	HS only	HS only	HOM2
n/a		GR only					MKC7
n/a	HS only	0%	HS only	HS only	HS only	HS only	DPS1
n/a		HS only		HS only	HS only	HS only	MSD1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	HIS1
n/a	HS only	HS only	HS only		GR only	HS only	ATP4
n/a			HS only	HS only	HS only	119%	ATP5

108%	268%	80%	153%	523%	89%	-63%	ATP1
173%	1027%	401%	317%	943%	188%	-30%	ATP2
n/a		HS only				GR only	ATP7
n/a	HS only			HS only			ATP16
n/a					GR only		ATP21
n/a		GR only	0%	HS only	GR only	GR only	ATP17
n/a	0%	0%	0%	0%	0%	GR only	ATP20
195%	HS only	345%	491%	345%	345%	100%	ATP3
n/a	HS only	HS only	HS only	HS only			ATP14
n/a					GR only	GR only	ATP18
n/a	HS only		HS only			HS only	STF2
n/a					HS only		HMI1
n/a						HS only	YKU70
n/a	0%	HS only	133%	HS only	100%		NAM7
n/a			HS only				ULS1
158%	1975%	52%	467%	1200%	272%	150%	HSC82
n/a	HS only	HS only	HS only	HS only	346%	HS only	HSP82
n/a		GR only			GR only		MDL1
49%	67%	-40%	24%	-8%	-38%	-73%	PDR12
20%	HS only	HS only	6%	HS only	HS only	-34%	PDR15
n/a	HS only		HS only				CHL1
n/a			HS only				DBP1
n/a	GR only					GR only	DBP10
n/a	HS only	30%	0%	0%	GR only		DBP10
28%	9%	29%	46%	51%	0%	-10%	DBP2
34%	76%	GR only	21%	GR only		89%	DBP3
n/a		HS only		HS only	0%		DBP3
n/a	225%	0%	HS only	HS only	0%		DBP4
n/a	50%	0%	236%	HS only	-50%	GR only	DBP5
n/a	0%	GR only	GR only	HS only	GR only		DBP6
n/a		HS only			HS only		DBP6
0%	-27%	0%	0%	50%	-52%	0%	DBP8
156%	26%	-19%	48%	109%	-86%	360%	DBP9
88%	145%	85%	128%	39%	0%	-49%	DED1
41%	30%	0%	44%	169%	-53%	-37%	DHH1
n/a	0%	GR only	100%	HS only	GR only		MTR4
38%	28%	-22%	77%	HS only	-31%	0%	DRS1
33%	100%	-45%	22%	800%	-56%	-45%	TIF1
n/a	0%	-69%	-50%	HS only	GR only		FAL1
6%	44%	-22%	41%	167%	-25%	29%	HAS1
n/a	0%	100%	HS only		0%	0%	MAK5
n/a				HS only			MAK5
49%	-39%	-30%	43%	123%	-39%	-55%	MSS116
n/a	HS only	HS only	HS only		GR only		ROK1
87%	114%	-53%	173%	53%	GR only	0%	SUB2
n/a					HS only		SUV3
n/a				GR only	HS only	HS only	RRP3

n/a	64%	50%	0%	HS only	GR only	GR only	RRP3
n/a	HS only	HS only	HS only	HS only	GR only		SPB4
n/a				GR only			ATG14
n/a		GR only					ATG16
n/a				GR only	HS only		ATG19
n/a		GR only	HS only				ATG2
n/a	HS only		HS only	HS only	HS only		ATG21
n/a	HS only	HS only					ATG29
n/a			HS only		HS only		ATG29
n/a				HS only			CIS1
n/a	HS only						BAR1
n/a	HS only	HS only	800%	154%	245%	HS only	ADE16
n/a	HS only	HS only	HS only	41%	173%	HS only	ADE17
n/a	HS only	HS only	HS only	HS only	HS only		ADE5,7
n/a	HS only	HS only	HS only	944%	422%	HS only	BAT2
n/a	500%	HS only	HS only	HS only		HS only	BAT1
n/a	0%	GR only	GR only	HS only	0%	GR only	BDF2
n/a	0%	0%	200%	317%	-52%	GR only	BEM1
n/a	0%	0%	100%	GR only	0%	GR only	BEM4
n/a	GR only	GR only			GR only		BUD4
n/a			HS only		HS only		BUD6
n/a		GR only	GR only		GR only	GR only	RAX1
85%	114%	0%	-36%	267%	0%	133%	ADE3
9%	0%	10%	33%	386%	10%	15%	MIS1
n/a				GR only			ERG2
n/a		GR only		HS only	GR only	GR only	CNB1
n/a	HS only	HS only		HS only	HS only		CMK2
n/a	HS only	HS only	HS only	HS only			FRQ1
n/a		GR only			GR only		CMD1
68%	36%	0%	135%	450%	-20%	0%	BCY1
n/a					HS only		TPK1
n/a				HS only			TPK2
n/a		GR only			HS only		TPK3
n/a	HS only		HS only	113%	113%	113%	NCE103
n/a				GR only			CPS1
n/a	HS only	HS only	HS only	121%	313%	HS only	DKA1
n/a				0%		HS only	YPP1
n/a		GR only					YPP1
n/a				HS only			YAT2
n/a	HS only	GR only	HS only		GR only	GR only	YMC1
n/a		HS only	HS only		GR only		YCK1
33%	-50%	-50%	0%	100%	0%	-67%	YCK2
n/a		GR only			GR only		YCK3
n/a	0%	-54%	0%	117%	0%	GR only	HRR25
n/a	HS only	HS only	HS only	HS only	HS only		CKB1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	CKB2
105%	238%	285%	184%	170%	17%	-26%	CHA1

n/a		HS only					CAT5
n/a	HS only	HS only	HS only	1136%	918%	1382%	CTT1
n/a	HS only		HS only	HS only			YER163C
114%	109%	-52%	227%	HS only	-52%	0%	MOB2
n/a	HS only	118%	30%	360%	35%	HS only	DBF2
0%	0%	134%	0%	27%	-36%	0%	CDC10
59%	70%	54%	76%	125%	0%	-41%	CDC11
17%	44%	43%	-10%	138%	-22%	-43%	CDC12
n/a	HS only		HS only	HS only	HS only		CDC24
n/a	59%	HS only	HS only	HS only	355%	0%	CDC28
51%	82%	59%	78%	69%	-37%	-24%	CDC3
n/a	GR only				HS only	HS only	CDC42
223%	775%	156%	413%	925%	275%	-33%	CDC48
n/a	HS only	0%	50%	HS only	GR only	GR only	CDC53
n/a				HS only	HS only		CDC54
n/a				HS only			CDC7
n/a	-33%	-44%	-85%	-67%	-76%	GR only	YLR413W
n/a	0%	0%	0%	HS only	0%	GR only	TAO3
n/a					GR only		WSC2
n/a	HS only	HS only	HS only	HS only		HS only	HSP150
n/a			HS only	GR only		HS only	PST1
n/a						GR only	CWP1
30%	-39%	-14%	-14%	-18%	-64%	-74%	ECM33
n/a						GR only	CHL4
n/a		HS only	HS only				CBF2
n/a	HS only	HS only	HS only	HS only	HS only	HS only	PRB1
n/a			GR only		GR only		CNM67
n/a			HS only		GR only		CHS5
n/a		0%	0%				CHS3
26%	0%	-50%	27%	433%	-65%	79%	ARO2
n/a						HS only	RLF2
n/a		HS only	HS only		HS only		EAF3
n/a			GR only				EAF7
n/a	0%	HS only	133%	HS only	133%	GR only	RSC30
n/a		HS only			HS only		RSC58
n/a	HS only		HS only				RSC8
n/a	HS only		HS only				RSC4
n/a	HS only	HS only	HS only	HS only	HS only	HS only	NPL6
n/a	HS only	HS only	HS only	HS only			RSC9
n/a	HS only	HS only	HS only	HS only	HS only		SFH1
n/a	HS only	350%	HS only	HS only	0%	HS only	CHD1
n/a			HS only				CSM3
n/a						GR only	CST9
n/a	HS only						CTF8
294%	314%	129%	640%	34%	26%	53%	CIT1
n/a					GR only		YAP1802
308%	775%	525%	750%	317%	208%	133%	CHC1

n/a	GR only	0%	HS only		GR only	GR only	CLC1
106%	567%	567%	150%	467%	180%	-63%	RET1
n/a	HS only	467%	HS only	HS only	HS only	HS only	SEC26
n/a	HS only	-64%	75%	HS only			SEC27
n/a		HS only		HS only	HS only		RET2
n/a	HS only	HS only	HS only	HS only	227%	HS only	SEC28
n/a			HS only				SEC21
n/a	HS only	HS only		HS only			RET3
n/a		GR only	HS only		GR only	HS only	COF1
n/a	HS only	100%	GR only	HS only			SWD2
n/a		HS only					COG4
n/a		HS only					COG5
n/a	HS only			HS only			COG7
n/a			GR only				RRI2
n/a	HS only						CSN9
n/a	800%	300%	1000%	HS only	0%	HS only	SEC16
n/a			GR only			GR only	CTR1
440%	GR only	GR only	980%	GR only	GR only	100%	CRN1
n/a	HS only		HS only		HS only	HS only	CCW12
n/a	HS only	HS only	HS only	HS only	HS only		YKL091C
n/a			GR only				CTK1
n/a		0%	0%	HS only			CTK3
111%	58%	23%	309%	HS only	100%	88%	URA7
n/a	HS only	HS only	HS only	HS only	HS only	HS only	URA8
n/a	GR only	GR only	GR only	GR only			PHO85
n/a	HS only	HS only	HS only	471%	1214%	HS only	DUG1
n/a			HS only				STR3
n/a	HS only	54%	HS only	HS only	367%	GR only	CYS4
n/a	HS only	111%	HS only	HS only	HS only		CYS3
n/a	100%	50%	HS only	HS only	100%	HS only	NFS1
n/a	HS only	HS only	HS only		HS only		LAP3
n/a						HS only	YNL247W
11%	-48%	-27%	0%	42%	-78%	-23%	CDD1
n/a						HS only	bI2
n/a			HS only				CBP2
n/a	GR only	HS only	0%		GR only		CBP6
n/a	HS only	HS only	HS only	HS only	HS only	HS only	COR1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	QCR2
n/a					HS only		QCR6
n/a	HS only	HS only	HS only	HS only	HS only	HS only	QCR7
56%	HS only	HS only	113%	HS only	113%	0%	RIP1
n/a	HS only			HS only			CYC3
50%	77%	-86%	32%	-68%	-24%	-68%	CYC1
n/a	HS only			HS only		GR only	COX5A
n/a					HS only		COX8
n/a	HS only						COX4
n/a	HS only	HS only	HS only	HS only	HS only	HS only	COX6

n/a	HS only	HS only					COX9
n/a	HS only	HS only	HS only	HS only	HS only	HS only	CTC1
n/a					HS only		ERG5
n/a	100%	GR only					CYK2
n/a				HS only			CYK3
n/a			HS only				NCS6
n/a				GR only			NAR1
n/a		HS only					NBP35
n/a		HS only	HS only	HS only	HS only		SER33
n/a	0%	0%	0%	0%	GR only		ARA2
n/a	HS only	HS only	HS only	HS only	HS only	HS only	ARA1
n/a	HS only	137%	HS only	HS only			DAD3
n/a	HS only	HS only	GR only		HS only	0%	MOB1
n/a	HS only		HS only				ERG4
n/a			HS only				PUT2
n/a	HS only	HS only	HS only	HS only	HS only		HEM2
n/a	-71%	-71%	0%	HS only	GR only	GR only	DCD1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	LIA1
n/a	HS only	HS only	HS only	HS only	HS only		DYS1
n/a	HS only	HS only	0%	0%	GR only	GR only	DFM1
n/a				GR only	GR only	GR only	DIP5
87%	154%	34%	117%	386%	34%	-58%	LPD1
62%	39%	39%	67%	19%	0%	-56%	PDA2
n/a	HS only	HS only	HS only	229%	HS only	HS only	KGD2
n/a		HS only			HS only		URA1
n/a	HS only	HS only	HS only	HS only			DAK1
n/a			HS only				DAK2
88%	120%	-47%	225%	817%	-47%	50%	ILV3
n/a	HS only	HS only	0%	HS only	0%		DIM1
n/a				HS only		HS only	ERG19
n/a			HS only				DLD1
n/a	HS only	HS only	HS only	HS only	HS only		DLD2
n/a	HS only	HS only	HS only	HS only	117%		DLD3
n/a		GR only			GR only		RAD17
n/a					GR only		LCD1
n/a		GR only	HS only				DUN1
n/a	GR only						RPH1
n/a			HS only		GR only		MSH1
n/a	GR only			HS only			POL1
n/a	GR only						HCS1
n/a			HS only				HYS2
n/a			HS only	HS only			POL2
n/a		GR only					POL5
n/a	GR only						REV3
n/a	HS only	100%	GR only	HS only	HS only		PRI1
n/a	GR only	GR only	0%				RAD52
n/a	133%	-73%	HS only	0%	GR only	GR only	RDH54

n/a			HS only				RAD16
n/a						HS only	RAD2
n/a		GR only	HS only				RAD50
n/a	HS only	HS only		HS only	HS only		RAD51
n/a			HS only				RAD9
n/a	GR only			GR only			DNA2
n/a				HS only			CDC47
n/a			HS only				MCM2
n/a	HS only	HS only		HS only	HS only		MCM6
n/a	HS only			HS only			TOP1
n/a	HS only		HS only	0%	100%		TOP2
n/a	HS only	0%	HS only				PAT1
n/a					HS only		APN1
n/a			HS only	HS only			MAG1
n/a		HS only	HS only				RAP1
n/a	-11%	-14%	0%	300%	-57%	HS only	RPA1
n/a	GR only	GR only		HS only	GR only		RPA12
233%	75%	75%	467%	467%	0%	0%	RPA2
n/a	GR only	GR only	HS only	GR only	GR only		RPA34
n/a	GR only	GR only			GR only		RPA43
n/a	-50%	GR only	213%	0%	0%	HS only	RPA49
n/a	600%	700%	1000%	700%	233%	HS only	RPB1
n/a	HS only		HS only	HS only			RPB11
n/a	HS only	333%	167%	HS only	167%		RPB2
n/a		HS only	HS only				RPB3
n/a		HS only		GR only			RPB4
n/a	HS only						RPC11
n/a	0%	HS only	HS only		100%	HS only	RET1
n/a	HS only			HS only	HS only	HS only	RPC34
n/a	HS only	HS only	HS only				RPC17
63%	86%	42%	157%	440%	66%	32%	RPC40
28%	0%	-56%	-56%	0%	GR only	0%	RPC19
n/a	0%	0%	HS only	0%	107%		RPB5
n/a		HS only			HS only		RPB8
0%	152%	152%	0%	HS only	GR only	0%	RPC10
n/a	HS only	87%	GR only	HS only	149%	HS only	RPB10
570%	371%	254%	1215%	662%	257%	76%	MDJ1
n/a		GR only					XDJ1
n/a				HS only			JEM1
15%	56%	-45%	31%	0%	27%	0%	SCJ1
n/a		GR only	GR only			GR only	DID4
n/a	HS only	GR only	HS only	HS only	0%		YLR422W
n/a	GR only	-52%	HS only	HS only	0%	GR only	DPM1
n/a			HS only				OST3
n/a	HS only	0%	0%	HS only	GR only		OST2
n/a		GR only	HS only		0%	-53%	WBP1
n/a					HS only		PMT2

n/a		HS only	HS only				PMT4
n/a			HS only				MRE11
n/a	HS only			HS only	GR only		MGM1
n/a	-26%	-34%	-69%	HS only	-63%	GR only	BRE1
n/a	HS only	HS only					DMA1
69%	15%	0%	77%	150%	-30%	-62%	RSP5
n/a		HS only	HS only	HS only	HS only		EMI1
n/a	GR only	GR only	400%		GR only	HS only	EDE1
41%	63%	52%	63%	-47%	-24%	-19%	TEF1
27%	0%	0%	0%	0%	0%	-54%	EFB1
n/a	-26%	113%	220%	0%	0%	HS only	CAM1
86%	24%	HS only	171%	29%	119%	0%	TEF4
34%	-16%	54%	34%	-48%	-11%	-33%	EFT1
35%	-32%	48%	0%	-21%	-13%	71%	YEF3
63%	243%	38%	187%	HS only	0%	60%	TUF1
n/a	GR only	0%			0%	GR only	ELO2
n/a	HS only	0%	HS only	HS only			IKI3
n/a	HS only	GR only		HS only	HS only		ELP3
n/a						HS only	ELP4
n/a	0%	0%	0%	HS only	GR only	GR only	IKI1
n/a	HS only	GR only	HS only	HS only			ELP6
n/a						HS only	PPN1
117%	50%	233%	233%	317%	108%	0%	EDC3
n/a	HS only	HS only	HS only	588%	1443%	182%	ENO1
1661%	3123%	2248%	3384%	992%	1258%	62%	ENO2
n/a			HS only				ERR1
n/a						HS only	ERR3
n/a					GR only		TSC13
n/a	HS only	HS only	HS only	600%	HS only	HS only	ETR1
n/a			HS only			HS only	ENT1
n/a	-69%	-50%	-63%	GR only	-50%	GR only	ENT2
n/a				GR only		GR only	ENT3
n/a	HS only	0%	HS only		GR only		ENT4
50%	0%	0%	100%		HS only	0%	ENT5
27%		0%	0%		GR only	-55%	ERV29
n/a	HS only	HS only	0%	HS only	GR only		ERV46
n/a					GR only	GR only	ERG28
n/a		59%	GR only	GR only	HS only	HS only	ERJ5
119%	238%	204%	238%	HS only	238%	0%	EMG1
n/a	HS only	0%	HS only		0%		ENP1
n/a	HS only	0%	HS only				TIF4632
n/a	0%	GR only	233%		-57%		TIF4631
13%	0%	-43%	-26%	147%	-32%	0%	SUP35
71%	49%	13%	89%	179%	89%	-53%	SUP1
n/a	HS only		HS only	HS only	124%		TIF11
n/a	GR only	120%	0%	GR only	GR only	HS only	SUI2
79%	33%	0%	157%	936%	-66%	0%	SUI3

35%	74%	0%	17%	369%	0%	-52%	GCD11
n/a	HS only	220%	HS only	HS only	HS only		YGR054W
25%	-48%	-70%	-9%	70%	-70%	-59%	TIF32
31%	-70%	-59%	37%	450%	-82%	100%	PRT1
n/a		GR only	-50%	GR only	-50%		NIP1
n/a	GR only					HS only	NIP1
n/a	233%	375%	GR only	233%	43%	GR only	TIF35
n/a			HS only				TIF35
n/a	HS only	111%	HS only	0%	0%	111%	TIF34
n/a		GR only			GR only		HCR1
n/a	HS only	114%	0%	HS only	HS only		TIF3
n/a	-80%	96%	-43%	HS only	63%	GR only	TIF45
n/a	0%	-38%	225%	0%	0%	GR only	TIF5
14%	35%	0%	0%	-28%	0%	-28%	HYP2
50%	0%	0%	233%	67%	-50%	333%	FUN12
n/a	107%	0%	HS only	HS only	HS only	GR only	TIF6
n/a	75%	0%	300%	300%	172%	HS only	SUI1
n/a	GR only	GR only	GR only				EXO70
n/a	HS only	HS only	HS only		HS only		SEC10
n/a	HS only	HS only	HS only	HS only			SEC15
n/a	GR only		HS only		HS only	HS only	SEC3
n/a			HS only	HS only	GR only		SEC5
n/a			0%	HS only	HS only		SEC6
n/a	-50%	100%	GR only	HS only	-50%		SEC8
n/a		GR only		HS only			EXO1
n/a		HS only					CSL4
n/a			HS only		HS only	HS only	RRP40
n/a					HS only		RRP43
n/a			HS only				RRP45
n/a	HS only						RRP46
n/a			GR only		HS only	HS only	DIS3
n/a	HS only	HS only	HS only	HS only	HS only	HS only	POB3
211%	HS only	0%	422%	800%	283%	0%	SPT16
n/a	HS only	HS only	HS only		HS only		CAP2
n/a	HS only	HS only	HS only	HS only	HS only		FSH1
n/a	HS only	HS only	HS only	HS only			FSH3
n/a			HS only				FPP1
99%	257%	-22%	154%	900%	129%	-44%	FAS2
8%	38%	18%	41%	300%	55%	25%	FAS1
n/a			HS only				YLR352W
n/a						GR only	FRE1
n/a	HS only	HS only		GR only	HS only	113%	HEM15
n/a			HS only	HS only			SAC6
98%	224%	340%	224%	750%	181%	29%	FPR3
n/a		HS only	HS only	HS only			FPR1
n/a	182%	138%	170%	HS only	37%	HS only	FPR4
n/a	GR only	GR only	HS only		GR only	GR only	FLC1

n/a	HS only	HS only	HS only	HS only	HS only		YHB1
n/a	HS only	GR only	HS only		GR only	0%	YCP4
n/a					HS only		FBP26
456%	HS only	538%	1311%	464%	349%	398%	FBA1
n/a	214%	HS only	HS only	443%	HS only	586%	FUM1
n/a	HS only	HS only	HS only	53%	380%	HS only	YEL047C
n/a	HS only	-63%	HS only	HS only	HS only	HS only	NOT1
n/a		HS only					NOT2
n/a		GR only					NOT4
n/a				HS only			NOT5
n/a						HS only	GIP2
n/a	HS only		HS only	0%	GR only	GR only	GIP4
n/a	214%	0%	343%	0%	-50%	GR only	EXG1
n/a	GR only	HS only	HS only			GR only	BGL2
n/a	HS only	HS only	HS only	567%	862%	132%	GLK1
n/a	HS only	0%	250%	HS only	HS only	HS only	GFA1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	ZWF1
n/a	HS only	HS only	HS only	GR only	100%		YMR099C
n/a	HS only	308%	HS only	HS only	HS only	HS only	PGI1
n/a		HS only			HS only		GID8
n/a			GR only	0%			CCR4
n/a	120%	-23%	175%	HS only	-53%	GR only	PRO1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	GAD1
n/a	100%	400%	267%	HS only			GLT1
n/a				HS only	0%		GSH1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	GLN1
n/a	125%	0%	250%	HS only	GR only		GUS1
65%	HS only	130%	130%	130%	283%	0%	GRX2
n/a		120%	HS only	HS only			GPX2
50%	200%	443%	200%	HS only	HS only	100%	GLR1
n/a	HS only	HS only	HS only	HS only	HS only	0%	GTT1
n/a				GR only			GTT2
n/a				HS only			GSH2
n/a	HS only	HS only	76%	HS only	HS only	HS only	TDH1
n/a	HS only	HS only	32%	147%	GR only		TDH2
21%	72%	94%	31%	210%	43%	-12%	TDH3
n/a	HS only	HS only	0%	HS only	HS only	GR only	GPD1
n/a		0%	0%		-53%		GPD2
n/a				HS only			GPT1
n/a	HS only	HS only	0%	HS only	-40%	GR only	GDE1
n/a				HS only	HS only		GCV3
n/a			HS only				GCV2
n/a	HS only	HS only		HS only	HS only	56%	GSY1
92%	HS only	2200%	266%	154%	125%	81%	GSY2
63%	HS only		275%	HS only	HS only	150%	GDB1
n/a	HS only	HS only	HS only	843%	471%	HS only	GPH1
n/a					GR only		KRE2

n/a	HS only	HS only	HS only	HS only	HS only	HS only	GRS1
n/a	HS only						GRS2
n/a	HS only	467%	HS only	HS only	HS only		GUA1
n/a	HS only	HS only					IMH1
n/a	GR only	0%	GR only	GR only	GR only	GR only	YSP2
n/a		HS only					GRH1
n/a	HS only		HS only	HS only			WHI2
n/a		HS only	HS only	HS only	HS only	HS only	FOL2
n/a	HS only	HS only					RIB1
n/a	HS only	HS only	HS only	HS only	HS only		MTG2
93%	71%	-39%	100%	250%	-42%	-86%	BEM2
n/a		GR only	GR only				GYP1
n/a	HS only						MSB3
n/a		HS only					GYP8
n/a			GR only				SAC7
n/a					HS only		GSP1
n/a	HS only		HS only	HS only			GSP2
n/a		HS only					GTR2
116%	151%	0%	233%	HS only	47%	0%	RBG1
9%	-31%	45%	-75%	0%	0%	-58%	RHO1
n/a	HS only	HS only	HS only	HS only	HS only		RHO3
n/a	110%	110%	-34%	0%	-52%	GR only	RHO5
n/a	HS only	HS only	HS only	HS only	HS only		YPT1
n/a		HS only		HS only	HS only		YPT7
n/a	HS only	0%		HS only			ARC1
n/a	HS only						LTE1
n/a	HS only		HS only	HS only	0%		GPB1
17%	-37%	367%	-14%	-30%	243%	20%	ASC1
n/a	HS only	HS only	HS only	HS only			STE18
n/a		HS only					GUK1
78%	259%	118%	118%	0%	65%	-39%	GAR1
0%	109%	-52%	50%	39%	-47%	50%	NHP2
159%	99%	0%	99%	828%	-50%	416%	NOP10
95%	73%	27%	154%	27%	-30%	-36%	CBF5
n/a	HS only						YBR242W
n/a	HS only	HS only	HS only	HS only	HS only		YGL101W
2802%	HS only	3633%	5833%	1300%	2733%	229%	HSP104
n/a	HS only	HS only	HS only	1527%	4133%	1640%	HSP26
n/a	HS only	HS only	HS only	347%	859%	850%	HSP42
476%	HS only	942%	1182%	596%	671%	229%	HSP60
n/a	HS only	HS only	HS only	1050%	HS only	HS only	HSP78
220%	1040%	295%	248%	320%	58%	689%	SSE1
n/a	HS only	HS only	HS only	357%	HS only	900%	SSE2
163%	152%	126%	409%	367%	201%	83%	SSA1
169%	140%	160%	410%	263%	168%	72%	SSA2
n/a			HS only				SSA3
n/a	HS only	HS only	HS only	560%	HS only	HS only	SSA4

41%	21%	-40%	37%	HS only	GR only	-46%	SSB1
43%	21%	-40%	36%	72%	-6%	-50%	SSB2
130%	562%	181%	260%	2490%	114%	0%	SSC1
n/a	HS only	120%	HS only	HS only	HS only	HS only	STI1
n/a	-75%	-25%	500%	0%	GR only	HS only	SEN1
n/a		HS only	GR only				HOT13
n/a	HS only	HS only	HS only	HS only	HS only		HAP1
n/a					HS only		GPG1
n/a	HS only	HS only	HS only	0%	GR only		COQ1
n/a			HS only				COQ3
n/a	HS only	HS only	HS only	HS only	HS only	HS only	HXK1
n/a	HS only	314%	HS only	HS only	HS only		HXK2
0%	HS only	0%	0%	HS only	0%	0%	HMO1
n/a		GR only	GR only		GR only	-67%	GNP1
80%	HS only	317%	124%	HS only	100%	-36%	HXT7
n/a	HS only	GR only	HS only		0%	HS only	TRK1
n/a		GR only					HOT1
n/a	HS only	HS only		HS only	HS only		HIS4
n/a	HS only	HS only	HS only	HS only			HTS1
n/a	GR only	GR only	-50%			GR only	GCN5
n/a		GR only					SAS3
n/a		HS only					ASF1
n/a		HS only					CTI6
n/a			HS only		HS only		HDA1
22%	-53%	0%	-44%	56%	-53%	0%	HOS3
n/a	HS only	HS only	HS only		HS only	HS only	RPD3
102%	0%	-56%	204%	129%	0%	0%	HHO1
42%	0%	0%	53%	161%	53%	-31%	HTA1
39%	52%	0%	43%	118%	52%	-34%	HTZ1
n/a	HS only	HS only		33%	GR only	HS only	HTB1
n/a	33%	74%	71%	HS only	0%	GR only	HTB2
n/a	-41%	288%	-56%	-41%	69%	HS only	HHT1
269%	227%	0%	478%	34%	-59%	-59%	HHF1
n/a	HS only	GR only	GR only				SET1
n/a		HS only				HS only	HNT1
n/a						HS only	HMT1
n/a	HS only	HS only	HS only		HS only		LYS4
41%	76%	0%	19%	0%	-43%	-63%	LYS20
n/a		HS only		GR only	HS only		HOM6
n/a	HS only	HS only	HS only	HS only	HS only		THR1
n/a		GR only	HS only		GR only		SNL1
n/a	0%	0%	HS only	HS only	GR only		AHA1
n/a	117%	383%	HS only	HS only	0%	117%	ERG13
n/a		HS only			HS only		HPT1
n/a	HS only	217%	0%		-50%	HS only	SRP1
n/a	HS only	0%	HS only	HS only	GR only		KAP95
n/a	HS only	0%	HS only				KAP123

n/a		HS only	HS only	HS only			ISN1
n/a	HS only	233%	133%	HS only	-79%	GR only	IST2
n/a			HS only				BNA2
n/a			HS only				BUD2
n/a			HS only				IRA1
n/a	HS only	-36%	HS only	HS only	GR only	GR only	SLI15
n/a				HS only	HS only		IES5
n/a	0%	-55%	0%	HS only	-55%	GR only	PHO88
n/a		GR only	0%	GR only	0%	GR only	PHO86
118%	118%	236%	236%	HS only	0%	0%	IPP1
n/a					HS only		IPP2
n/a	HS only	380%	HS only	HS only	815%		IMD2
n/a		GR only	HS only	HS only			VIP1
n/a	100%	100%	100%	HS only	GR only		ISC1
n/a					HS only		INP52
n/a	-75%	-80%	50%	100%	GR only		INP53
n/a	HS only			HS only			SUC1
n/a		GR only	0%				ISU1
n/a					GR only		ISU2
n/a				HS only			AFT1
n/a	HS only	HS only		HS only			IAH1
95%	111%	233%	189%	111%	40%	0%	IDH1
70%	626%	119%	261%	288%	169%	120%	IDH2
n/a		50%	HS only	HS only	GR only	GR only	IDP3
32%	0%	-24%	-20%	0%	-47%	-85%	IDP1
n/a	HS only	HS only	HS only	HS only			ILS1
n/a	HS only	HS only		HS only	HS only		IDI1
n/a				HS only			ISW1
n/a						HS only	ISW2
n/a	HS only			HS only			IOC3
n/a	HS only	HS only	HS only	HS only			IOC4
n/a	HS only	HS only	HS only	HS only	HS only		APJ1
n/a					HS only		KAR4
n/a	0%	-40%	120%	HS only	GR only		KEL1
86%	131%	-30%	95%	HS only	-49%	-78%	ILV5
n/a	-50%	100%	0%	56%	GR only		YBL032W
n/a	HS only		HS only				YLL032C
n/a						GR only	KRE5
n/a		GR only			GR only		CIN8
n/a		GR only					KAR3
n/a	0%	HS only	HS only				KIP2
n/a				HS only			SMY1
n/a	HS only						NUF2
n/a	HS only	HS only	HS only	HS only	HS only		BNA5
n/a		HS only	HS only				LAH1
n/a	HS only	HS only	HS only	HS only	490%	490%	GLO1
n/a			HS only				LRE1

n/a		GR only					#VALUE!
n/a	HS only	GR only	HS only	HS only			ERG11
n/a	-50%	-50%	110%		100%		LSG1
n/a				GR only			LSB1
26%	-45%	-28%	24%	0%	-24%	-28%	LSB3
n/a				HS only			ASP1
n/a	HS only	HS only		HS only			PPM2
n/a						HS only	SOG2
n/a	HS only	0%	HS only	HS only	HS only	HS only	CDC60
160%		GR only	320%	HS only	0%	0%	YDR266C
n/a			GR only				TGL3
n/a					HS only		TGL5
n/a		0%		HS only			LIP5
25%	300%	180%	250%	180%	0%	300%	FAA1
n/a		HS only					FAA3
n/a	HS only	1040%	HS only	HS only	900%		FAA4
n/a				GR only		HS only	LTP1
n/a	HS only	HS only	HS only	244%	125%	525%	GLY1
19%	-42%	-75%	-52%	-25%	-42%	-89%	HXT1
15%	-52%	-74%	-51%	-62%	-44%	-82%	HXT3
n/a	GR only		GR only				PLB1
n/a	HS only	-67%	HS only	HS only	HS only		NTE1
n/a		0%		HS only	HS only		KRS1
n/a				GR only			MSK1
n/a			HS only				YOR111W
n/a				GR only			ALR1
n/a						HS only	ALR2
n/a	HS only	452%	2186%	662%	2957%	HS only	ALD6
n/a	HS only	HS only	HS only	HS only	HS only	HS only	MDH1
18%	189%	-40%	35%	76%	0%	0%	MDH3
n/a		GR only					MLS1
n/a		GR only					MCT1
n/a				HS only			MNR2
n/a	0%	0%	0%	HS only	0%	HS only	DCW1
n/a	0%	0%	0%	HS only	0%	GR only	MNN9
n/a		GR only					VAN1
67%	20%	-15%	92%	116%	-54%	-42%	MPG1
n/a	HS only	114%	HS only	HS only			PMI40
n/a		HS only	GR only				MKK2
n/a					0%		PBS2
n/a	0%	GR only	500%	HS only	GR only	HS only	MHP1
n/a		HS only		HS only	HS only		MATA1
n/a	HS only		HS only	HS only	HS only		MRC1
n/a	HS only						MED11
n/a					GR only		GAL11
n/a	HS only	HS only	HS only	HS only	HS only		SRB2
n/a	130%	HS only	HS only	HS only	HS only		SRB6

n/a						HS only	NUT1
n/a					HS only		MED8
n/a	GR only						RIM4
n/a	125%	0%	56%	125%	GR only	HS only	MSC3
n/a				GR only			MSC6
n/a	HS only			HS only			MCA1
125%	1650%	1213%	1900%	724%	2463%	1650%	MAP1
n/a	HS only	HS only	HS only	100%	0%	0%	MAP2
n/a	475%	225%	HS only	100%	100%	0%	MES1
n/a					HS only		MMS1
n/a		HS only			HS only		YBR261C
n/a		HS only	HS only	HS only			MDN1
n/a			GR only				MCM10
n/a	HS only	HS only	HS only	HS only	HS only		MCM5
109%	119%	0%	146%	0%	-54%	-73%	FIS1
n/a		HS only		HS only			ICL2
n/a		GR only	GR only	HS only	GR only	GR only	ODC2
n/a			HS only	HS only			MAM33
n/a	GR only	GR only	GR only	GR only			ATP10
n/a	0%	GR only	0%	HS only	GR only	GR only	RIM2
n/a					GR only		TCM62
n/a			HS only		HS only	HS only	MCX1
n/a				GR only			NTG1
28%	-50%	0%	-55%	0%	100%	0%	YHM2
n/a						HS only	YME2
n/a				HS only	HS only		ERV1
n/a	-37%	HS only	383%	HS only	GR only		MGM101
n/a	HS only	HS only		HS only	GR only		MTG1
n/a			HS only	HS only			MRS11
n/a			HS only	GR only			PAM18
n/a	HS only	GR only	0%	HS only		GR only	PAM16
n/a		GR only					TIM21
17%	27%	26%	-21%	217%	-57%	-55%	TIM44
n/a		HS only		0%		0%	TOM20
n/a	HS only	HS only				GR only	TOM40
n/a		HS only					TOM6
n/a	100%	HS only	-38%	0%	GR only	GR only	TOM70
n/a		GR only					OCT1
n/a						HS only	MMT1
n/a	GR only		0%			GR only	NUC1
n/a	HS only		HS only	HS only	HS only		IML2
n/a			488%	113%	0%	HS only	OM45
220%	1003%	501%	513%	138%	152%	73%	POR1
n/a	HS only						SCY_3392
n/a	-55%						OAC1
n/a	HS only			HS only			MPM1
244%	250%	392%	550%	HS only	250%	62%	PRX1

76%	26%	-47%	71%	108%	20%	-80%	MIR1
n/a			HS only				FMP38
135%	185%	48%	269%	67%	-21%	0%	YDJ1
n/a		GR only					AFG3
n/a	0%	GR only	0%		GR only	GR only	RCA1
n/a					HS only		GEM1
n/a		0%		HS only		HS only	MAS2
n/a	HS only	HS only	HS only	HS only	HS only	0%	MAS1
n/a	-50%	100%	0%	0%	GR only		FUS3
n/a	HS only	HS only		HS only	HS only		HOG1
n/a				HS only			KSS1
n/a		HS only	HS only				SLT2
n/a	HS only					HS only	CSM1
n/a	HS only	HS only	HS only	HS only	HS only		GRX5
n/a		GR only	GR only			GR only	MSB1
n/a	HS only	HS only	HS only				RNA15
n/a	HS only	HS only	HS only	HS only			YTH1
n/a	HS only	HS only		HS only	HS only		CTH1
45%	0%	-41%	35%	480%	-35%	-55%	MEX67
n/a				HS only		GR only	GFD1
n/a	HS only	GR only	0%				MTR2
n/a	HS only	290%	254%	91%	408%	HS only	MRT4
n/a				HS only	GR only		PUF2
n/a	GR only	HS only		GR only			PUF3
n/a	0%	243%	0%	HS only	GR only		DCP1
n/a	HS only	HS only			HS only		DCP2
n/a	HS only	HS only	HS only	HS only	HS only	0%	MEU1
n/a	HS only	HS only			HS only		TRM112
n/a		-43%	HS only		HS only		MRD1
178%	221%	299%	316%	66%	-42%	-40%	MBF1
n/a	-54%	70%	117%	0%	-72%		MLC1
1%	-17%	-48%	-22%	25%	-59%	-21%	BBC1
n/a		HS only		GR only	GR only		MYO1
n/a	100%	0%	HS only	GR only	GR only		MYO2
29%	23%	0%	92%	16%	-41%	150%	MYO3
113%	-53%	-45%	225%	-60%	-61%	0%	MYO5
n/a					GR only		TRM1
n/a	HS only	HS only	HS only	HS only	HS only		TRP1
n/a		HS only		HS only			AML1
n/a		GR only	GR only	HS only	GR only	GR only	NHA1
n/a			HS only				HPA3
n/a	HS only	HS only	HS only	HS only	HS only	HS only	HST2
n/a	HS only	GR only	100%		GR only		SIR2
n/a	HS only		HS only	100%		100%	MAE1
n/a	HS only		HS only	HS only			NPY1
n/a	0%	-67%		HS only	-78%	GR only	CBR1
n/a			-28%				CBR1

20%	GR only	100%	59%	HS only		100%	MCR1
n/a	HS only	0%	HS only	HS only	HS only	HS only	ADH6
n/a	HS only	682%	HS only	576%	788%	53%	OYE2
n/a					HS only		OYE3
n/a	HS only	HS only	HS only				NCP1
n/a	HS only	HS only	HS only	550%	550%	350%	GRE3
n/a	HS only	HS only	HS only	805%	562%	520%	YDL124W
n/a	HS only	HS only	HS only				GRE2
n/a	HS only	HS only	HS only	HS only	HS only		GDH1
n/a				GR only		HS only	GDH3
n/a						GR only	NBP1
n/a	0%	-39%	0%	260%	-55%	GR only	EGD2
n/a			HS only		0%	HS only	EGD1
n/a		HS only					RPI1
n/a	GR only						PMD1
114%	0%	-52%	229%	475%	-63%	0%	NAN1
n/a	HS only	HS only	HS only	850%	688%	1150%	NTH1
n/a	HS only	HS only	HS only	HS only	HS only		NIF3
n/a	HS only	HS only	240%	HS only	HS only	HS only	PNC1
n/a	HS only		HS only	HS only	HS only	HS only	NRK1
n/a				HS only		GR only	NMA1
n/a	HS only	HS only	HS only	HS only	HS only		NPT1
n/a	HS only	HS only		HS only	HS only		BNA6
n/a	HS only	HS only	HS only	HS only	HS only		NFU1
n/a	GR only	GR only	GR only	GR only	GR only	HS only	NPR1
n/a			HS only				SNG1
n/a			GR only				NCE101
19%	-59%	63%	0%	0%	63%	-39%	NCE102
n/a	HS only			HS only			NHP6B
n/a		HS only					UPF3
n/a	HS only	HS only	HS only	HS only	HS only	HS only	ARD1
n/a		HS only	HS only				NAT1
n/a	GR only	GR only	100%	GR only		HS only	MDM20
n/a		HS only	HS only				MAK3
84%	44%	-17%	204%	130%	0%	35%	NUG1
n/a	0%	GR only	HS only		-53%		NSR1
3%	0%	-50%	-60%		0%	-67%	NUM1
n/a			HS only				NAB2
n/a			HS only	GR only			SNF4
n/a	HS only	HS only	HS only	HS only			STH1
18%	0%	-77%	-31%	93%	-40%	-68%	BFR1
n/a	HS only	HS only				HS only	NTF2
0%	100%	-50%	0%	0%	-67%	0%	NOP14
n/a	0%	HS only	0%	HS only	0%	HS only	NOC2
n/a		HS only	HS only	HS only		GR only	NOC4
n/a	HS only	100%	HS only	100%	HS only		NOC3
0%	247%	73%	0%	220%	40%	0%	NOG1

19%	33%	0%	-15%	22%	-18%	-53%	NOG2
n/a	0%	114%	200%	0%	GR only	GR only	URB1
n/a	HS only	HS only					URB2
89%	329%	77%	179%	250%	-44%	0%	NOP12
n/a	GR only	-50%	HS only		HS only		NOP13
44%	0%	-69%	188%	100%	GR only	100%	NPL3
0%	79%	0%	0%	80%	-30%	0%	NOP4
30%	135%	9%	42%	113%	17%	-18%	NOP56
42%	163%	43%	41%	115%	19%	-43%	NOP58
n/a	HS only	0%	HS only	HS only	132%	0%	NOP6
92%	40%	-14%	-17%	300%	-61%	167%	NET1
n/a	HS only	HS only	GR only	HS only		HS only	ASM4
n/a	HS only	0%	HS only	HS only	0%	HS only	GLE2
n/a			HS only				NDC1
n/a	-20%	38%	0%	HS only	-50%	GR only	NIC96
n/a	100%	GR only	100%	0%	0%	HS only	NSP1
n/a	HS only	GR only	0%		GR only	GR only	NUP100
64%	117%	-54%	78%	200%	GR only	-50%	NUP116
n/a					HS only		NUP133
n/a	0%	-60%	150%	HS only	-60%	GR only	NUP145
n/a	GR only	GR only	150%	0%	GR only		NUP157
0%	-78%	-43%	0%	100%	-71%	0%	NUP159
n/a	HS only	-67%	HS only	HS only	-33%	100%	NUP170
n/a	GR only	0%	200%	HS only	GR only		NUP188
n/a	HS only	100%	100%	HS only	GR only	GR only	NUP192
n/a		GR only	HS only				NUP2
n/a				GR only			NUP49
n/a	0%	0%	117%	0%	117%	GR only	NUP57
n/a	0%	0%	HS only		GR only	GR only	NUP60
n/a	-71%	-56%	71%	0%	0%	GR only	NUP82
43%	20%	-25%	0%	400%	0%	-87%	POM152
n/a	100%	-50%	-69%	-50%	GR only	GR only	POM34
n/a	0%	367%	0%	111%	233%		SEH1
38%	0%	34%	77%	HS only	67%	0%	YNK1
n/a				HS only	HS only		NAP1
n/a		HS only	HS only				FSP2
43%	90%	-24%	-6%	35%	-64%	-92%	YOR1
n/a	HS only	HS only	HS only	HS only	HS only		REX2
n/a	HS only	HS only	HS only	HS only	HS only		CAR2
n/a			HS only			GR only	OSM1
40%	43%	-13%	80%	40%	-50%	0%	OSH2
n/a	0%	-54%	0%	100%	GR only		OSH3
50%	0%	-68%	100%	HS only	0%	0%	OSH6
n/a	111%	20%	36%	HS only	GR only	HS only	PBP1
n/a	HS only	HS only	HS only	HS only			PBP2
n/a			HS only				PAN3
n/a	HS only			HS only			REP1

n/a	109%	HS only					REP2
n/a	-50%	650%	HS only	HS only	HS only	HS only	ARO1
n/a		HS only	HS only		HS only		MXR1
n/a			GR only			GR only	PTR2
4%	333%	333%	125%	183%	0%	117%	CPR6
n/a	0%	HS only	121%	HS only	GR only		ESS1
146%	1652%	217%	655%	683%	267%	364%	CPR1
n/a		HS only	HS only				PTH2
n/a	GR only	HS only	GR only				PWP1
n/a	57%	0%	57%	HS only	-73%		PWP2
n/a	HS only		GR only	GR only	HS only	0%	DOT5
n/a						GR only	HYR1
n/a	0%	47%	HS only	0%	78%	606%	TSA1
n/a	HS only	HS only	412%	HS only			TSA2
n/a	HS only	442%	HS only	67%	0%	121%	AHP1
n/a			HS only			GR only	SPS19
56%	HS only		111%	GR only	HS only	0%	TES1
n/a	HS only	HS only	HS only				PEX8
n/a			HS only				FOX2
n/a	HS only						PEX17
n/a			HS only				PEX11
n/a	HS only	HS only					PEX5
1%	242%	0%	-20%	175%	-37%	-21%	FAT2
n/a		GR only					PIP2
n/a	60%	-55%	340%	0%	0%	HS only	NOP7
n/a	0%	-52%			GR only	GR only	PAD1
n/a	HS only		HS only			HS only	FRS2
n/a	HS only	480%	HS only	360%	1080%		FRS1
n/a	GR only	GR only	GR only	GR only	-71%	GR only	STE2
n/a			HS only	HS only		GR only	PHM7
n/a					GR only		PEM1
1%	30%	-37%	27%	-20%	-18%	26%	NPC2
n/a						HS only	VPS34
144%	-36%	-36%	244%	56%	-64%	-44%	SLM1
n/a		GR only			GR only		SLM2
n/a					HS only		PIK1
n/a	GR only	50%	HS only	HS only	GR only	GR only	STT4
n/a	HS only	HS only	HS only	HS only			CSR1
n/a			HS only	GR only	HS only	GR only	PDR16
n/a					HS only		PDR17
n/a		HS only	HS only				ARO3
n/a	HS only	HS only			HS only		ARO4
n/a		HS only	HS only				YMR278W
n/a			HS only		HS only		PGM1
n/a	HS only	HS only	HS only	683%	508%	200%	PGM2
18%	9%	-42%	18%	42%	-46%	54%	PGK1
495%	1846%	4037%	1068%	404%	1527%	78%	GPM1

n/a		HS only	HS only	HS only	HS only		GPM2
n/a	GR only	GR only	0%	HS only	GR only	GR only	SAC1
n/a		GR only	0%			GR only	SPO14
n/a	1959%	1959%	2985%	1048%	705%	HS only	SEC53
n/a		100%		HS only	0%	GR only	ADE2
n/a	HS only	HS only		HS only			ADE6
n/a	HS only	HS only		HS only	HS only		RIM20
n/a	200%	HS only	100%	HS only	0%	HS only	TPA1
32%	48%	59%	8%	39%	36%	-57%	PMA1
n/a						GR only	FTR1
23%	7%	19%	-24%	-12%	-26%	-70%	PDR5
n/a					GR only		SNI1
n/a	HS only	HS only	HS only	HS only	HS only		PCC1
n/a			HS only				PAP1
n/a	114%	0%	HS only	HS only	0%		POP2
n/a	-71%	0%	-71%		0%	GR only	PAP2
7%	34%	-39%	-8%	384%	0%	-22%	PAB1
n/a	HS only	HS only	HS only	314%	247%	136%	PAA1
n/a	HS only	HS only					FMS1
n/a	83%	64%	-25%	0%	-67%	GR only	TPO1
n/a	HS only		HS only	HS only	HS only	HS only	TPO2
n/a	HS only	GR only	120%	HS only	0%	GR only	TPO3
n/a			HS only		GR only		TPO4
n/a				GR only			TPP1
n/a	HS only	HS only	HS only	HS only	HS only		HEM3
247%	HS only	HS only	900%	810%	550%	406%	ALD4
n/a	HS only						PAC10
n/a				HS only	HS only		GIM3
n/a	HS only	GR only	HS only	HS only			GIM5
n/a				HS only			PML1
n/a					GR only	GR only	PML39
n/a		GR only	GR only	GR only			PRP19
n/a			HS only		GR only		PRP16
n/a			HS only				PRP22
68%	-14%	0%	72%	19%	-39%	-65%	PRP43
n/a			GR only				PRP2
n/a	HS only						ISY1
n/a				HS only	GR only		RDS3
n/a					GR only		URN1
n/a	HS only	0%	HS only	HS only	0%		ESF1
n/a	HS only	GR only	0%		-52%		PNO1
n/a		HS only	HS only	HS only	0%		RIX1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	BDH2
n/a	-64%	GR only	-64%	-64%	-64%	GR only	GAS3
85%	GR only	100%	100%	0%	GR only	-69%	SLC1
n/a				HS only	HS only		NAS2
n/a	HS only	HS only		HS only			NAS6

n/a				HS only	GR only	HS only	PDH1
n/a	HS only	HS only	HS only	HS only	HS only		ACO2
n/a	HS only			HS only			YMR087W
n/a	HS only		HS only	HS only	HS only		ALT2
n/a			HS only		HS only		ALT1
n/a	0%	0%	0%	HS only			MNN10
n/a		GR only	HS only		HS only	GR only	MNN11
30%	-50%	0%	0%	400%	GR only	-60%	ECM16
n/a	GR only	GR only	HS only	GR only	-56%		DHR2
n/a		HS only	HS only	HS only	HS only		YOL057W
n/a		GR only					SNT1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	AIM45
n/a	HS only	HS only	HS only	59%			YGR207C
n/a	HS only	HS only	100%			HS only	YOR356W
n/a	HS only	HS only	HS only	HS only			SCW4
n/a	GR only	GR only			GR only		UTR2
n/a					HS only		HOS2
n/a			HS only				NIT3
229%	400%	277%	628%	1446%	HS only	170%	IMD3
n/a	GR only	GR only	GR only	HS only	61%		IMD4
n/a						GR only	ALG9
n/a	GR only	HS only	-50%	GR only			KTR3
n/a	0%	-55%	HS only	HS only	GR only	HS only	ARX1
n/a	GR only	GR only	0%		GR only	GR only	FSF1
n/a						HS only	ARH1
n/a		GR only	GR only				MSS4
n/a		0%	GR only				DNF1
n/a	100%	GR only	-75%	GR only	GR only	GR only	DNF2
n/a	HS only		HS only	HS only			AIM10
n/a	HS only	GR only	HS only	HS only			ZTA1
n/a		GR only	GR only				HSL1
n/a						GR only	KKQ8
n/a					HS only		YBR028C
n/a				HS only			YDL025C
n/a			GR only				YNR047W
n/a	HS only	HS only	HS only	HS only	HS only		YOL045W
n/a	HS only	GR only	HS only				YOL100W
n/a			HS only				BIT2
n/a	GR only						HMS1
n/a	0%	GR only	HS only	HS only	GR only	0%	STB4
n/a		GR only	GR only		GR only	GR only	AQR1
94%	109%	-24%	109%	479%	0%	-78%	PHB1
107%	195%	0%	134%	720%	120%	-80%	PHB2
n/a	GR only	GR only	-55%	GR only	GR only		LAS17
n/a			GR only				PFS1
n/a	HS only	HS only	HS only	HS only			PBA1
n/a	HS only						ADD66

n/a	HS only	HS only	HS only	HS only	936%	HS only	PRE10
n/a	HS only	HS only	HS only		HS only	HS only	PRE1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	PRE7
n/a	546%	1177%	HS only	HS only	1438%	HS only	SCL1
n/a	HS only	HS only	HS only	588%	736%	HS only	PRE2
n/a	HS only	HS only	HS only	HS only	HS only	HS only	PRE3
n/a		HS only		0%	GR only	GR only	PRE4
279%	771%	1000%	771%	149%	214%	214%	PRE5
115%	0%	59%	231%	HS only	130%	0%	PRE6
n/a	HS only	HS only					PUP1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	PUP2
n/a	HS only	HS only	HS only	63%	134%	134%	PUP3
n/a	HS only	HS only	HS only	231%	369%	HS only	PRE9
n/a	HS only	HS only	HS only	HS only	HS only	HS only	PRE8
n/a		HS only	HS only	HS only	-56%		CIC1
n/a	0%	0%	0%		GR only	GR only	AFR1
n/a		HS only		HS only			AIM2
n/a	HS only				GR only		AIR2
n/a	HS only	HS only	HS only	0%	0%	HS only	APA1
n/a	-50%	GR only	HS only			HS only	ARG5,6
n/a	0%	GR only	400%	HS only	GR only		ASK10
n/a	114%	60%	0%	HS only	0%		AST1
n/a			HS only				AST2
n/a						GR only	ATP11
n/a			HS only				ATP13
n/a			HS only				BCH2
n/a	HS only	HS only		HS only	HS only		BCP1
n/a	0%	0%	0%	HS only	0%	GR only	BFR2
n/a					HS only		BIM1
15%	HS only	GR only	88%	717%	-54%	58%	BMH1
n/a	GR only	-29%	HS only	508%		HS only	BMH2
n/a	HS only	GR only	50%		GR only		BNI1
20%	133%	43%	40%	HS only	-70%	0%	BOI1
n/a	HS only		HS only	HS only	GR only		BOI2
n/a	0%	GR only	183%	83%	GR only	HS only	BSP1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	BTN2
n/a			GR only				BUR2
n/a	HS only	HS only	100%	GR only	GR only		BZZ1
n/a						HS only	CAF130
n/a				HS only			CAJ1
n/a	-53%	GR only	-53%	HS only	HS only	GR only	CBP3
n/a	HS only	HS only	HS only	HS only	HS only		CGI121
28%	57%	0%	57%	227%	0%	0%	CMS1
n/a		HS only					CSF1
n/a	GR only						CWH43
n/a	HS only	HS only	HS only	344%	HS only	HS only	DCS2
93%	242%	438%	186%	HS only	0%	0%	MPD1

175%	200%	50%	350%	HS only	0%	0%	DOP1
n/a		HS only	HS only				DSE1
n/a			0%				EAP1
n/a		GR only			GR only		EBS1
n/a	HS only	HS only				HS only	ECM30
100%	100%	100%	200%	-50%	0%	0%	EFR3
n/a		GR only					FAF1
n/a	HS only			HS only	HS only		RAM2
n/a		GR only	HS only		GR only		FMP27
n/a	HS only	HS only	HS only	HS only	HS only	HS only	FMP52
n/a						HS only	FYV10
n/a	125%	0%	125%	HS only	0%	GR only	GCN20
n/a	HS only	HS only	HS only	55%	0%	0%	GCY1
n/a						HS only	GDS1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	GVP36
n/a	HS only	HS only		HS only	HS only		HAM1
n/a			HS only				HBT1
n/a			HS only	HS only			HGH1
n/a	HS only						HIR1
n/a				HS only			HIR2
n/a		GR only	GR only				HIT1
n/a	HS only	GR only	0%		GR only		HLJ1
n/a			GR only				IGO2
n/a			HS only				PIH1
n/a	GR only	HS only	GR only	GR only	GR only	0%	ISD11
n/a	HS only			HS only			IVY1
n/a	HS only	357%	HS only	HS only	HS only		KES1
n/a	HS only	-73%	167%	67%	GR only		PKC1
76%	27%	53%	151%	97%	-45%	0%	MCK1
n/a		GR only				HS only	SCY1
n/a	120%	0%	HS only	HS only	GR only	0%	KRI1
n/a						HS only	LDB16
n/a	-50%	0%	0%		GR only		LDB19
211%	759%	162%	421%	HS only	98%	0%	LSM12
n/a			HS only				LTV1
n/a			HS only				MAK11
n/a		HS only	HS only	HS only	HS only		MAK16
n/a		HS only	HS only				YKL162C
n/a	625%	463%	875%	388%	525%	HS only	MKT1
n/a						GR only	MLP1
n/a		GR only	HS only	HS only	GR only	HS only	MLP2
63%	HS only	713%	92%	HS only	66%	-34%	MMF1
n/a	GR only	GR only	GR only				MON2
29%	22%	22%	-15%	33%	-46%	-73%	MRH1
n/a	HS only	HS only					AIM30
n/a	HS only			HS only			MSO1
n/a	HS only						MSS18

n/a		GR only	0%	HS only	GR only		MUK1
n/a			HS only				NAM1
n/a						HS only	NAM8
n/a	HS only	GR only	GR only	HS only	GR only		NBA1
n/a			HS only		0%		NIP100
58%	0%	GR only	0%	HS only	-71%	117%	NIP29
n/a			HS only				NIS1
n/a	GR only	0%	GR only		GR only		NNF2
n/a		GR only					NSG1
n/a	HS only	HS only	HS only	HS only	HS only		NTA1
n/a	GR only		0%		GR only	GR only	NUD1
n/a	67%	-81%	24%	67%	-91%	GR only	NUF1
n/a		HS only	HS only	HS only	100%		OCA4
n/a	HS only	GR only	HS only		GR only		OPY1
n/a		0%	0%	GR only	GR only		PAM1
n/a	0%	0%	0%	HS only	HS only	GR only	PAR32
n/a	116%	-50%	0%	GR only	GR only	GR only	PBP4
n/a						HS only	PCF11
n/a					GR only		PDC2
n/a	HS only	HS only	120%	HS only			PET54
n/a	HS only	HS only	HS only	HS only	HS only	HS only	SDS22
n/a		HS only		HS only			PTC1
n/a			HS only				PTC2
n/a	HS only		HS only		HS only		CDC55
n/a	0%	GR only	240%	0%			PSP2
n/a	225%	41%	-69%	129%	GR only		PXR1
n/a					HS only	-69%	PXR1
n/a				0%	GR only		RFS1
n/a	GR only	GR only	HS only	HS only	HS only		ROD1
n/a		GR only	HS only				SCD6
21%	-64%	-73%	-41%	-12%	-69%	-82%	SCP160
119%	100%	175%	238%	69%	-41%	0%	SDA1
n/a	GR only			GR only			SDS23
n/a					HS only		SDS23
n/a	HS only		0%			GR only	SFK1
n/a						GR only	SIP3
n/a		HS only					SIP5
74%	304%	190%	208%	350%	53%	61%	SIS1
n/a			HS only				SKG3
n/a		GR only			0%		SKT5
95%	GR only	GR only	300%	GR only	-88%	110%	SLA2
n/a					HS only		SLM4
n/a	HS only			GR only			SNI2
18%	11%	-26%	-55%	0%	-62%	-92%	SNQ2
n/a	117%	-54%	HS only	HS only	0%		SOF1
7%	-82%	GR only	-36%	75%	-82%	-50%	SPA2
n/a	HS only	HS only			HS only	HS only	SPT2

n/a	HS only		0%				SPT3
n/a		HS only	HS only				SRN2
n/a			HS only	0%			SSD1
n/a			GR only				SSO1
n/a						HS only	SSO2
n/a	GR only	-26%	GR only	HS only	-53%		SST2
n/a						HS only	STB6
35%	0%	0%	0%	64%	-69%	-69%	SUR7
n/a			HS only				TEX1
n/a	-55%	0%	HS only	HS only	GR only		THO1
31%	-56%	-61%	-10%	-50%	-80%	-72%	TIF31
n/a		0%	-55%	HS only	GR only		TMA23
n/a			HS only		HS only		GOS1
n/a	225%	-28%	HS only	475%	-83%	-56%	SEC1
100%	-47%	274%	26%	42%	122%	227%	SEC13
39%	200%	174%	79%	13%	70%	0%	SEC23
15%	29%	14%	29%	150%	-31%	0%	SEC24
5%	-29%	59%	109%	14%	10%	100%	SEC31
n/a	0%	0%	0%	0%	0%	GR only	SSS1
n/a				HS only			UPS1
34%	-10%	0%	9%	74%	-38%	-60%	URA2
n/a	HS only	HS only		HS only			URE2
n/a			HS only				VAB2
n/a	HS only	GR only	HS only		HS only		WHI3
n/a		HS only	0%	HS only	HS only	HS only	WHI4
n/a			HS only				YGP1
n/a		GR only			0%	0%	YOP1
89%	HS only	126%	177%	HS only	39%	0%	YRO2
n/a	-35%	-35%	35%	0%	GR only		YSC84
n/a		GR only	GR only		GR only		YSP1
n/a					GR only	GR only	ZPS1
50%	226%	1067%	163%	HS only	589%	63%	PST2
n/a				GR only			HEM14
n/a		HS only	HS only				YJL010C
n/a	HS only		0%	HS only	GR only	HS only	PUF6
n/a	HS only	HS only	HS only	HS only	HS only		PNP1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	YNL274C
4%			108%	0%		100%	YEL020C
n/a		HS only	HS only	HS only			FAP7
n/a	HS only			HS only			YPL088W
n/a		HS only	GR only	GR only			IRC3
n/a	GR only	0%	100%	HS only	HS only	GR only	ECM32
n/a			HS only		75%	HS only	YLR419W
n/a		HS only			HS only		YDL086W
n/a				GR only	GR only		YML082W
n/a		HS only	HS only			HS only	YGR012W
n/a		HS only	HS only				INO80

n/a	HS only				HS only		INO80
n/a			HS only				YGR201C
n/a				HS only			HFD1
8%	0%	0%	-50%	HS only	-67%	-67%	FLC3
n/a	HS only	HS only	HS only	HS only	HS only	HS only	EMI2
n/a	HS only				HS only		YLR126C
n/a	HS only	0%	GR only		GR only	GR only	HOC1
n/a						HS only	YLF2
n/a		HS only	HS only	HS only			YER134C
0%	-52%	-52%	0%		0%	0%	YHM1
n/a	GR only		GR only				PET127
n/a						GR only	DET1
39%	102%	-22%	49%	533%	0%	-30%	YHR020W
n/a		GR only	HS only		GR only		AXL1
n/a						HS only	YHL018W
n/a					HS only		BUD16
n/a			HS only				YPR127W
n/a			HS only		GR only	GR only	FMP46
n/a	HS only	380%	HS only	HS only		HS only	YPR1
n/a	HS only	HS only	HS only	HS only		HS only	YLR143W
n/a	340%	180%	180%	HS only	120%	HS only	NOP2
n/a		GR only			GR only		YOR071C
n/a	HS only	HS only	HS only	HS only	HS only		YOR251C
n/a		GR only					SEF1
n/a	HS only	HS only	HS only	HS only	HS only		YKL033W-A
n/a	HS only	HS only	HS only	HS only	HS only	HS only	YOR131C
n/a	HS only	HS only	HS only	HS only	HS only	HS only	YGL039W
n/a	HS only	HS only	HS only	HS only	HS only	HS only	YGL157W
n/a			GR only		HS only	HS only	API2
n/a						GR only	YCL042W
n/a	HS only						YGR137W
n/a		HS only					YIR020W-A
n/a			GR only	GR only			YOR318C
n/a	HS only	HS only		HS only			YDR020C
63%	125%	475%	225%	350%	0%	100%	YLL029W
n/a	80%	-64%	HS only	HS only	180%	HS only	YIL108W
n/a		HS only					YLR455W
n/a					HS only		PDX3
n/a		HS only					PRO3
n/a				HS only			PYC1
379%	380%	1136%	767%	185%	165%	9%	PDC1
n/a						GR only	PDC6
0%	350%	100%	63%	HS only	HS only	63%	PDX1
56%	12%	311%	51%	17%	-15%	-61%	PDA1
90%	152%	135%	125%	68%	31%	-54%	PDB1
168%	1569%	890%	330%	465%	278%	-7%	PYK1
n/a	HS only	HS only	HS only	HS only	HS only		PYK2

93%	0%	-37%	117%	100%	-68%	-68%	QDR2	
n/a	HS only	0%	HS only	HS only	HS only	HS only	GDI1	
n/a	HS only	GR only	HS only	HS only		HS only	YRB1	
0%	HS only		250%			250%	RAS2	
19%	0%	-38%	-38%	HS only	-52%	0%	RSR1	
n/a	225%	225%	53%	HS only	GR only		RAI1	
n/a			HS only	HS only			RMI1	
n/a			GR only				RCY1	
n/a	HS only	0%	204%	108%	60%	HS only	RVS161	
n/a	100%	100%	HS only	0%	-50%	HS only	RVS167	
n/a					HS only		PRP20	
n/a		GR only					RTT103	
n/a	HS only						ADR1	
n/a						HS only	PHO2	
n/a	GR only	GR only					SIR3	
n/a	-60%	0%	HS only	HS only	GR only		SIR4	
n/a				HS only			RFA2	
n/a	HS only	HS only	HS only	HS only	HS only		RFA3	
75%	33%	50%	150%	HS only	-68%	0%	RFC1	
27%	102%	26%	-17%	293%	-64%	-70%	RFC2	
n/a	GR only	GR only	244%	HS only	GR only		RFC3	
n/a	HS only	GR only	HS only	HS only	HS only		RFC4	
n/a	0%	0%	HS only	HS only	0%	HS only	RFC5	
0%	109%	-52%	0%	-38%	-52%	0%	RTN1	
n/a	HS only		HS only	HS only		182%	RTN2	
n/a					GR only		RFX1	
n/a						GR only	RHB1	
n/a			HS only				RGD1	
n/a		GR only	HS only		150%	GR only	ROM2	
n/a	HS only	GR only	HS only		GR only		LRG1	
n/a	HS only	GR only	HS only	HS only	0%	GR only	RGD2	
n/a		GR only		HS only			RNT1	
n/a			HS only					#VALUE!
n/a	HS only		HS only				RPM2	
n/a	GR only		HS only				RPP1	
n/a						HS only	RNY1	
n/a		HS only					POP8	
n/a					HS only		RNR1	
n/a	HS only	HS only	HS only	HS only	HS only	HS only	RNR2	
n/a		HS only					RNR4	
n/a		HS only		HS only			SML1	
n/a	0%	100%	0%	HS only	HS only		PRS1	
4%	HS only	0%	-71%	120%	HS only	-79%	PRS3	
n/a		HS only	HS only	HS only	HS only		PRS5	
n/a		HS only					RKM1	
n/a	HS only	HS only		HS only			RKM3	
n/a	HS only			HS only			VAR1	

n/a	-66%	41%	0%	HS only	GR only		KRR1
n/a	0%	0%	HS only				RRP1
217%	HS only	60%	433%	120%	0%	0%	RRP12
n/a		GR only				HS only	RRP15
n/a			0%	HS only	HS only		RRP7
n/a		HS only			GR only		RRP8
0%	120%	120%	0%	HS only	0%	0%	RRP9
n/a	HS only	0%	HS only	GR only			RSA3
n/a	GR only	HS only	GR only		0%		RRB1
n/a		HS only		HS only	HS only		SQT1
n/a	HS only	HS only	HS only		HS only		RIX7
n/a	121%	121%	58%	HS only	0%	HS only	NOP15
n/a		HS only					ALB1
n/a	-63%	GR only	0%	60%	-71%	GR only	BMS1
59%	109%	109%	109%	227%	57%	227%	BRX1
n/a	GR only	HS only	GR only		HS only		ENP2
n/a	300%	0%	0%	200%	-67%	GR only	ERB1
n/a	0%	50%	HS only	HS only	0%	-50%	MAK21
n/a	HS only	HS only	HS only	HS only	HS only	HS only	NOP53
n/a	HS only	GR only		HS only	GR only		NSA2
n/a	0%	-55%	0%	HS only	GR only	GR only	RLP24
n/a				HS only	HS only		RLP7
n/a		HS only			HS only		SLX9
n/a			GR only				SSF2
n/a		HS only	HS only				UTP30
n/a				HS only	HS only		YTM1
n/a					GR only		SDO1
n/a	120%	0%	120%	HS only	-55%		RPF1
43%	30%	0%	23%	108%	-67%	-63%	SSZ1
n/a		GR only	HS only	HS only	HS only		RRF1
n/a	HS only			HS only			HRT1
n/a	GR only		-53%		222%	HS only	RCL1
68%	38%	36%	153%	0%	-14%	17%	YRA1
n/a	GR only	GR only	GR only	0%	0%	HS only	REX4
n/a					HS only		NGL2
n/a		HS only					SSU72
n/a	GR only		HS only				TFB3
n/a	HS only	HS only	HS only	HS only			NAB6
57%	114%	0%	0%	114%	0%	114%	SRO9
n/a	HS only	HS only	HS only	HS only		233%	NDI1
51%	144%	-44%	102%	46%	-32%	0%	NOP1
12%	28%	5%	9%	121%	0%	33%	RRP5
121%	114%	-35%	357%	0%	0%	114%	EBP2
n/a	GR only	HS only		HS only			FCF1
n/a				HS only	HS only		FYV7
n/a	0%	0%		HS only	GR only		UTP23
696%	391%	176%	1514%	653%	300%	122%	RVB1

n/a	HS only	0%	100%	HS only	0%		RVB2
n/a	HS only	HS only	HS only	HS only	HS only		PRD1
n/a			GR only				PEP4
n/a		GR only	HS only	0%	0%	-50%	LYS1
n/a	GR only						SAM3
192%	HS only	64%	333%	333%	56%	-50%	SAM1
n/a	GR only				HS only		SGF29
n/a	HS only	HS only	HS only	HS only	HS only	HS only	DCS1
n/a	HS only	HS only	HS only	380%	HS only	HS only	SEC14
n/a		HS only			HS only		SFB2
n/a	HS only	57%	267%	367%	GR only	HS only	SFB3
n/a					HS only		ESP1
n/a	0%	GR only	0%	HS only	0%		YJU3
14%	-19%	24%	-52%	0%	-28%	-80%	SHM2
n/a	HS only		HS only				SHM1
n/a	HS only	GR only			GR only		LCB1
n/a	HS only	-50%	0%	0%	GR only		KIN1
113%	-40%	-32%	142%	100%	-72%	-83%	AKL1
n/a	GR only	GR only	GR only				BCK1
n/a		GR only	GR only	HS only	GR only		SGV1
n/a	GR only	GR only	HS only	0%	GR only	GR only	CBK1
n/a		HS only	HS only	HS only			CHK1
n/a					0%		CLA4
n/a	35%				GR only	GR only	DBF20
n/a	0%	-33%	100%		0%		GCN2
21%	-78%	-13%	-37%	0%	-78%	-79%	GIN4
n/a			0%				HAL5
88%	100%	0%	125%	225%	0%	-50%	HRK1
n/a	HS only		HS only		GR only		KIC1
n/a	-50%	-75%	0%	-63%	-73%	GR only	KIN2
n/a	GR only	GR only	GR only		GR only		KIN4
n/a	HS only		200%	HS only	GR only	GR only	KSP1
n/a	GR only		HS only		0%	GR only	MEC1
n/a						HS only	PKH1
n/a		HS only					PKH3
n/a	GR only	GR only	HS only	HS only	100%	HS only	PTK2
n/a	HS only	HS only	HS only	HS only	HS only	HS only	RIO2
n/a			HS only				SCH9
n/a	GR only	33%	100%	HS only		GR only	TOR1
n/a	33%	0%	167%	200%	0%	GR only	TOR2
n/a			HS only				VPS15
n/a		HS only	HS only				YPK1
n/a		HS only					SIT4
181%	248%	57%	315%	315%	0%	-46%	GLC7
n/a					HS only		PPH21
n/a		HS only					PPH22
n/a	HS only	-44%	HS only	HS only	GR only	HS only	PPZ1

n/a					HS only		TYE7
0%	HS only	0%	100%	HS only	200%	100%	SES1
74%	103%	0%	115%	367%	19%	-33%	SHS1
n/a	HS only	HS only	HS only	HS only	HS only		YJL068C
n/a			HS only	GR only			SRP101
n/a	HS only	HS only		HS only			SRP54
n/a					HS only		SRP68
n/a			HS only				SRP72
n/a	114%	-53%	114%	114%	HS only	HS only	GBP2
n/a	125%	HS only	GR only	HS only	125%	HS only	RIM1
n/a		GR only					PDS5
n/a		HS only	HS only	HS only	HS only		SAR1
n/a		HS only		HS only			SGT2
n/a		HS only					SME1
n/a		GR only					SMD1
n/a	0%	0%	0%	HS only		GR only	SMD2
n/a	HS only		0%	HS only		GR only	SMD3
n/a		GR only			GR only		SMB1
n/a	122%	0%	HS only	HS only	GR only		LSM1
n/a		GR only		HS only			ENA1
n/a						GR only	ENA2
n/a	100%	-69%	0%		100%		SAS10
n/a		GR only			GR only		SAS4
n/a		GR only	0%		GR only		SAS5
n/a		HS only					MVP1
n/a	115%	GR only	0%	HS only	-53%	GR only	SNX3
n/a	HS only	HS only	HS only	HS only	HS only	HS only	SPE3
n/a	HS only	HS only		HS only	HS only		LCB4
n/a			GR only				LCB5
65%	HS only	242%	184%	340%	0%	54%	LSP1
25%	691%	949%	351%	691%	243%	400%	PIL1
n/a			0%				DPL1
29%	-28%	-28%	-22%	388%	-71%	-79%	SPC42
n/a			HS only				RMD1
n/a	HS only	HS only	HS only				RMD8
n/a					HS only		SPO73
n/a				HS only			SPO77
n/a	GR only						SPG5
n/a		HS only		HS only	0%	0%	ERG6
n/a		GR only			HS only	HS only	SUT1
50%	67%	167%	167%	HS only	167%	67%	SMC1
n/a	HS only		HS only				SMC2
n/a	60%	-60%	300%	HS only	-75%		SMC3
n/a	GR only		0%		GR only		SMC4
n/a			HS only				SMC6
n/a		HS only		HS only	GR only		RAD27
n/a	HS only	GR only	HS only	HS only	100%	HS only	SVL3

n/a						HS only	YJL045W
n/a	HS only	HS only	HS only	340%	60%	GR only	SDH1
n/a	HS only	HS only	HS only	108%			SDH2
n/a						HS only	SCY_1267
n/a				GR only			EMI5
n/a	HS only	HS only	HS only	HS only	HS only		UGA2
n/a	HS only	HS only	HS only	HS only	HS only	120%	LSC1
n/a	HS only		HS only	HS only			LSC2
n/a					HS only		MET3
n/a	HS only	HS only		GR only		HS only	SKI3
n/a	0%	130%	130%	0%	GR only	GR only	SOD1
n/a	HS only	HS only	HS only	114%	0%	400%	SOD2
n/a	HS only	GR only					SGD1
n/a	HS only		HS only	HS only	HS only		SUM1
75%	-75%	0%	150%		GR only	300%	SYP1
n/a	HS only			HS only			MPT5
n/a	61%	0%	0%	222%	-38%	HS only	SRP40
138%	383%	-79%	277%	0%	0%	0%	STM1
298%	HS only	HS only	655%	HS only		59%	FMP45
107%	0%	0%	214%	HS only	0%	0%	HSV2
n/a			HS only				SNF5
n/a				HS only			YOR338W
n/a				HS only			SWC3
n/a			HS only			HS only	SWC4
n/a	-67%	25%	-50%	HS only	0%	GR only	KOG1
46%	50%	-67%	42%		-33%	-50%	TCO89
n/a		GR only	HS only		GR only		AVO1
n/a	0%	GR only	GR only			0%	AVO2
25%	-50%	0%	-50%	HS only	-50%	0%	LST8
n/a			HS only			HS only	MOT1
n/a	0%	HS only	HS only				SPT15
n/a		HS only	HS only				YTA7
n/a	108%	0%	HS only	HS only	HS only		CCT2
58%	0%	-26%	54%	HS only	-52%	-63%	CCT4
n/a	HS only	317%		HS only	HS only		CCT5
n/a	HS only	GR only		HS only	GR only		CCT3
67%	78%	25%	233%	HS only	-28%	100%	CCT8
n/a		0%		HS only	HS only		CCT6
n/a			GR only			HS only	EST2
n/a		GR only					RIF1
n/a					HS only		TIP1
n/a						HS only	THI6
n/a					GR only		THI7
n/a			GR only				THI72
n/a	HS only	HS only	HS only	345%	HS only	HS only	TRR1
n/a			HS only			HS only	TRX3
n/a	HS only		HS only				THO2

n/a			HS only				SRY1
65%	133%	33%	92%	268%	65%	-38%	ILV1
n/a	HS only	HS only	HS only	600%	350%	HS only	THS1
n/a			HS only	HS only			MST1
n/a		HS only			HS only		TMP1
n/a					GR only	GR only	TOF2
n/a	HS only	HS only	HS only	HS only	HS only		RAF1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	NQM1
175%	HS only	HS only	350%	HS only	HS only	0%	TAL1
n/a					GR only		MIG3
n/a	HS only	GR only	HS only	240%	-79%		DST1
0%	-67%	-58%	0%	233%	-71%	0%	SPT5
n/a					GR only		IWS1
n/a	HS only	HS only					PDR1
n/a	HS only						TFC3
n/a	HS only	HS only	HS only				TFC7
n/a			HS only		HS only	HS only	TOA2
n/a		GR only	0%		GR only	GR only	SUA7
n/a	HS only	HS only	HS only			GR only	TAF1
n/a		HS only		HS only			TAF11
n/a			GR only				TAF4
n/a	HS only	117%	-54%	HS only	233%		TAF6
n/a	HS only	HS only		HS only			TAF9
n/a		HS only					SNF2
n/a	GR only	GR only	GR only	HS only	GR only		MOT3
n/a	HS only	-53%	HS only	HS only	0%	GR only	ADA2
n/a	HS only	HS only	HS only	HS only	HS only	HS only	WTM1
n/a				HS only			WTM2
n/a		HS only					ASH1
n/a	0%				GR only		DOT6
n/a			HS only	HS only			GAT1
n/a				HS only			RXT2
n/a		HS only					RXT3
n/a					HS only		UME1
n/a			HS only				OPI1
n/a	HS only	-50%	100%		GR only		TRA1
n/a	HS only	HS only	HS only	HS only	HS only	HS only	SCP1
n/a	HS only	680%	HS only	HS only	HS only	HS only	TKL1
n/a	HS only	HS only	HS only	200%	HS only	HS only	TKL2
n/a	HS only	HS only	HS only	HS only	HS only		GCN3
n/a	HS only		HS only	HS only	-56%		GCD7
n/a	HS only			HS only			GCD2
n/a		HS only	HS only				GCD1
n/a	0%	-26%	-11%	152%	-83%	GR only	RLI1
n/a	HS only	HS only					TMA10
n/a		0%	0%	HS only	HS only		TMA20
n/a	GR only		0%		GR only		TMA22

n/a	-37%	0%	0%	HS only	GR only	GR only	TMA46
n/a	HS only	HS only	GR only	HS only	GR only		TMA7
n/a			100%				GCN1
315%	425%	144%	630%	630%	0%	0%	TMA19
n/a	HS only	GR only	HS only				SEC62
n/a		HS only					SEC72
n/a		HS only					TMN2
n/a	0%	0%	HS only	HS only	GR only		TRS120
n/a		GR only					TRS130
n/a	HS only		HS only				TRS20
n/a	0%	112%	0%	0%	0%	GR only	BET3
n/a				113%		HS only	TRS23
n/a	HS only	GR only	0%	HS only	0%	GR only	TRS31
n/a	HS only		HS only				TRS33
n/a		HS only			GR only		TY1A-A
n/a		HS only	GR only	HS only	HS only		TY1B-BL
n/a	GR only	GR only	HS only		GR only		TY1A-BR
n/a		HS only		HS only	HS only		TY1A-DR1
n/a		GR only					TY1B-DR1
n/a						GR only	TY1A-DR2
n/a	HS only						TY1A-DR3
n/a	HS only					HS only	TY1B-DR3
n/a			GR only				TY1A-DR6
n/a	43%				GR only	GR only	TY1B-GR2
n/a			GR only	HS only		HS only	TY1A-JR2
n/a		GR only	HS only				TY1B-JR2
n/a						HS only	TY1B-ML1
n/a			GR only	GR only		GR only	TY1B-MR2
n/a		GR only				HS only	TY1A-NL1
n/a	39%		HS only	GR only	GR only		TY1B-NL1
n/a				HS only	HS only		TY1A-NL2
n/a	10%	GR only	HS only	GR only	GR only	-10%	TY1A-OL
n/a		HS only	GR only	HS only	HS only		TY1B-OL
n/a			HS only				TY1B-PR2
n/a	GR only	GR only			GR only	GR only	TY1B-PR3
n/a	HS only	HS only			HS only		TY2A-B
n/a		HS only	0%	59%			TY2B-B
n/a						HS only	TY2A-DR1
n/a	GR only	GR only			GR only	GR only	TY2B-DR3
n/a	HS only						TY2B-F
n/a					HS only		TY2B-GR1
n/a		GR only					TY3B-I
n/a					HS only		TY4B-J
n/a	HS only	HS only			HS only		TPS3
433%	HS only	HS only	2267%	200%	717%	1400%	TSL1
n/a	HS only	HS only	1933%	800%	667%	HS only	TPS2
3%	0%	-40%	60%	GR only	GR only	67%	TCB1

n/a	0%	67%	67%		GR only		TCB2
33%	20%	-46%	67%	150%	-48%	0%	TCB3
n/a						GR only	TGS1
70%	1164%	115%	397%	HS only	641%	536%	TPI1
n/a				HS only			TRM82
n/a			HS only				TRM82
n/a	HS only	HS only	HS only	114%	HS only		TPT1
n/a						HS only	RIT1
n/a	GR only	GR only	GR only			GR only	TYW1
n/a			HS only	HS only			TRM12
n/a		HS only	HS only	HS only	HS only		DUS3
n/a						HS only	TAD1
n/a	HS only	HS only	HS only	244%	400%	HS only	TRP5
n/a	229%	HS only	HS only	HS only	GR only		WRS1
n/a					HS only		MSW1
179%	GR only	HS only	357%		-53%	0%	TUB1
n/a	HS only	GR only		HS only			TUB3
n/a	114%	229%	229%	229%	-53%	GR only	TUB2
n/a		GR only			HS only		PTP3
58%	100%	-33%	50%	HS only	-50%	-67%	CDC14
n/a			HS only		HS only	HS only	YVH1
n/a	HS only	238%	HS only	HS only	HS only		TYS1
n/a	HS only		HS only				MSY1
n/a		HS only	HS only	HS only			HSH155
n/a	112%	-53%	0%	112%	-53%	GR only	IMP3
n/a	0%	109%	0%	0%	0%	HS only	IMP4
52%	86%	0%	44%	HS only	-36%	-60%	UTP10
n/a		GR only	GR only		GR only		UTP11
n/a		GR only	HS only				DIP2
n/a	GR only	200%	GR only	0%	GR only		UTP13
n/a		HS only				GR only	UTP14
18%	54%	54%	0%	-35%	117%	-35%	UTP15
0%	-55%	0%	0%	HS only		0%	UTP18
n/a		GR only	HS only				UTP20
n/a		133%	133%	0%	HS only	GR only	UTP21
50%	25%	-32%	16%	100%	-48%	-84%	UTP22
n/a	175%	HS only	63%	HS only	0%	HS only	UTP4
n/a					HS only		UTP5
n/a	0%	GR only	100%	HS only	-50%	GR only	UTP6
n/a	317%	0%	167%	78%	-76%	HS only	UTP7
n/a	-36%	-56%	0%	375%	0%	GR only	UTP8
n/a	500%	-35%	HS only	HS only	GR only	GR only	UTP9
120%	0%	-35%	240%	HS only	-35%	0%	MPP10
n/a	HS only			HS only			LSM2
n/a	HS only	HS only	HS only	HS only			LSM3
n/a	0%	HS only		HS only	-54%		LSM4
n/a	HS only	0%	HS only	HS only	0%	HS only	LSM5

n/a	624%	0%	0%	HS only			LSM6
n/a	0%	0%	0%	HS only		GR only	LSM7
n/a			GR only				COQ5
n/a	HS only				HS only		COQ6
n/a		GR only					UBP10
n/a		HS only					UBP15
22%	-17%	-26%	17%	-57%	-63%	-27%	UBP3
n/a		HS only					UBP5
n/a	GR only	0%	GR only	HS only	0%	GR only	UBP7
n/a	HS only	HS only		HS only	HS only		YUH1
n/a	-70%	GR only	HS only	HS only	GR only	HS only	BUL1
n/a	HS only	-30%	0%	HS only	0%	GR only	BUL2
72%	357%	212%	68%	0%	0%	-76%	UBI1
n/a		100%	HS only	HS only		HS only	UBA1
n/a			HS only	HS only			UBC7
n/a	0%	GR only	0%	0%			MDY2
n/a	HS only	133%	HS only	HS only	HS only	HS only	SMT3
n/a	GR only		GR only				ULP1
n/a	0%	-70%	483%		HS only	GR only	BRE5
n/a	HS only	HS only	HS only	HS only			UBX4
n/a	HS only	HS only	HS only				UBX6
n/a			HS only				UAP1
n/a					GR only		ALG7
n/a	HS only	HS only	HS only		HS only		YDR061W
n/a		HS only	HS only	HS only	GR only	HS only	YNR070W
n/a			HS only			HS only	YOL075C/YOL074C
n/a				GR only			FUN30
n/a		GR only			GR only	GR only	YHR031C
n/a				GR only			YLR247C
n/a	0%	0%	0%	0%	HS only	HS only	YAL044W-A
n/a		HS only	HS only				YJR015W
n/a	HS only	HS only	HS only	HS only			YBR056W
257%	1022%	737%	592%	1048%	269%	78%	OLA1
n/a	HS only	HS only	HS only	HS only	HS only		YGR173W
n/a		GR only	HS only				YGR210C
n/a	HS only		HS only		GR only		YDL133W
n/a	HS only	GR only		HS only	GR only	GR only	YOL019W
n/a				HS only			YPL041C
n/a	HS only			HS only	HS only	HS only	YIL064W
n/a	HS only	HS only	HS only	HS only	-52%		FMP41
n/a		HS only					Q0255
n/a	HS only						YNL260C
n/a	HS only	HS only	HS only	179%	0%	329%	YHL021C
n/a				HS only			YIR036C
n/a	HS only	HS only	HS only	HS only	HS only	HS only	YJR096W
n/a		HS only					YKL071W
n/a	HS only	HS only	HS only	HS only	HS only	HS only	YMR226C

n/a	HS only		HS only	HS only	HS only		YFR006W
138%	0%	-69%	225%	HS only	GR only	-50%	YPR091C
n/a	HS only		HS only				YPR115W
n/a	HS only	HS only	HS only	HS only	HS only	HS only	YNL010W
n/a					HS only	HS only	YNL194C
n/a			HS only	HS only			IRC10
n/a						HS only	JIP4
n/a	HS only	HS only	HS only	HS only	HS only		MRP8
n/a	HS only	GR only	GR only	GR only	GR only	GR only	RSN1
n/a		GR only	0%		GR only	GR only	YBL086C
n/a		HS only					YBL095W
n/a		GR only					YBR108W
n/a	HS only						YBR191W-A
n/a		HS only					YBR225W
n/a			HS only				YBR246W
n/a					HS only		YBR259W
n/a				HS only	HS only		YBR271W
n/a			GR only		HS only		YCR016W
n/a		0%	HS only		GR only		YDL012C
n/a	HS only	HS only	GR only	HS only	HS only	GR only	YDL144C
n/a	-54%	-54%	383%	HS only	GR only		YDR348C
n/a		HS only		HS only	HS only	HS only	YDR391C
n/a				0%			YEL007W
n/a						GR only	YEL043W
n/a			HS only				YER137C
n/a		HS only					YER041W
n/a		HS only	HS only	HS only			YER080W
n/a	HS only	0%	113%				YGL082W
n/a		HS only					YGR110W
n/a	HS only			HS only	HS only		YGR117C
n/a	HS only	HS only	HS only	HS only			YGR127W
n/a	HS only		GR only				YGR130C
n/a		HS only	0%		HS only		YGR203W
n/a			HS only	HS only			YGR266W
n/a		GR only	HS only	HS only	GR only		YGR283C
n/a			HS only	HS only		GR only	YHR080C
n/a	HS only	61%	0%	HS only	GR only	HS only	YHR097C
n/a	577%	33%	91%	203%	-42%	GR only	YHR127W
n/a		0%	0%				YHR146W
n/a	HS only	HS only	HS only	HS only			YHR209W
n/a	GR only	GR only	0%	GR only	-69%		YIL091C
n/a				HS only			YIL127C
n/a	GR only	GR only	33%		GR only	GR only	YIR003W
0%	HS only	0%	0%	HS only	0%	0%	YJL133C-A
0%	HS only	0%	-53%	-53%	113%	-53%	YJL171C
n/a	HS only			HS only			YJL217W
n/a	HS only		HS only	GR only	HS only	0%	YJR046W

n/a			HS only		GR only		YJR111C
n/a		HS only		HS only	HS only		YJR142W
n/a	GR only	0%	GR only	GR only	GR only		YKL054C
n/a			GR only				YKL070W
n/a	HS only	0%	HS only	HS only	GR only	HS only	YKL077W
n/a	HS only		HS only				YKL098W
n/a		0%	0%		GR only		YKL105C
n/a		HS only	HS only		109%		YKL128C
n/a	HS only						YKL130C
n/a		HS only	HS only	HS only			YKL151C
n/a	HS only	HS only	HS only	HS only			YKL215C
n/a	HS only	HS only	HS only	HS only			YKR011C
n/a	HS only					GR only	YKR023W
n/a	HS only	HS only	HS only	HS only	HS only		YKR043C
n/a	0%	0%	111%	HS only	GR only	GR only	YKR070W
n/a	HS only	0%	HS only	HS only	HS only		YLR104W
n/a				HS only			YLR149C
n/a				0%			YLR177W
n/a			HS only				YLR179C
n/a	HS only	HS only	HS only	HS only	HS only	HS only	YLR301W
n/a	GR only		GR only			HS only	YLR361C-A
n/a			HS only				YLR392C
n/a		HS only		HS only	HS only		YLR460C
n/a				HS only			YML020W
n/a					GR only		YML050W
n/a			HS only				YML079W
n/a	111%	GR only	GR only	HS only		GR only	YML119W
n/a		GR only	GR only	HS only	HS only		YMR003W
13%	300%	-50%	75%	425%	-25%	100%	YMR031C
n/a	133%	0%	43%	0%	GR only	HS only	YMR086W
n/a						HS only	YMR098C
n/a						HS only	YMR124W
n/a	HS only	HS only	HS only	HS only	HS only		YMR152W
n/a			GR only				YMR157C
n/a	HS only			HS only	HS only	0%	YMR178W
n/a		HS only	HS only	HS only	0%		YMR196W
n/a				HS only			YMR244C-A
n/a						HS only	YMR258C
n/a			HS only	HS only			YMR262W
n/a	57%	110%	-52%	HS only	0%		YMR310C
294%	533%	1078%	533%	378%	185%	-55%	YMR315W
n/a			GR only				YMR317W
n/a	0%	GR only		HS only	GR only		YNL022C
n/a	HS only	HS only	HS only		HS only		YNL108C
n/a	HS only	HS only	HS only	HS only	HS only	HS only	YNL134C
n/a				HS only			YNL181W
n/a				HS only			YNL193W

n/a		HS only	HS only	0%		0%	YNL200C
36%	122%	122%	0%	65%	-39%	-73%	YNL208W
n/a	HS only	HS only	HS only	HS only	HS only		YNL313C
n/a	HS only	HS only	HS only	HS only	HS only		YOL022C
n/a			HS only				YOL083W
n/a		HS only					YOL086W-A
n/a	HS only	HS only	HS only	113%	175%	0%	YOR051C
n/a			GR only				YOR112W
83%	HS only	GR only	167%	GR only	GR only	0%	YOR227W
n/a	HS only		HS only	HS only	HS only		YOR289W
n/a	GR only		HS only				YOR304C-A
n/a	GR only	HS only	0%	HS only	GR only	GR only	YOR316C-A
n/a		HS only					YPL034W
n/a	HS only	GR only			GR only		YPL245W
n/a	HS only						YPR074W-A
n/a	HS only	HS only	HS only	325%	325%		YGR250C
n/a	120%	HS only	HS only	HS only	HS only		YPL184C
n/a						HS only	TBS1
n/a	0%		0%	0%			YKR064W
n/a		GR only					ESBP6
n/a			HS only				YOL087C
n/a			HS only				FMP40
n/a					HS only		YKL069W
n/a		GR only					YGR021W
n/a		HS only					YJR008W
59%	HS only		118%		GR only	0%	YLL023C
n/a	HS only	GR only	HS only	HS only	0%	GR only	YLR064W
n/a	HS only						YER156C
57%	0%	-60%	33%	156%	-74%	-81%	KRE33
n/a	HS only	HS only	HS only	HS only	HS only	HS only	YBR137W
n/a			0%				YCL057C-A
n/a			HS only		HS only		YPL225W
n/a		GR only					YOR287C
n/a	HS only						YCR090C
n/a		GR only	HS only	0%	GR only		YBL028C
n/a			HS only				YGL250W
n/a					HS only		YCL047C
n/a		HS only					YBR141C
n/a	HS only	HS only		HS only			YDR161W
n/a		HS only					YPR045C
n/a	HS only	HS only	HS only	HS only	HS only		YHR009C
n/a	HS only	-50%	HS only	HS only	GR only		YNR021W
n/a		GR only					YKR021W
27%	119%	0%	0%	0%	-81%	-54%	YCR087C-A
n/a	HS only	HS only	HS only	0%	0%	0%	FUR1
n/a		HS only					HEM12
n/a	HS only	HS only		HS only	HS only	HS only	HEM4

83%	123%	344%	212%	212%	329%	46%	UGP1
n/a	0%	GR only	GR only	GR only	GR only	HS only	ATH1
n/a	HS only	783%	HS only	HS only	350%	GR only	APE1
n/a	HS only						VMA22
n/a		HS only		HS only	HS only		VID30
n/a			HS only				PEP3
n/a	333%	100%	167%	200%	-50%	GR only	PEP5
n/a		HS only	HS only		HS only	GR only	IML1
n/a	GR only						VAM7
n/a	HS only	-67%	0%	HS only	GR only	GR only	VAC8
133%	290%	87%	224%	124%	-40%	-42%	VPS1
n/a		HS only	HS only				VPS13
n/a		HS only	GR only	HS only			VPS20
n/a	HS only						VPS21
n/a		HS only	0%				VPS26
n/a	0%	108%	0%	HS only	HS only	HS only	VPS29
n/a			HS only	GR only			VPS3
n/a	GR only						VPS30
n/a	HS only	0%		HS only	GR only		VPS33
n/a	HS only	GR only	HS only	HS only	133%	HS only	VPS35
n/a	GR only	GR only					VPS41
n/a	HS only						VPS5
n/a			HS only			0%	VPS54
n/a					HS only		VPS66
n/a	HS only	0%	HS only	HS only	HS only		DID2
n/a	HS only	0%		GR only		GR only	VTC2
n/a	HS only	0%	HS only	0%	0%	0%	SNF7
n/a		HS only					SNF8
n/a	120%	0%	GR only	120%	-69%	GR only	VAP1
n/a	HS only	HS only	HS only	HS only	HS only		VAS1
n/a	GR only	GR only	0%		GR only		VRP1
n/a				HS only			FAT1
64%	0%	0%	128%	-52%	-52%	0%	SCS2
46%	-54%	-60%	0%	HS only	-80%	-92%	SEC18
15%	226%	219%	321%	242%	275%	292%	TFP1
n/a	50%	GR only	500%	HS only	GR only	GR only	VPH1
640%	2008%	563%	1515%	293%	269%	234%	VMA2
n/a	HS only		HS only	HS only	HS only		VMA5
n/a	HS only	HS only	HS only	HS only	HS only	HS only	VMA6
n/a	HS only	-54%	0%	HS only		GR only	VMA8
n/a					HS only		VMA4
n/a			HS only				VMA10
n/a	0%			HS only	0%	GR only	YBL104C/YBL103C-A
n/a						HS only	YCR072C
50%		GR only	100%	HS only	HS only	0%	YMR102C
n/a			HS only		HS only		YPL247C
n/a		HS only					YFL010C

n/a		GR only			GR only		YRF1-1
n/a			GR only			GR only	YRF1-3
n/a		HS only					YBP2
76%	-40%	445%	270%	118%	-40%	118%	GIS2
n/a					HS only		RME1
n/a		HS only	HS only				RTS2
n/a	HS only			HS only	GR only		SFP1
n/a	HS only	GR only	HS only		GR only	HS only	STP3
n/a					GR only		YPR022C
n/a	GR only	0%	60%	HS only	0%	GR only	ZUO1

Average emPAI value						Response to Heat Shock			
Growth			Heat Shock			Fold Increase			Stan
Wildtype	**Knockout**	**Mutant**	**Wildtype**	**Knockout**	**Mutant**	**Wildtype**	**Knockout**	**Mutant**	**Wildtype**
0.13	0.205	0.13	1.37	1.08	0.56	10.54	5.27	4.31	3.15
0	0	0	1.37	0.85	0	HS Only	HS Only		
0	0	0	0.09	0.18	0.135	HS Only	HS Only	HS Only	
0.41	0.66	0.285	0.3	0.385	0.41	0.73	0.58	1.44	0.72
0.28	0.23	0.28	0.455	0.33	0.675	1.63	1.43	2.41	
0.08	0.13	0.28	0.13	0.14	0.14	1.63	1.08	0.50	0.18
0	0	0	0	0.07	0		HS Only		
0.38	0.38	0.505	0.34	0.225	0.265	0.89	0.59	0.52	0.17
0.145	0.31	0.31	0.14	0.105	0.14	0.97	0.34	0.45	0.96
0	0	0.065	0.445	0.355	0.48	HS Only	HS Only	7.38	
0	0.565	0.34	0.565	0.34	0.79	HS Only	0.60	2.32	
0	0	0.33	0	0.33	0.76		HS Only	2.30	
1.15	0.86	0.63	1.75	1.67	1.75	1.52	1.94	2.78	0.20
0.07	0	0	0.07	0	0.07	1.00		HS Only	
0	0	0	0.07	0	0.15	HS Only		HS Only	
0	0.15	0.07	0.15	0.155	0.15	HS Only	1.03	2.14	
0	0	0	0.195	0.33	0.15	HS Only	HS Only	HS Only	
0.14	0.39	0	0.305	0.49	0.48	2.18	1.26	HS Only	0.86
0	0.08	0	0.41	0.26	0.26	HS Only	3.25	HS Only	
0	0	0	0.15	0.23	0.07	HS Only	HS Only	HS Only	
0.03	0	0.03	0.03	0.03	0.03	1.00	HS Only	1.00	
0	0	0	0.285	0.57	0.22	HS Only	HS Only	HS Only	
0	0	0	0	0.21	0		HS Only		
0.03	0.03	0.03	0.03	0.03	0.03	1.00	1.00	1.00	
0	0	0	0	0.07	0		HS Only		
0	0.09	0	0.09	0.145	0.2	HS Only	1.61	HS Only	
0	0	0	0.08	0.08	0.08	HS Only	HS Only	HS Only	
0	0	0	0.29	0.13	0	HS Only	HS Only		
0	0	0	0	0.08	0.11		HS Only	HS Only	
0	0	0	0.135	0	0	HS Only			
0.03	0	0.03	0.06	0.065	0.095	2.00	HS Only	3.17	
0	0	0	0.16	0.16	0.16	HS Only	HS Only	HS Only	
0.09	0	0	0.09	0.135	0.135	1.00	HS Only	HS Only	
0	0.1	0	0.52	0.74	0.75	HS Only	7.40	HS Only	
0	0.1	0.1	0.265	0.265	0.21	HS Only	2.65	2.10	
0	0	0	0.09	0	0.09	HS Only		HS Only	
0.25	0	0.25	0.405	0.405	0.405	1.62	HS Only	1.62	0.88
0	0	0	0.455	0.28	0.63	HS Only	HS Only	HS Only	
0.08	0.08	0.08	0.08	0.17	0.17	1.00	2.13	2.13	
0	0.09	0.09	0.09	0.19	0.3	HS Only	2.11	3.33	
0	0	0	0.06	0.06	0.095	HS Only	HS Only	HS Only	
0	0	0	0.1	0.1	0.1	HS Only	HS Only	HS Only	
0.09	0	0	0	0	0	0.00			

0	0	0	0.16	0.25	0.16	HS Only	HS Only	HS Only	
0.22	0.22	0.22	0	0.22	0	0.00	1.00	0.00	
0	0	0.13	0.29	0.28	0.205	HS Only	HS Only	1.58	
0	0.15	0	0.15	0.335	0.15	HS Only	2.23	HS Only	
0	0.37	0.37	0.37	0.37	0.37	HS Only	1.00	1.00	
0	0.06	0	0.13	0.13	0.06	HS Only	2.17	HS Only	
0	0	0	0	0.1	0		HS Only		
0	0	0	0	0.12	0.12		HS Only	HS Only	
0	0	0	0.12	0.185	0.12	HS Only	HS Only	HS Only	
0	0.11	0	0.17	0.17	0.51	HS Only	1.55	HS Only	
0	0.09	0	0.09	0	0.09	HS Only	0.00	HS Only	
0	0	0	0.22	0.28	0.22	HS Only	HS Only	HS Only	
0	0	0	0.205	0.28	0	HS Only	HS Only		
0	0	0	0.815	0.47	0.47	HS Only	HS Only	HS Only	
0	0.11	0	0.11	0.11	0.11	HS Only	1.00	HS Only	
0.23	0.23	0.23	0.23	0.23	0.23	1.00	1.00	1.00	
0	0	0	0.03	0	0	HS Only			
0.03	0	0.03	0.03	0.03	0	1.00	HS Only	0.00	
0	0	0	0	0.18	0		HS Only		
0	0	0	0	0.06	0		HS Only		
0	0	0	0.22	0.04	0	HS Only	HS Only		
0	0.14	0.245	0	2.325	1.295		16.61	5.29	
0.09	0	0.09	0.09	0.09	0.09	1.00	HS Only	1.00	
0.09	0.09	0.09	0	0.09	0	0.00	1.00	0.00	
0.63	0	0.64	0	0	0.63	0.00		0.98	
0.44	0.64	0	1.35	1.505	1.08	3.07	2.35	HS Only	
1.065	3.205	7.255	2.79	5.015	6.98	2.62	1.56	0.96	8.13
5.775	8.72	11.6	3.64	4.03	5.42	0.63	0.46	0.47	0.02
1.67	1.38	2.025	1.96	3.025	2.24	1.17	2.19	1.11	0.30
4.61	4.4	7.81	2.635	3.43	3.43	0.57	0.78	0.44	0.20
38.3	0	0	16.725	21.295	19.58	0.44	HS Only	HS Only	
59.36	27.805	42.175	0	0	0	0.00	0.00	0.00	
4.225	4.495	5.445	3.1	2.11	3.1	0.73	0.47	0.57	0.57
6.465	5.83	6.465	7.435	5.83	6.465	1.15	1.00	1.00	0.59
16.705	16.705	28.95	13.315	20.375	14.495	0.80	1.22	0.50	0.26
7.985	11.38	13.52	11.685	8.51	12.335	1.46	0.75	0.91	0.78
1.375	5.83	3.895	2.55	2.965	2.625	1.85	0.51	0.67	1.08
11.74	17.7	28.665	7.025	8.035	11.405	0.60	0.45	0.40	0.65
10.31	19.02	34.645	6.125	7.135	7.915	0.59	0.38	0.23	0.66
1.895	2.7	6.33	1.89	1.665	1.665	1.00	0.62	0.26	0.91
6.74	7.66	10.33	7.185	13.405	6.74	1.07	1.75	0.65	0.81
3.01	13.44	9.925	6.41	20.29	0.95	2.13	1.51	0.10	1.58
1.72	9.34	6.41	6.41	20.29	7.195	3.73	2.17	1.12	
11.575	18.33	98.11	9.01	9.01	21.935	0.78	0.49	0.22	0.58
0.915	0.52	1.58	0.88	0.88	0.375	0.96	1.69	0.24	0.72
6.14	8.96	8.96	6.31	4.875	8.09	1.03	0.54	0.90	0.36
5.05	3.59	4.42	4.42	2.485	4.42	0.88	0.69	1.00	0.63

0.63	1.345	2.41	2.04	1.82	0	3.24	1.35	0.00	
1.69	0	2.45	0	0	2.55	0.00		1.04	
7.565	6.55	11.83	5.605	3.3	4.95	0.74	0.50	0.42	0.23
3.495	18.34	11.67	10.45	36.305	24.255	2.99	1.98	2.08	2.22
2.56	0	27.875	18.34	36.305	44.08	7.16	HS Only	1.58	
4.405	1.095	2.365	0.61	1.095	0.61	0.14	1.00	0.26	
1.54	0.6	1.54	0	0.6	1.54	0.00	1.00	1.00	
4.78	4.495	6.35	3.395	2.4	3.47	0.71	0.53	0.55	0.16
24.2	38.4	44.85	17.75	10.99	11.66	0.73	0.29	0.26	0.86
0.78	9.045	2.28	4.745	2.06	1.585	6.08	0.23	0.70	12.46
2.2	3.34	9.86	2.81	4.21	5.42	1.28	1.26	0.55	0.82
0.855	0.855	1.435	0.855	1.435	0.71	1.00	1.68	0.49	0.00
14.94	19.99	52.89	8.315	9.065	8.135	0.56	0.45	0.15	0.10
3.44	5.63	5.225	2.5	4.025	4.67	0.73	0.71	0.89	0.11
2.245	7.515	8.56	2.5	2.54	4.195	1.11	0.34	0.49	0.18
2.715	2.125	5.805	2.335	2.715	2.56	0.86	1.28	0.44	0.28
1.92	2.715	4.03	1.89	2.36	5.15	0.98	0.87	1.28	0.34
0	0	0	0	2.93	1.49		HS Only	HS Only	
0.07	0.07	0	0.805	0.7	0.305	11.50	10.00	HS Only	
0	0	0	0	0.1	0.1		HS Only	HS Only	
0.09	0.195	0.125	0.195	0.205	0.325	2.17	1.05	2.60	0.05
0.03	0.045	0.06	0.06	0	0	2.00	0.00	0.00	
0	0.19	0.71	1.39	0.55	1.13	HS Only	2.89	1.59	
0	0	0	0.185	0.12	0.12	HS Only	HS Only	HS Only	
0	0	0	0	0.13	0.13		HS Only	HS Only	
0.18	0.18	0.18	0.18	0.18	0.18	1.00	1.00	1.00	0.00
0	0	0.12	0	0	0			0.00	
0	0	0	0	0.13	0.13		HS Only	HS Only	
0.11	0	0	0.11	0	0	1.00			
0	0	0	0.665	0.36	0.525	HS Only	HS Only	HS Only	
0	0	0	0.08	0.23	0.125	HS Only	HS Only	HS Only	
0	0	0.2	0.2	0.2	0.2	HS Only	HS Only	1.00	
0	0.26	0	0	0	0		0.00		
0	0.21	0.21	0.21	0.34	0.21	HS Only	1.62	1.00	
0	0	0	0.08	0.08	0.17	HS Only	HS Only	HS Only	
0	0	0.41	0.695	0.695	0.98	HS Only	HS Only	2.39	
0	0.32	0	0	0.32	0.32		1.00	HS Only	
0.125	0	0	0.17	0.125	0.175	1.36	HS Only	HS Only	0.80
0	0	0.18	0.18	0	0	HS Only		0.00	
0.25	0.25	0.41	0.25	0.25	0	1.00	1.00	0.00	
0	0	0	0.1	0.2	0	HS Only	HS Only		
0	0	0	0.11	0.11	0	HS Only	HS Only		
0.33	0.33	0.33	0.33	0.555	0.33	1.00	1.68	1.00	
0	0	0	0.2	0.2	0.2	HS Only	HS Only	HS Only	
0	0	0	0.23	0	0	HS Only			
0	0	0	0.15	0	0.33	HS Only		HS Only	
0	0.13	0.21	0.13	0.29	0.13	HS Only	2.23	0.62	

0	0	0	0.12	0	0	HS Only			
0	0	0	0	0.11	0		HS Only		
0	0	0	0.15	0.33	0.33	HS Only	HS Only	HS Only	
0.04	0	0.04	0.23	0.205	0.33	5.75	HS Only	8.25	
0	0.2	0	0.73	0.44	0.2	HS Only	2.20	HS Only	
0.6	0.94	1.17	1.05	0.85	1.06	1.75	0.90	0.91	1.77
0.36	0	0.36	0	0.36	0.36	0.00	HS Only	1.00	
3.59	0.925	1.975	0.925	0.925	0.6	0.26	1.00	0.30	
0	0.82	0.35	0	0	0.35		0.00	1.00	
0.06	0	0	0.09	0.19	0	1.50	HS Only		
1.68	1.01	1.03	1.85	2.075	2.32	1.10	2.05	2.25	0.54
2.32	1.265	4.49	1.325	2.88	2.04	0.57	2.28	0.45	0.00
1.57	0.88	0	0.825	0.67	1.25	0.53	0.76	HS Only	0.04
0	0	2.725	0	2.31	0		HS Only	0.00	
2.34	3.045	3.315	3.885	3.16	2.835	1.66	1.04	0.86	0.20
1.12	0.57	0.83	0.83	0.83	1.15	0.74	1.46	1.39	
0.735	0.57	0.83	0	0.83	0.57	0.00	1.46	0.69	
3.775	2.37	2.74	3.82	4.81	2.075	1.01	2.03	0.76	0.55
0	0	3.71	0	2.78	0		HS Only	0.00	
2.815	1.33	2.17	1.68	2.84	2.34	0.60	2.14	1.08	0.37
0.995	1.705	1.375	0.84	0.995	0.71	0.84	0.58	0.52	0.19
1.325	1.5	1.53	0.755	0.995	1.5	0.57	0.66	0.98	0.32
7.525	5.86	11.91	3.185	4.665	3.96	0.42	0.80	0.33	0.09
10.85	5.465	11.91	3.185	5.13	3.96	0.29	0.94	0.33	
1.69	1.485	1.405	1.485	1.31	1.405	0.88	0.88	1.00	0.98
2.54	0.87	4.67	0.735	1.215	1.845	0.29	1.40	0.40	0.01
1.665	1.125	2.32	1.39	1.73	1.71	0.83	1.54	0.74	0.74
7.62	5.745	7.62	4.245	5.965	4.66	0.56	1.04	0.61	0.04
1.78	2.72	3.165	2.905	3.025	2.245	1.63	1.11	0.71	0.78
1.51	1.765	2.325	2.07	2.69	1.11	1.37	1.52	0.48	
0.63	0.455	0.63	0.455	0.63	0.455	0.72	1.38	0.72	
47.07	64.82	336.39	34.525	27.195	132.31	0.73	0.42	0.39	0.12
5.145	4.56	7.295	3.2	3.35	3.66	0.62	0.73	0.50	0.21
4.32	2.495	5.81	2.16	3.235	2.395	0.50	1.30	0.41	
3.43	5.12	4.6	5.12	3.525	4.63	1.49	0.69	1.01	0.27
8.185	8.865	25.545	10.61	9.73	3.09	1.30	1.10	0.12	0.03
4.6	4.6	5.275	3.52	4.06	5.57	0.77	0.88	1.06	
5.95	4.6	0	0	0	0	0.00	0.00		
3.395	2.695	3.97	2.695	3.06	2.145	0.79	1.14	0.54	0.53
1.04	1.48	2.83	1.48	1.115	1.9	1.42	0.75	0.67	0.46
1.475	1.37	2	2.295	3.22	3.94	1.56	2.35	1.97	0.19
1.15	0.48	0.91	0.29	0.48	0.67	0.25	1.00	0.74	0.00
2.67	1.535	2.985	1.785	2.1	1.925	0.67	1.37	0.64	0.32
3.065	3.535	4.96	3.065	4.15	1.625	1.00	1.17	0.33	0.00
4.08	3.015	0	4.08	4.08	2.87	1.00	1.35	HS Only	
2.48	1.365	3.31	1.365	1.365	1.505	0.55	1.00	0.45	0.11
0	0	2.38	0	0	0			0.00	

4.52	6.01	7.66	5.09	5.82	4.635	1.13	0.97	0.61	0.75
4.61	4.91	5.93	7.3	4.155	6.95	1.58	0.85	1.17	0.54
0	24.99	0	0	0	2.27		0.00	HS Only	
23.555	32.805	60.765	54.6	18.11	30.08	2.32	0.55	0.50	6.69
0.64	0	1.17	0	1.7	0.64	0.00	HS Only	0.55	
0	0	0	0.68	0	0	HS Only			
0.72	0.78	0.72	1.25	0.515	1.335	1.74	0.66	1.85	0.00
2.145	1.275	3.345	1.01	1.275	1.275	0.47	1.00	0.38	0.27
1.675	2.445	2.285	1.42	1.885	1.82	0.85	0.77	0.80	0.55
0.23	0.235	0.11	0.23	0.17	0.235	1.00	0.72	2.14	0.00
0	0	0	1.76	1.33	1.33	HS Only	HS Only	HS Only	
1.365	3.23	2.315	2.27	3.59	2.87	1.66	1.11	1.24	0.74
1.11	0.975	1.57	1.395	1.235	0	1.26	1.27	0.00	0.04
0	0	0	0	0	2.04			HS Only	
2.37	2.59	3.115	2.075	1.855	1.405	0.88	0.72	0.45	0.44
2.81	3.335	4.49	2.23	2.59	2.6	0.79	0.78	0.58	0.29
3.12	1.86	3.405	2.52	2.01	1.86	0.81	1.08	0.55	
1.775	1.99	2.895	1.99	1.56	2.5	1.12	0.78	0.86	0.19
0	0	0	0.16	0.245	0.16	HS Only	HS Only	HS Only	
0.18	0.525	0.18	0.525	0.525	0.65	2.92	1.00	3.61	0.98
0.13	0.06	0	0.095	0.13	0	0.73	2.17		
0.14	0.105	0.16	0.36	0.455	0.285	2.57	4.33	1.78	0.20
0.22	0.185	0.2	0.62	0.705	0.49	2.82	3.81	2.45	
0	0.07	0.07	0.74	0.915	0.605	HS Only	13.07	8.64	
0	0	0	0.21	0	0.47	HS Only		HS Only	
0	0	0	0.82	0.745	0.875	HS Only	HS Only	HS Only	
0	0	0	0	0.1	0		HS Only		
0.235	0.385	0.235	0.965	0.56	0.75	4.11	1.45	3.19	2.73
0.225	0.255	0.16	0.705	0.705	0.43	3.13	2.76	2.69	1.71
0.06	0	0	0	0	0	0.00			
0.32	0.59	0.555	0.52	0.59	0.64	1.63	1.00	1.15	0.45
0.35	0.35	0.36	0.665	0.845	1.125	1.90	2.41	3.13	
0.09	0.18	0.18	0.41	0.79	0.46	4.56	4.39	2.56	
1.19	1.745	1.515	1.22	1.115	1.2	1.03	0.64	0.79	0.41
0	0	0	0	0.27	0.095		HS Only	HS Only	
0.075	0.075	0.075	0.1	0.125	0.1	1.33	1.67	1.33	0.71
0	0	0	0	0.08	0.08		HS Only	HS Only	
0.04	0.04	0.18	0.23	0.305	0.31	5.75	7.63	1.72	
0.14	0.09	0.09	0	0	0.09	0.00	0.00	1.00	
0	0.29	0	0	0	0		0.00		
0	0	0	0	0	0.12			HS Only	
0.105	0.23	0.125	0	0	0.27	0.00	0.00	2.16	
0.065	0.125	0.08	0.05	0.03	0.23	0.77	0.24	2.88	
1.48	1.485	0.345	0.575	0.64	2.035	0.39	0.43	5.90	0.06
0	0.1	0.1	0.1	0.1	0.1	HS Only	1.00	1.00	
0.05	0	0.11	0.05	0.05	0.05	1.00	HS Only	0.45	
0	0	0	0.08	0.11	0.11	HS Only	HS Only	HS Only	

0.07	0.07	0	0.105	0.07	0.07	1.50	1.00	HS Only	
0	0	0.04	0	0	0.105			2.63	
0.225	0.605	0.37	0.87	0.605	0.75	3.87	1.00	2.03	6.03
0.08	0.08	0	0	0	0.28	0.00	0.00	HS Only	
0.09	0.245	0.14	0.245	0.36	0.44	2.72	1.47	3.14	0.86
0.64	0.285	0.18	0.18	0.285	0.41	0.28	1.00	2.28	
0.54	0.67	0.43	0.97	1.005	0.58	1.80	1.50	1.35	0.65
0.35	0.22	0.35	0.22	0.22	0.51	0.63	1.00	1.46	0.38
0.11	0.42	0.285	0.275	0.195	0.475	2.50	0.46	1.67	0.81
0	0	0	0.04	0	0.04	HS Only		HS Only	
0	0.05	0	0	0	0		0.00		
0	0	0	0.27	0.44	0	HS Only	HS Only		
0	0.13	0.06	0	0	0		0.00	0.00	
0	0	0	0.25	0.25	0	HS Only	HS Only		
0	0	0	0	0.18	0		HS Only		
0	0	0	0	0.09	0.09		HS Only	HS Only	
0	0.1	0	0.21	0.1	0	HS Only	1.00		
0.07	0.15	0.15	1.6	1.505	0.415	22.86	10.03	2.77	
0.15	0.45	0.15	0.15	0.15	0.15	1.00	0.33	1.00	
0	0	0	0.14	0	0.14	HS Only		HS Only	
0.07	0.07	0.07	0.21	0.255	0.07	3.00	3.64	1.00	
0	0	0	0.07	0	0	HS Only			
0	0.06	0	0	0	0		0.00		
0	0	0	0.15	0.07	0	HS Only	HS Only		
0	0	0	0	0.07	0		HS Only		
0	0	0	0.04	0.04	0.055	HS Only	HS Only	HS Only	
1.265	2.485	5.14	2.155	1.22	2.92	1.70	0.49	0.57	0.77
0	0	0	0.39	0.22	0.14	HS Only	HS Only	HS Only	
0	0.18	0.18	0.18	0.18	0	HS Only	1.00	0.00	
0.07	0	0	0	0	0	0.00			
0.11	0.24	0.11	0.11	0.11	0.11	1.00	0.46	1.00	
0.19	0.09	0.09	0.09	0	0	0.47	0.00	0.00	
0.13	0.095	0.13	0.095	0.13	0.13	0.73	1.37	1.00	
0.06	0	0	0	0	0.06	0.00		HS Only	
0.085	0.46	0.35	0.145	0.085	0.175	1.71	0.18	0.50	0.14
0	0	0	0	0.04	0		HS Only		
0	0	0	0.05	0	0	HS Only			
2.115	3.465	1.925	8.38	10.5	7.425	3.96	3.03	3.86	1.64
0.09	0.09	0.31	0.53	0.48	0.35	5.89	5.33	1.13	0.00
0	0	0	0	0.09	0		HS Only		
0	0	0	0.51	0.44	0	HS Only	HS Only		
0	0.06	0	0.18	0	0.12	HS Only	0.00	HS Only	
0.13	0.06	0	1.055	0.99	0.885	8.12	16.50	HS Only	
0.55	0.45	0.13	2.95	3.13	2.88	5.36	6.96	22.15	
0	0	0	0.06	0	0	HS Only			
0.08	0.16	0.08	0	0	0.08	0.00	0.00	1.00	
0.2	0.2	0.095	0.365	0.45	0.51	1.83	2.25	5.37	

0.16	0.16	0.08	0.08	0.08	0.08	0.50	0.50	1.00	
0.17	0	0	0.17	0	0.17	1.00		HS Only	
0	0	0	0	0	0.05			HS Only	
0	0	0.03	0.03	0.03	0.09	HS Only	HS Only	3.00	
0.14	0.225	0.14	0.14	0.14	0.14	1.00	0.62	1.00	
0	0.08	0.08	0.215	0.08	0.36	HS Only	1.00	4.50	
0	0	0	0	0	0.07			HS Only	
0.12	0.19	0.12	0.12	0.12	0	1.00	0.63	0.00	0.00
0	0.04	0	0	0	0.04		0.00	HS Only	
0	0.11	0.11	0.25	0.175	0.11	HS Only	1.59	1.00	
0	0	0	0.22	0.22	0.22	HS Only	HS Only	HS Only	
0	0	0	0	0.05	0		HS Only		
0	0	0	0	0.15	0		HS Only		
0	0	0	0.09	0	0	HS Only			
0	0	0	0.2	0.13	0	HS Only	HS Only		
0	0.07	0	0.07	0.07	0.07	HS Only	1.00	HS Only	
0.05	0.025	0.03	0.04	0	0.02	0.80	0.00	0.67	
0	0	0	0	0	0.04			HS Only	
0.07	0	0	0	0	0	0.00			
0.2	0	0	0.2	0	0	1.00			
0	0.045	0.03	0.03	0.03	0.045	HS Only	0.67	1.50	
0.06	0.06	0	0.06	0	0	1.00	0.00		
0.21	0.21	0.21	0.21	0.21	0.21	1.00	1.00	1.00	
0	0	0	0.09	0.18	0	HS Only	HS Only		
0	0.03	0	0	0	0		0.00		
0.02	0	0	0	0	0	0.00			
0	0.02	0.02	0	0	0		0.00	0.00	
0	0	0	0.545	0.405	0.155	HS Only	HS Only	HS Only	
0	0	0	0	0.07	0		HS Only		
0	0	0	0.08	0.16	0	HS Only	HS Only		
0	0	0	0.14	0.105	0	HS Only	HS Only		
0	0	0	0.08	0.08	0.25	HS Only	HS Only	HS Only	
0	0	0	0.05	0.05	0.1	HS Only	HS Only	HS Only	
0	0	0.05	0.05	0	0	HS Only		0.00	
0	0	0	0.54	0.59	0.255	HS Only	HS Only	HS Only	
0.27	0.17	0.17	0.485	0.27	0.17	1.80	1.59	1.00	1.79
0	0.06	0	0.24	0.345	0.11	HS Only	5.75	HS Only	
0	0	0	0.06	0.06	0	HS Only	HS Only		
0	0.08	0	0.695	0.57	0.46	HS Only	7.13	HS Only	
0.07	0.07	0.07	0.105	0.07	0.07	1.50	1.00	1.00	
0	0.09	0	0.62	0.63	0.14	HS Only	7.00	HS Only	
0	0.06	0	0	0	0		0.00		
0	0.06	0	0.09	0.06	0.18	HS Only	1.00	HS Only	
0	0	0	0.05	0.05	0.05	HS Only	HS Only	HS Only	
0	0	0	0.45	0.53	0.305	HS Only	HS Only	HS Only	
0	0.13	0	0.13	0.29	0.13	HS Only	2.23	HS Only	
0	0	0.16	0.16	0.16	0.35	HS Only	HS Only	2.19	

0.16	0.39	0.51	0.755	0.715	0.74	4.72	1.83	1.45	1.80
0.37	0.955	1.21	4.015	3.57	2.585	10.85	3.74	2.14	0.59
0	0	0.19	0	0.19	0		HS Only	0.00	
0	0	0	0.22	0	0	HS Only			
0	0.35	0	0	0	0		0.00		
0	0.34	0.34	0.34	0	0.34	HS Only	0.00	1.00	
0.29	0.29	0.29	0.29	0.29	0.29	1.00	1.00	1.00	0.00
0.11	0.11	0.11	0.355	0.49	0.435	3.23	4.45	3.95	
0	0	0	0.27	0.27	0.27	HS Only	HS Only	HS Only	
0	0.61	0.61	0	0	0		0.00	0.00	
0	0	0	0.4	0	0.68	HS Only		HS Only	
0	0	0	0	0.04	0		HS Only		
0	0	0	0	0	0.05			HS Only	
0.03	0.07	0.03	0.05	0.105	0.07	1.67	1.50	2.33	
0	0	0	0	0	0.02			HS Only	
0.065	0.445	0.24	1	0.995	0.98	15.38	2.24	4.08	5.48
0	0.24	0	0.86	0.945	1.01	HS Only	3.94	HS Only	
0	0.05	0	0	0	0		0.00		
0.375	0.565	0.695	0.48	0.345	0.45	1.28	0.61	0.65	0.53
0	0	0.37	0.2	0.275	0.315	HS Only	HS Only	0.85	
0	0	0	0.04	0	0.04	HS Only		HS Only	
0	0	0	0	0	0.58			HS Only	
0.1	0	0.03	0	0	0	0.00		0.00	
0.03	0.1	0.1	0.03	0.13	0.1	1.00	1.30	1.00	
1.38	1.63	1.155	1.71	1.89	1.38	1.24	1.16	1.19	0.30
0.34	0.7	0.345	0.6	0	0.51	1.76	0.00	1.48	
0	0.6	0	0.51	0.65	0	HS Only	1.08		
0.04	0.105	0	0.13	0.105	0.13	3.25	1.00	HS Only	
0.14	0.14	0.105	0.175	0.105	0.47	1.25	0.75	4.48	
0.05	0.05	0.05	0.05	0	0	1.00	0.00	0.00	
0	0	0	0	0.05	0		HS Only		
0.245	0.33	0.2	0.24	0.245	0.2	0.98	0.74	1.00	0.55
0.17	0.36	0.17	0.26	0.17	0.33	1.53	0.47	1.94	0.59
2.92	3.97	4.39	5.215	5.06	5.26	1.79	1.27	1.20	0.75
0.2	0.39	0.43	0.35	0.275	0.445	1.75	0.71	1.03	0.99
0.03	0.205	0.06	0.03	0	0.12	1.00	0.00	2.00	
0.18	0.18	0.085	0.23	0.135	0.135	1.28	0.75	1.59	
0.22	0.725	0.53	0.72	0.365	0.49	3.27	0.50	0.92	4.95
0.08	0.21	0.16	0.08	0.08	0.08	1.00	0.38	0.50	
0.6	0.96	0.62	1.085	0.735	0.855	1.81	0.77	1.38	0.87
0.04	0.04	0.04	0.04	0.06	0.105	1.00	1.50	2.63	
0	0	0	0.08	0	0	HS Only			
0.385	0.475	0.475	0.445	0.31	0.465	1.16	0.65	0.98	1.15
0	0.18	0	0.06	0.06	0.06	HS Only	0.33	HS Only	
0.11	0.415	0.11	0.19	0.15	0.24	1.73	0.36	2.18	0.43
0	0	0	0	0.09	0		HS Only		
0.2	0	0	0	0.36	0.13	0.00	HS Only	HS Only	

0.45	0.405	0.45	0.595	0.54	0.54	1.32	1.33	1.20	
0	0.05	0	0.05	0.05	0.05	HS Only	1.00	HS Only	
0.09	0	0	0	0	0	0.00			
0	0.22	0	0	0	0		0.00		
0.08	0	0	0	0.08	0	0.00	HS Only		
0	0.02	0	0	0	0.02		0.00	HS Only	
0	0	0	0.06	0.06	0.06	HS Only	HS Only	HS Only	
0	0	0	0.15	0.15	0	HS Only	HS Only		
0	0	0	0	0.15	0.15		HS Only	HS Only	
0	0	0	0.17	0	0	HS Only			
0	0	0	0.06	0	0	HS Only			
0.24	0.11	0.05	0.61	0.495	0.45	2.54	4.50	9.00	
0.17	0.11	0	0.205	0.3	0.235	1.21	2.73	HS Only	
0	0	0	0.18	0.3	0.13	HS Only	HS Only	HS Only	
0.09	0.18	0	0.94	1.025	0.575	10.44	5.69	HS Only	
0.08	0	0	0.545	0.48	0.22	6.81	HS Only	HS Only	
0.05	0.05	0.05	0.05	0.05	0	1.00	1.00	0.00	
0.12	0.215	0.06	0.215	0.15	0.18	1.79	0.70	3.00	2.24
0.05	0.05	0.05	0.05	0.05	0.1	1.00	1.00	2.00	
0.02	0.02	0	0	0	0	0.00	0.00		
0	0	0	0	0.04	0.04		HS Only	HS Only	
0	0.19	0.11	0	0	0		0.00	0.00	
0.05	0.11	0.07	0.13	0.11	0.07	2.60	1.00	1.00	1.08
0.23	0.435	0.37	0.365	0.48	0.47	1.59	1.10	1.27	2.73
0.15	0	0	0	0	0	0.00			
0	0.19	0.19	0.19	0	0	HS Only	0.00	0.00	
0	0	0	0.07	0.11	0	HS Only	HS Only		
0	0	0	0.17	0.17	0.17	HS Only	HS Only	HS Only	
0	0.23	0	0	0	0		0.00		
0.165	0.55	0.295	0.39	0.495	0.525	2.36	0.90	1.78	2.93
0	0	0	0	0.08	0		HS Only		
0	0	0	0.08	0	0	HS Only			
0	0.08	0	0	0.08	0		1.00		
0.15	0.15	0.15	0.32	0.32	0.235	2.13	2.13	1.57	
0.06	0	0	0	0	0	0.00			
0.75	0.32	0	0.99	1.165	2.555	1.32	3.64	HS Only	
0.04	0	0	0.04	0	0.04	1.00		HS Only	
0	0.04	0	0	0	0		0.00		
0	0	0	0.03	0	0	HS Only			
0	0.11	0.11	0.11	0	0.11	HS Only	0.00	1.00	
0	0.06	0	0	0.06	0.06		1.00	HS Only	
0.09	0.12	0.12	0.09	0.09	0.06	1.00	0.75	0.50	1.06
0	0.06	0	0	0	0		0.00		
0.06	0.095	0.13	0.095	0.06	0.13	1.58	0.63	1.00	0.82
0	0	0	0.11	0.11	0.24	HS Only	HS Only	HS Only	
0	0	0	0.12	0.12	0.12	HS Only	HS Only	HS Only	
0.62	0.875	1.235	1.86	1.76	1.805	3.00	2.01	1.46	0.49

0	0	0	0	0.14	0		HS Only		
0.11	0.11	0.11	1.085	0.965	1.56	9.86	8.77	14.18	
0	0	0	0.31	0	0.3	HS Only		HS Only	
0.11	0.23	0.11	0.17	0.11	0.235	1.55	0.48	2.14	
0.05	0.17	0.23	0.265	0.3	0.175	5.30	1.76	0.76	
0.59	0.62	0.835	0.67	0.67	0.835	1.14	1.08	1.00	0.19
0.39	0.79	0.855	0.73	1.005	0.965	1.87	1.27	1.13	0.39
0.97	1.525	1.975	1.72	1.65	1.54	1.77	1.08	0.78	0.66
0	0	0	0.04	0.04	0.04	HS Only	HS Only	HS Only	
0.22	0.11	0.11	0.425	0.5	0.23	1.93	4.55	2.09	
0.635	1.01	1.005	1.12	1.01	1.335	1.76	1.00	1.33	0.09
0.17	0	0	0	0.17	0.17	0.00	HS Only	HS Only	
0.04	0.12	0.1	0.38	0.355	0.245	9.50	2.96	2.45	1.06
0	0.1	0.06	0.06	0.08	0.12	HS Only	0.80	2.00	
0	0	0	0.03	0.07	0	HS Only	HS Only		
0	0	0	0.06	0	0	HS Only			
0.15	0.24	0.3	0.075	0.1	0.05	0.50	0.42	0.17	0.24
0.01	0.01	0.02	0.01	0.01	0.03	1.00	1.00	1.50	
0	0.07	0	0	0	0		0.00		
0	0	0	0.185	0.12	0.12	HS Only	HS Only	HS Only	
0.08	0	0	0	0	0.16	0.00		HS Only	
0	0	0.15	0	0	0			0.00	
0.965	1.115	1.115	0.665	0.7	0.65	0.69	0.63	0.58	0.15
0	0	0.07	0	0	0			0.00	
0	0	0	0	0.03	0.03		HS Only	HS Only	
0	0	0	0.16	0.19	0.075	HS Only	HS Only	HS Only	
0	0.11	0.05	0	0	0		0.00	0.00	
0	0.05	0	0	0	0.15		0.00	HS Only	
0	0.03	0.03	0	0.03	0.03		1.00	1.00	
0.35	0.97	0.405	0.74	0.4	0.59	2.11	0.41	1.46	3.06
0	0	0	0	0	0.05			HS Only	
0	0	0	0	0.08	0.08		HS Only	HS Only	
0	0	0.07	0	0	0			0.00	
0.03	0.03	0.03	0.03	0.07	0.07	1.00	2.33	2.33	
0	0	0	0	0.06	0		HS Only		
0	0	0	0.06	0	0.06	HS Only		HS Only	
0	0	0	0.05	0	0.05	HS Only		HS Only	
0	0	0	0.11	0.15	0.11	HS Only	HS Only	HS Only	
0	0	0	0.05	0.11	0.05	HS Only	HS Only	HS Only	
0	0	0	0.11	0.07	0.15	HS Only	HS Only	HS Only	
0	0.02	0	0.145	0.055	0.125	HS Only	2.75	HS Only	
0	0	0	0	0	0.1			HS Only	
0	0	0.07	0	0	0			0.00	
0	0	0	0.25	0	0	HS Only			
0.41	0.295	0.34	0.745	0.48	1.4	1.82	1.63	4.12	1.98
0	0.06	0	0	0	0		0.00		
0.05	0.08	0.06	0.3	0.31	0.325	6.00	3.88	5.42	3.24

0.14	0.14	0.14	0	0.14	0.29	0.00	1.00	2.07	
0.03	0.04	0.08	0.185	0.17	0.115	6.17	4.25	1.44	0.71
0	0.03	0	0.105	0.12	0.05	HS Only	4.00	HS Only	
0	0.11	0.04	0.04	0.04	0.07	HS Only	0.36	1.75	
0	0	0	0.06	0.06	0	HS Only	HS Only		
0	0.11	0	0.305	0.43	0.58	HS Only	3.91	HS Only	
0	0	0	0	0	0.03			HS Only	
0	0	0	0.17	0.17	0	HS Only	HS Only		
0	0.38	0	0	0	0.555		0.00	HS Only	
0	0.1	0.1	0.1	0.2	0	HS Only	2.00	0.00	
0	0	0	0	0.04	0		HS Only		
0	0	0	0	0.08	0		HS Only		
0	0	0	0.11	0	0	HS Only			
0	0	0.05	0	0	0			0.00	
0	0	0	0.19	0	0	HS Only			
0.01	0.02	0.01	0.075	0.035	0.07	7.50	1.75	7.00	
0	0	0.08	0	0	0			0.00	
0.24	0.155	0.05	0	0	0.32	0.00	0.00	6.40	
0	0	0	0.29	0.29	0.29	HS Only	HS Only	HS Only	
0	0	0	0.27	0.215	0.46	HS Only	HS Only	HS Only	
0	0	0.06	0	0	0			0.00	
0	0.1	0.1	0.1	0.1	0.1	HS Only	1.00	1.00	
0.24	0.31	0.175	0.275	0.5	0.45	1.15	1.61	2.57	
0	0	0	0.085	0.14	0.085	HS Only	HS Only	HS Only	
0.16	0.1	0.1	0	0	0	0.00	0.00	0.00	
0.14	0.07	0	0.745	0.92	0.61	5.32	13.14	HS Only	
0	0	0	0	0	0.07			HS Only	
0	0.095	0.06	0.13	0.24	0.13	HS Only	2.53	2.17	
0	0.18	0	0.23	0.33	0.18	HS Only	1.83	HS Only	
0.07	0.105	0	0.175	0.175	0.18	2.50	1.67	HS Only	
0	0	0	0.13	0.095	0.06	HS Only	HS Only	HS Only	
0	0	0	0	0	0.08			HS Only	
2.005	7.45	4.295	1.655	2.29	3.62	0.83	0.31	0.84	0.63
0	0	0	0	0	0.07			HS Only	
0	0	0	0	0	0.1			HS Only	
0.2	0.2	0.2	0	0.2	0.2	0.00	1.00	1.00	
0	0	0	0.48	0.32	0.33	HS Only	HS Only	HS Only	
0	0	0	0.6	0.6	0.48	HS Only	HS Only	HS Only	
0	0	0	0	0.22	0		HS Only		
0	0	0	0.785	0.42	0.58	HS Only	HS Only	HS Only	
0	0.16	0.16	0.16	0.34	0.25	HS Only	2.13	1.56	
0	0	0	0.12	0	0	HS Only			
28.64	71.04	38.04	19.38	23.39	28.64	0.68	0.33	0.75	1.02
0	0	0.22	0.22	0	0	HS Only		0.00	
0	0	0	0	0.44	0		HS Only		
0	0	0	0.22	0	0	HS Only			
0	0	0	1.17	0.98	0.5	HS Only	HS Only	HS Only	

0	0	0	0.57	0.57	0	HS Only	HS Only		
0	0	0	0.11	0.11	0.165	HS Only	HS Only	HS Only	
0	0	0	0	0.06	0		HS Only		
0.05	0.05	0	0.1	0	0	2.00	0.00		
0	0	0	0.04	0	0	HS Only			
0	0	0	0	0	0.09			HS Only	
0.07	0	0	0	0	0	0.00			
0	0	0	0	0.1	0		HS Only		
0	0	0	0.07	0.07	0.07	HS Only	HS Only	HS Only	
0.09	0.09	0.09	0.09	0.09	0.09	1.00	1.00	1.00	0.00
0	0	0	0.31	0.5	0.195	HS Only	HS Only	HS Only	
0	0.35	0	0.83	0.83	0.35	HS Only	2.37	HS Only	
0	0	0.155	0.1	0.1	0.1	HS Only	HS Only	0.65	
0	0	0	0.06	0	0.06	HS Only		HS Only	
0	0	0	0	0	0.06			HS Only	
0	0	0	0.255	0.39	0.1	HS Only	HS Only	HS Only	
0.34	0.405	0.22	0.22	0.1	0.34	0.65	0.25	1.55	
0	0	0	0.335	0.28	0.155	HS Only	HS Only	HS Only	
0	0	0	0.27	0.27	0.17	HS Only	HS Only	HS Only	
0.09	0.09	0.09	0.09	0.09	0.09	1.00	1.00	1.00	
0.05	0.05	0.05	0	0	0	0.00	0.00	0.00	
0.39	0.67	0.685	1.235	0.9	0.7	3.17	1.34	1.02	1.64
0.59	0.645	0.595	0.76	0.76	0.565	1.29	1.18	0.95	0.14
0.07	0	0	0.23	0.11	0.11	3.29	HS Only	HS Only	
0	0	0	0	0.1	0		HS Only		
0	0	0	0.215	0.06	0.25	HS Only	HS Only	HS Only	
0	0	0	0	0	0.06			HS Only	
0.155	0.47	0.12	0.55	0.25	0.285	3.55	0.53	2.38	4.93
0	0.1	0.1	0.155	0.1	0.1	HS Only	1.00	1.00	
0	0	0	0.08	0	0.08	HS Only		HS Only	
0	0	0	0	0	0.05			HS Only	
0	0	0	0.16	0.09	0.12	HS Only	HS Only	HS Only	
0	0.06	0	0.21	0.17	0.13	HS Only	2.83	HS Only	
0	0.08	0	0	0	0		0.00		
0	0.04	0	0	0	0		0.00		
0	0.06	0	0	0	0.06		0.00	HS Only	
0.04	0	0	0	0	0	0.00			
0	0.03	0	0	0	0.03		0.00	HS Only	
0.04	0	0	0.02	0	0	0.50			
0.05	0	0	0	0	0	0.00			
0	0	0	0	0	0.06			HS Only	
0	0	0	0.01	0	0.01	HS Only		HS Only	
0	0.03	0	0	0	0		0.00		
0.02	0	0	0	0	0	0.00			
0	0.08	0.08	0.08	0.12	0	HS Only	1.50	0.00	
0.14	0.14	0.07	0	0	0.07	0.00	0.00	1.00	
0.03	0.09	0.07	0.05	0.03	0.07	1.67	0.33	1.00	0.94

0	0	0	0	0	0.04			HS Only	
0	0	0	0	0	0.03			HS Only	
0	0.02	0	0	0	0.02		0.00	HS Only	
0	0	0	0.08	0.17	0	HS Only	HS Only		
0	0	0	0	0	0.02			HS Only	
0.02	0	0	0	0	0	0.00			
0	0	0	0.04	0	0	HS Only			
0	0	0	0	0	0.04			HS Only	
0	0	0	0.06	0.045	0	HS Only	HS Only		
0	0	0	0.04	0	0	HS Only			
0.02	0.02	0	0.045	0.04	0.07	2.25	2.00	HS Only	
0	0.04	0	0.04	0.04	0.04	HS Only	1.00	HS Only	
0	0	0	0	0.09	0		HS Only		
0	0	0	0.11	0	0.11	HS Only		HS Only	
0	0	0	0	0.04	0.04		HS Only	HS Only	
0.11	0.14	0.16	0.16	0.09	0.13	1.45	0.64	0.81	2.20
0.28	0.28	0	0.28	0	0	1.00	0.00		
0.055	0.14	0.03	0.155	0.17	0.1	2.82	1.21	3.33	2.77
0.14	0.14	0	0	0	0.14	0.00	0.00	HS Only	
0.1	0.1	0	0	0	0	0.00	0.00		
0.12	0.12	0.08	0.08	0.16	0.205	0.67	1.33	2.56	0.35
0.02	0.04	0.02	0.15	0.18	0.14	7.50	4.50	7.00	0.71
0	0	0	0.455	0	0.28	HS Only		HS Only	
0	0.03	0.03	0.12	0.105	0.08	HS Only	3.50	2.67	
0	0	0	0	0.1	0.1		HS Only	HS Only	
0.14	0	0	0	0.14	0	0.00	HS Only		
0	0	0	0.3	0	0	HS Only			
0.03	0.03	0	0.03	0.045	0.03	1.00	1.50	HS Only	
0	0	0	0.1	0.1	0.1	HS Only	HS Only	HS Only	
0	0	0	0.2	0.44	0.2	HS Only	HS Only	HS Only	
0.39	0.9	0.51	1.08	1.385	1.035	2.77	1.54	2.03	2.50
0.23	0.375	0.375	0.23	0.23	0.23	1.00	0.61	0.61	0.00
0.15	0.15	0	0.15	0.23	0.15	1.00	1.53	HS Only	0.00
0	0	0	0	0.22	0		HS Only		
0.52	0.52	0.52	0.915	1.31	0.52	1.76	2.52	1.00	
0	0.82	0.47	0.82	1.68	0.47	HS Only	2.05	1.00	
0.17	0.245	0.17	0.99	0.87	1.04	5.82	3.55	6.12	2.05
0	0.07	0	0	0	0		0.00		
0	0	0	0.05	0	0	HS Only			
0.18	0.51	0.39	0.23	0.465	0.45	1.28	0.91	1.15	0.39
0	0.14	0.14	0	0	0		0.00	0.00	
0	0.02	0	0.02	0.02	0.03	HS Only	1.00	HS Only	
0.25	0.185	0.12	0.25	0.12	0.25	1.00	0.65	2.08	
0	0	0	0	0	0.09			HS Only	
0	0.26	0.26	0.26	0.26	0.26	HS Only	1.00	1.00	
0	0.07	0.15	0	0.07	0.11		1.00	0.73	
0	0	0	0	0.04	0		HS Only		

0	0	0	0	0.04	0.04		HS Only	HS Only	
0	0	0	0	0	0.05			HS Only	
0	0.04	0	0.055	0	0	HS Only	0.00		
0.19	0.265	0.215	0.115	0.14	0.09	0.61	0.53	0.42	
0	0	0	0.08	0.08	0	HS Only	HS Only		
0.19	0.28	0.235	0.3	0.235	0.27	1.58	0.84	1.15	0.95
0	0	0	0.17	0.17	0.17	HS Only	HS Only	HS Only	
0.05	0.035	0.02	0	0	0.06	0.00	0.00	3.00	
65.615	64.98	98.92	64.73	71.4	124.85	0.99	1.10	1.26	0.78
0.35	0.35	0.35	0.35	0.35	0.255	1.00	1.00	0.73	0.00
0.25	0.12	0.25	0.205	0.21	0.525	0.82	1.75	2.10	0.19
0.4	0.16	0.4	0.505	0.725	0.7	1.26	4.53	1.75	0.03
1.84	1.505	2.495	1.25	1.745	2.575	0.68	1.16	1.03	0.22
0.745	0.7	0.74	0.545	0.77	0.91	0.73	1.10	1.23	0.08
0.07	0.195	0.15	0.285	0.24	0.335	4.07	1.23	2.23	
0.09	0.09	0.09	0	0.09	0	0.00	1.00	0.00	
0	0.02	0	0.02	0.02	0.05	HS Only	1.00	HS Only	
0	0.06	0	0.06	0.06	0	HS Only	1.00		
0	0	0	0	0	0.07			HS Only	
0.1	0.1	0.1	0.1	0.1	0.1	1.00	1.00	1.00	
0	0.12	0	0.185	0	0.25	HS Only	0.00	HS Only	
0	0	0	0	0	0.05			HS Only	
0.09	0.12	0.09	0.215	0.325	0.23	2.39	2.71	2.56	1.89
2.26	1.09	1.09	12.995	22.845	6.755	5.75	20.96	6.20	
1.405	1.615	1.53	21.315	28.96	11.785	15.17	17.93	7.70	15.07
0	0	0	0	0	0.16			HS Only	
0	0	0	0	0	0.08			HS Only	
0	0.1	0	0	0	0		0.00		
0.09	0	0	0.7	0.72	0.57	7.78	HS Only	HS Only	
0	0	0	0	0	0.105			HS Only	
0.105	0.1	0.16	0.05	0.05	0.1	0.48	0.50	0.63	
0.08	0	0.08	0	0	0	0.00		0.00	
0	0.2	0	0.13	0.13	0.13	HS Only	0.65	HS Only	
0.08	0.08	0.08	0.08	0.08	0.12	1.00	1.00	1.50	
0	0.1	0.16	0	0.1	0.1		1.00	0.63	
0	0.08	0.08	0.08	0.08	0.08	HS Only	1.00	1.00	
0	0.22	0.48	0	0	0		0.00	0.00	
0.11	0.22	0.11	0	0.285	0.11	0.00	1.30	1.00	
0.13	0.205	0.205	0.36	0.645	0.36	2.77	3.15	1.76	
0	0.06	0	0.06	0.06	0.13	HS Only	1.00	HS Only	
0	0.03	0	0.07	0.03	0.03	HS Only	1.00	HS Only	
0.03	0.07	0.03	0.03	0.03	0.1	1.00	0.43	3.33	
0.23	0.405	0.405	0.34	0.25	0.34	1.48	0.62	0.84	1.04
0.655	1.11	0.89	1.25	1.59	1.05	1.91	1.43	1.18	0.91
0	0.21	0	0.21	0.47	0.21	HS Only	2.24	HS Only	
0.1	0.1	0.1	0	0.22	0.1	0.00	2.20	1.00	
0.325	0.93	0.465	0.93	0.555	0.89	2.86	0.60	1.91	6.39

0.24	0.52	0.395	0.61	0.52	0.37	2.54	1.00	0.94	2.09
0	0.05	0	0.13	0.13	0.16	HS Only	2.60	HS Only	
0.175	0.445	0.315	0.15	0.135	0.245	0.86	0.30	0.78	0.83
0.155	0.27	0.155	0.15	0.085	0.225	0.97	0.31	1.45	3.68
0.04	0.08	0.08	0	0.04	0.04	0.00	0.50	0.50	
0.12	0	0	0	0	0.04	0.00		HS Only	
0.12	0.26	0.25	0.4	0.57	0	3.33	2.19	0.00	0.00
0	0	0	0	0	0.4			HS Only	
0.09	0.14	0.09	0.09	0.19	0.19	1.00	1.36	2.11	
0	0.12	0	0	0	0		0.00		
0	0.07	0.15	0.15	0.15	0.15	HS Only	2.14	1.00	
0.75	0.42	0.735	0.335	0.77	0.75	0.45	1.83	1.02	
0.08	0.17	0.08	0.08	0.12	0.26	1.00	0.71	3.25	0.00
1.67	1.435	2.315	1.725	1.435	2.08	1.03	1.00	0.90	0.44
0.06	0.185	0.045	0.08	0.135	0.165	1.33	0.73	3.67	0.47
0.14	0.14	0.14	0.215	0.215	0.14	1.54	1.54	1.00	
0.51	0.975	0.31	1.24	1.585	0.975	2.43	1.63	3.15	1.59
0.05	0.05	0.05	0	0	0	0.00	0.00	0.00	
0	0	0	0.04	0.04	0.07	HS Only	HS Only	HS Only	
0	0	0	0.07	0.14	0.1	HS Only	HS Only	HS Only	
0.02	0	0	0	0.02	0.02	0.00	HS Only	HS Only	
0	0.03	0	0.03	0	0.03	HS Only	0.00	HS Only	
0	0	0.04	0.04	0.04	0.04	HS Only	HS Only	1.00	
0.06	0.06	0.06	0.03	0.075	0	0.50	1.25	0.00	
0	0.04	0	0.09	0	0	HS Only	0.00		
0	0	0	0	0.11	0		HS Only		
0	0	0	0	0.29	0.215		HS Only	HS Only	
0	0	0	0	0.17	0		HS Only		
0	0	0	0	0	0.35			HS Only	
0	0	0	0.15	0	0	HS Only			
0	0	0.03	0	0.03	0.03		HS Only	1.00	
0	0	0	0.15	0.06	0.19	HS Only	HS Only	HS Only	
0.03	0.09	0.06	0.305	0.175	0.25	10.17	1.94	4.17	
0	0	0	0.23	0.11	0.23	HS Only	HS Only	HS Only	
0	0	0	0.205	0.205	0.13	HS Only	HS Only	HS Only	
0	0	0	0.25	0.25	0.12	HS Only	HS Only	HS Only	
0	0	0	0	0	0.09			HS Only	
0.045	0.125	0.11	0.225	0.15	0.19	5.00	1.20	1.73	4.55
0.095	0.14	0.125	0.21	0.185	0.17	2.21	1.32	1.36	1.85
0	0	0	0	0	0.04			HS Only	
0	0	0.05	0	0	0			0.00	
0.08	0	0.08	0.08	0.17	0.17	1.00	HS Only	2.13	
0	0	0	0.05	0	0.05	HS Only		HS Only	
0.165	0.205	0.3	0.745	0.775	0.63	4.52	3.78	2.10	3.72
0	0	0	0.31	0.31	0.31	HS Only	HS Only	HS Only	
0.17	0.32	0.27	0.48	0.625	0.55	2.82	1.95	2.04	
0.04	0.04	0.04	0	0	0.04	0.00	0.00	1.00	

0	0	0	0.215	0.26	0.36	HS Only	HS Only	HS Only	
0	0.14	0.14	0.14	0	0.14	HS Only	0.00	1.00	
0	0	0	0	0.07	0		HS Only		
0.42	0.63	0.305	2.875	3.225	2.385	6.85	5.12	7.82	
0.07	0	0.07	0.3	0.35	0.39	4.29	HS Only	5.57	1.62
0.15	0.15	0	0.27	0.475	0.19	1.80	3.17	HS Only	
0	0.08	0	0.045	0.035	0.06	HS Only	0.44	HS Only	
0	0	0	0	0.16	0		HS Only		
0	0.05	0	0	0	0		0.00		
0	0	0	0.11	0	0	HS Only			
0	0	0	0	0	0.06			HS Only	
0.04	0.04	0.04	0.04	0	0.04	1.00	0.00	1.00	
0.07	0.105	0.07	0.145	0.07	0.31	2.07	0.67	4.43	1.52
0.11	0	0.11	0	0.22	0.22	0.00	HS Only	2.00	
0.21	0.13	0.28	1.195	1	0.95	5.69	7.69	3.39	
0	0.04	0.04	0.09	0.065	0.09	HS Only	1.63	2.25	
0	0	0	0.13	0.165	0.13	HS Only	HS Only	HS Only	
0.11	0.11	0	0.22	0.285	0.22	2.00	2.59	HS Only	
0	0.12	0	0.365	0.575	0.305	HS Only	4.79	HS Only	
0	0	0	0	0.07	0		HS Only		
0.04	0	0.04	0.04	0	0	1.00		0.00	
0.25	0.39	0.25	0.445	0.25	0.44	1.78	0.64	1.76	
0	0	0	0.3	0.23	0.285	HS Only	HS Only	HS Only	
0.03	0.01	0.03	0.07	0.05	0.11	2.33	5.00	3.67	
0	0.05	0	0.05	0.05	0	HS Only	1.00		
0	0	0	0.645	0.835	0.665	HS Only	HS Only	HS Only	
0.04	0.065	0.04	0.09	0.09	0.14	2.25	1.38	3.50	
0.23	0.23	0.23	0.38	0.705	0.38	1.65	3.07	1.65	
0	0.2	0	0.2	0.44	0.2	HS Only	2.20	HS Only	
0.07	0.07	0.07	0.21	0.475	0.175	3.00	6.79	2.50	
0	0	0.14	0.14	0.215	0.305	HS Only	HS Only	2.18	
0.14	0	0	0	0	0	0.00			
0	0	0	0.06	0	0	HS Only			
0	0	0.78	2.42	2.49	1.075	HS Only	HS Only	1.38	
1.87	2.82	1.87	3.715	2.82	2.47	1.99	1.00	1.32	
1.88	2.765	2.7	4.53	4.43	2.84	2.41	1.60	1.05	0.98
0	0	0.08	0.08	0.125	0.08	HS Only	HS Only	1.00	
0	0.11	0.07	0	0.07	0.07		0.64	1.00	
0	0	0	0.04	0	0	HS Only			
0	0.05	0.05	0.05	0.04	0.05	HS Only	0.80	1.00	
0	0	0	0.2	0.2	0	HS Only	HS Only		
0	0	0	0	0	0.06			HS Only	
0	0	0.09	0.19	0.19	0.14	HS Only	HS Only	1.56	
0.24	0.14	0.515	0.645	0.73	1.495	2.69	5.21	2.90	
0	0	0.08	0.04	0.04	0.25	HS Only	HS Only	3.13	
0.07	0.07	0	0.555	0.5	0.775	7.93	7.14	HS Only	
0	0.07	0	0	0	0		0.00		

0	0	0	0.38	0.415	0.305	HS Only	HS Only	HS Only	
0	0	0	0.05	0	0	HS Only			
0	0.06	0	0.2	0.235	0.06	HS Only	3.92	HS Only	
0	0	0	0.03	0.03	0	HS Only	HS Only		
0.02	0.045	0.03	0	0.02	0	0.00	0.44	0.00	
0	0	0	0	0.09	0		HS Only		
0	0	0	0.135	0	0.06	HS Only		HS Only	
0	0	0	0.28	0.46	0.205	HS Only	HS Only	HS Only	
0	0	0	0.09	0.2	0	HS Only	HS Only		
0	0	0	0.06	0.06	0.06	HS Only	HS Only	HS Only	
0.055	0.275	0.095	0.13	0.165	0.125	2.36	0.60	1.32	1.26
0	0.05	0.05	0	0	0		0.00	0.00	
0	0	0	0.05	0	0	HS Only			
0	0	0	0	0.06	0		HS Only		
0	0	0.05	0	0	0			0.00	
0	0	0	0	0.32	0		HS Only		
0	0	0	0.23	0	0.15	HS Only		HS Only	
0	0	0	0	0.09	0		HS Only		
0.53	0.735	0.465	1.33	0.89	0.93	2.51	1.21	2.00	
0.57	0.55	1.52	0.445	0.675	0.445	0.78	1.23	0.29	0.22
0	0	0	0.14	0.14	0.14	HS Only	HS Only	HS Only	
0.1	0.155	0.21	0.155	0.155	0.21	1.55	1.00	1.00	0.78
0	0	0	0.34	0.25	0.34	HS Only	HS Only	HS Only	
0	0	0	0.16	0.25	0	HS Only	HS Only		
0	0.09	0	0.09	0.09	0	HS Only	1.00		
0	0	0	0.02	0	0	HS Only			
0	0.04	0	0.04	0.04	0.04	HS Only	1.00	HS Only	
1.85	0.495	1.635	1.215	2.095	1.58	0.66	4.23	0.97	0.05
0	0	0	0.69	0.69	0.69	HS Only	HS Only	HS Only	
0	0	0	0	0.18	0		HS Only		
0.27	0.27	0.39	0.49	0.49	0.37	1.81	1.81	0.95	1.83
1	1.96	0.8	1.67	1	1.2	1.67	0.51	1.50	0.49
1.095	2.365	1.095	4.405	1.58	3.15	4.02	0.67	2.88	5.15
0.83	1.21	0.72	1.205	1.135	0.99	1.45	0.94	1.38	0.32
0	0	0	0.13	0	0	HS Only			
0	0	0	0.225	0.31	0.14	HS Only	HS Only	HS Only	
0.07	0.03	0.05	0.915	0.985	1.005	13.07	32.83	20.10	
0.33	0.15	0.15	5.37	6.915	3.99	16.27	46.10	26.60	
0.17	0.17	0.08	0.57	1.125	0.91	3.35	6.62	11.38	
0.49	0.335	0.37	2.96	2.935	2.79	6.04	8.76	7.54	
0.04	0	0	0.385	0.185	0.39	9.63	HS Only	HS Only	
0.15	0.35	0.17	0.81	0.79	0.79	5.40	2.26	4.65	5.09
0.14	0	0.05	0.535	0.53	0.57	3.82	HS Only	11.40	
1.5	2.32	2	4.865	5.98	6.67	3.24	2.58	3.34	1.52
1.545	2.16	2.01	4.47	5.695	6.595	2.89	2.64	3.28	0.87
0	0	0	0	0	0.9			HS Only	
0.35	0	0	2.15	2.315	2.23	6.14	HS Only	HS Only	

3.77	5.345	4.29	4.295	3.3	4.085	1.14	0.62	0.95	
3.255	5.52	4.43	4.58	4.2	4.185	1.41	0.76	0.94	0.36
0.22	0.76	1.095	2.42	1.895	2.655	11.00	2.49	2.42	13.63
0	0.05	0	0.3	0.14	0.235	HS Only	2.80	HS Only	
0.025	0.04	0.01	0.01	0.03	0.035	0.40	0.75	3.50	0.53
0	0	0.28	0	0.28	0		HS Only	0.00	
0	0	0	0.02	0.055	0.02	HS Only	HS Only	HS Only	
0	0	0	0	0.25	0		HS Only		
0.07	0.14	0	0.07	0.07	0.14	1.00	0.50	HS Only	
0	0	0	0	0	0.1			HS Only	
0	0	0	0.67	0.675	0.43	HS Only	HS Only	HS Only	
0	0.07	0	0.105	0.29	0.14	HS Only	4.14	HS Only	
0	0.13	0.13	0.13	0.13	0.13	HS Only	1.00	1.00	
0	0.075	0.125	0	0	0.05		0.00	0.40	
0	0.06	0.32	0.285	0.185	0.405	HS Only	3.08	1.27	
0	0.03	0	0.03	0.03	0.03	HS Only	1.00	HS Only	
0	0.04	0	0	0	0		0.00		
0	0	0	0.04	0.04	0	HS Only	HS Only		
0	0	0	0.09	0.12	0.12	HS Only	HS Only	HS Only	
0.07	0.07	0.105	0	0	0.07	0.00	0.00	0.67	
0	0.04	0	0	0	0		0.00		
0	0	0	0	0.11	0		HS Only		
0	0	0	0	0.06	0		HS Only		
0	0	0	0	0.04	0.04		HS Only	HS Only	
0.14	0.14	0.17	0.115	0.09	0.115	0.82	0.64	0.68	0.76
0	0	0	0.07	0.11	0.2	HS Only	HS Only	HS Only	
0.365	0.745	0.28	0.545	0.565	0.565	1.49	0.76	2.02	0.91
0.61	0.825	1.665	1.1	1.1	1.59	1.80	1.33	0.95	1.14
1.01	1.275	1.54	1.87	1.54	1.605	1.85	1.21	1.04	0.46
4.17	5.53	0	5.53	7.26	4.17	1.33	1.31	HS Only	
4.17	4.85	4.85	5.53	6.395	9.44	1.33	1.32	1.95	
0.93	0.395	0.55	0.55	0.93	0.395	0.59	2.35	0.72	0.00
85.405	145.025	90.52	145.025	90.52	244.93	1.70	0.62	2.71	1.36
0	0.03	0.03	0.03	0	0	HS Only	0.00	0.00	
0	0	0	0	0.21	0.21		HS Only	HS Only	
0	0	0	0	0	0.09			HS Only	
0	0	0	0.05	0.05	0.05	HS Only	HS Only	HS Only	
0.295	0.44	0.67	0.39	0.345	0.525	1.32	0.78	0.78	0.54
0.09	0	0	0	0.145	0	0.00	HS Only		
0	0	0	0.19	0.14	0.09	HS Only	HS Only	HS Only	
0	0.2	0	0	0	0.2		0.00	HS Only	
0.09	0.09	0	0.09	0.09	0.09	1.00	1.00	HS Only	
0.06	0.06	0.06	0.13	0.175	0.13	2.17	2.92	2.17	
0	0	0	0	0.14	0		HS Only		
0	0.09	0.06	0.12	0.125	0.09	HS Only	1.39	1.50	
0	0.04	0	0.04	0.04	0.04	HS Only	1.00	HS Only	
0	0.03	0	0.03	0.03	0.06	HS Only	1.00	HS Only	

0	0	0	0.07	0.07	0.07	HS Only	HS Only	HS Only	
0	0.085	0.03	0.07	0.065	0.07	HS Only	0.76	2.33	
0	0	0	0	0	0.07			HS Only	
0	0	0	0	0	0.03			HS Only	
0	0	0	0	0	0.02			HS Only	
0	0.115	0.09	0.09	0.09	0.09	HS Only	0.78	1.00	
0	0	0	0.26	0.26	0	HS Only	HS Only		
0.17	0.38	0.275	0.275	0.17	0.17	1.62	0.45	0.62	
0.1	0.1	0.1	0	0.1	0.1	0.00	1.00	1.00	
0.11	0.11	0.11	0.24	0.24	0.24	2.18	2.18	2.18	
0	0	0	0	0.1	0		HS Only		
0	0.2	0	0.96	1.395	0.63	HS Only	6.98	HS Only	
0	0.03	0	0.03	0	0.03	HS Only	0.00	HS Only	
0.07	0.07	0.07	0.105	0.14	0.14	1.50	2.00	2.00	
0	0	0	0	0.03	0		HS Only		
0.075	0.105	0.06	0.045	0.03	0.09	0.60	0.29	1.50	1.24
0	0	0	0.06	0	0	HS Only			
0	0.21	0.21	0	0	0.21		0.00	1.00	
0	0.22	0	0	0	0		0.00		
0	0	0	0.05	0	0	HS Only			
0	0	0	0.205	0.13	0	HS Only	HS Only		
0.09	0.195	0.245	0.19	0.36	0.425	2.11	1.85	1.73	0.00
0.3	0.61	0.83	1.485	1.505	2.415	4.95	2.47	2.91	2.39
0	0.16	0.54	0.16	0.24	0.43	HS Only	1.50	0.80	
1.055	1.465	2.415	1.055	0.91	0.985	1.00	0.62	0.41	0.00
0	0	0	0.03	0.09	0.03	HS Only	HS Only	HS Only	
0	0	0	0.11	0.17	0	HS Only	HS Only		
0	0	0	0.03	0	0	HS Only			
0	0	0	0	0	0.03			HS Only	
0	0	0	0.04	0	0	HS Only			
0	0	0	0.06	0.06	0.06	HS Only	HS Only	HS Only	
0	0	0	0.12	0.195	0.06	HS Only	HS Only	HS Only	
0	0	0	0	0.09	0		HS Only		
0.05	0.095	0.05	0.05	0.03	0.11	1.00	0.32	2.20	
0.26	0.545	0.37	0.54	0.315	0.4	2.08	0.58	1.08	
0.18	0.09	0.18	0.185	0.18	0.18	1.03	2.00	1.00	0.75
0	0	0	0.04	0	0.04	HS Only		HS Only	
0	0	0.02	0	0	0			0.00	
0	0.03	0	0	0	0		0.00		
0	0.04	0	0	0	0		0.00		
0.05	0	0	0.05	0.05	0.05	1.00	HS Only	HS Only	
0	0	0	0.05	0	0	HS Only			
0	0	0	0.07	0	0	HS Only			
0	0	0	0.15	0.11	0.07	HS Only	HS Only	HS Only	
0	0	0	0	0.11	0.11		HS Only	HS Only	
0	0.1	0.1	0.665	0.945	0.945	HS Only	9.45	9.45	
0	0	0	0	0	0.06			HS Only	

0	0.12	0	0	0	0		0.00		
0	0.06	0	0.09	0	0.06	HS Only	0.00	HS Only	
0.1	0.075	0.1	0.05	0.075	0.21	0.50	1.00	2.10	
0.14	0	0	0	0	0	0.00			
0.285	0.37	0.37	0.19	0.275	0.375	0.67	0.74	1.01	0.32
0	0	0	0.09	0	0	HS Only			
0	0	0	0.04	0.04	0	HS Only	HS Only		
0	0	0	0	0	0.08			HS Only	
0	0.03	0	0.06	0.075	0.06	HS Only	2.50	HS Only	
0	0.075	0.05	0.05	0.05	0.13	HS Only	0.67	2.60	
0	0	0.05	0	0	0			0.00	
0	0	0	0	0.04	0		HS Only		
0	0.08	0	0.16	0.08	0	HS Only	1.00		
0.05	0.095	0.095	0.17	0.14	0.345	3.40	1.47	3.63	0.85
0	0	0	0	0.05	0		HS Only		
0	0.05	0	0.465	0.535	0.31	HS Only	10.70	HS Only	
0.2	0	0	0	0	0.2	0.00		HS Only	
0.18	0.08	0.08	0.56	0.545	0.56	3.11	6.81	7.00	
0.275	0.275	0.595	0.18	0.12	0.185	0.65	0.44	0.31	0.12
0.36	0.395	0.65	0.15	0.15	0.22	0.42	0.38	0.34	0.07
0.05	0	0.05	0	0	0	0.00		0.00	
0	0.06	0	0.03	0.02	0.04	HS Only	0.33	HS Only	
0	0.05	0	0.05	0.08	0	HS Only	1.60		
0.05	0	0	0	0	0	0.00			
0	0	0	0	0	0.14			HS Only	
0.04	0	0	0	0	0	0.00			
0	0	0	0	0	0.04			HS Only	
0.21	0.18	0.07	1.52	1.87	1.03	7.24	10.39	14.71	
0	0	0	0.155	0.405	0.7	HS Only	HS Only	HS Only	
0.595	1.52	1.665	1.3	1.215	1.895	2.18	0.80	1.14	0.80
0	0.06	0	0	0	0		0.00		
0	0.09	0	0	0	0		0.00		
0	0	0	0.03	0	0	HS Only			
0.07	0.07	0.07	0.07	0.07	0.07	1.00	1.00	1.00	
0.08	0.08	0.08	0.08	0.08	0.08	1.00	1.00	1.00	
0	0.06	0	0	0	0		0.00		
0.695	1.19	1.015	1.1	0.78	1.15	1.58	0.66	1.13	0.68
0	0.07	0	0.11	0.15	0.07	HS Only	2.14	HS Only	
0	0	0.06	0	0.06	0		HS Only	0.00	
0	0.05	0	0	0.05	0		1.00		
0.05	0.045	0.02	0.035	0	0.085	0.70	0.00	4.25	
0	0	0	0.25	0.25	0	HS Only	HS Only		
0	0	0	0.03	0.06	0.03	HS Only	HS Only	HS Only	
0	0	0	0.25	0	0	HS Only			
0	0.03	0	0	0	0		0.00		
0	0	0	0.35	0.35	0.56	HS Only	HS Only	HS Only	
0.27	0	0	0.62	0.445	0.27	2.30	HS Only	HS Only	

0	0	0	0	0	0.03			HS Only	
0	0	0	0	0.14	0		HS Only		
0.04	0	0	0	0	0	0.00			
0.04	0.09	0.09	0.09	0.09	0.14	2.25	1.00	1.56	0.00
0.04	0	0	0	0	0	0.00			
0	0	0	0.11	0	0	HS Only			
0.125	0.08	0.08	1.4	1.55	1.5	11.20	19.38	18.75	6.55
0.08	0.08	0.08	0.16	0.12	0.08	2.00	1.50	1.00	
0.04	0.04	0.04	0.155	0.105	0.11	3.88	2.63	2.75	2.65
0	0	0	0	0.02	0		HS Only		
0	0	0	0	0.14	0		HS Only		
0	0	0	0.01	0.01	0.01	HS Only	HS Only	HS Only	
0	0	0.05	0	0	0			0.00	
0	0	0	0.04	0.06	0.04	HS Only	HS Only	HS Only	
0.21	0.46	0.615	0.335	0.335	0.67	1.60	0.73	1.09	0.84
0	0	0	0.05	0.11	0	HS Only	HS Only		
0	0.22	0.165	0.11	0	0	HS Only	0.00	0.00	
0	0	0	0.26	0	0.12	HS Only		HS Only	
0.11	0.11	0.11	0	0	0	0.00	0.00	0.00	
0.09	0.135	0.135	0.09	0	0.18	1.00	0.00	1.33	
0	0.06	0	0	0	0		0.00		
0	0	0	0	0.06	0.06		HS Only	HS Only	
0.08	0	0	0	0	0	0.00			
0.165	0.165	0.3	0.11	0.22	0.165	0.67	1.33	0.55	0.35
0	0	0	0	0	0.04			HS Only	
0	0	0	0.37	0.17	0	HS Only	HS Only		
0.41	0.41	0.12	0.19	0.26	0.58	0.46	0.63	4.83	
0	0.09	0	0.09	0.18	0	HS Only	2.00		
0	0	0	0.37	0	0.37	HS Only		HS Only	
0.21	0	0	0	0	0.21	0.00		HS Only	
0	0.23	0.23	0.23	0	0.23	HS Only	0.00	1.00	
0	0.13	0	0	0	0		0.00		
0.285	0.59	0.43	0.59	0.43	0.285	2.07	0.73	0.66	1.34
0.18	0	0.18	0.18	0.18	0.18	1.00	HS Only	1.00	
0	0	0.09	0.09	0.09	0	HS Only	HS Only	0.00	
0	0	0	0	0.63	0		HS Only		
0.05	0.22	0.19	0.075	0.05	0.1	1.50	0.23	0.53	0.71
0	0.04	0	0	0	0		0.00		
0	0	0	0	0	0.06			HS Only	
0.1	0	0.1	0	0	0.1	0.00		1.00	
0	0	0	0.04	0.04	0.04	HS Only	HS Only	HS Only	
0.08	0.08	0.08	0.17	0.08	0.32	2.13	1.00	4.00	
0.8	1.355	0.8	3.635	5.09	2.265	4.54	3.76	2.83	6.11
0	0	0	0.04	0	0	HS Only			
0.22	0	0	0.1	0	0	0.45			
0	0	0	0.13	0	0	HS Only			
0.12	0.12	0.19	0.42	0.505	0.6	3.50	4.21	3.16	

0.605	1.31	1.465	0.975	1.13	1.11	1.61	0.86	0.76	0.58
0	0	0	0	0	0.11			HS Only	
0.82	1.68	1.365	1.645	1.73	2.71	2.01	1.03	1.99	0.84
0	0.04	0	0	0	0		0.00		
0.04	0.04	0.04	0.04	0	0.04	1.00	0.00	1.00	
0	0	0	0	0.05	0		HS Only		
0	0.07	0	0.07	0.07	0.07	HS Only	1.00	HS Only	
0	0	0.07	0.07	0.07	0.07	HS Only	HS Only	1.00	
0.135	0.09	0.09	0.09	0.18	0.09	0.67	2.00	1.00	0.35
0	0	0	0.195	0.11	0	HS Only	HS Only		
0	0	0	0.08	0	0	HS Only			
0	0	0	0	0.06	0.06		HS Only	HS Only	
0	0	0	0.17	0	0.17	HS Only		HS Only	
0	0	0	0.655	0.355	0.82	HS Only	HS Only	HS Only	
0	0.03	0.03	0	0	0		0.00	0.00	
0	0	0	0.11	0.11	0.11	HS Only	HS Only	HS Only	
0	0	0	0.15	0.15	0.15	HS Only	HS Only	HS Only	
0	0	0	0.1	0.1	0	HS Only	HS Only		
0.17	0.23	0.14	0.29	0.14	0.14	1.71	0.61	1.00	3.39
0	0	0.17	0.17	0	0	HS Only		0.00	
0	0.18	0.18	0.18	0	0.18	HS Only	0.00	1.00	
0.46	0.21	0.13	0.67	0.895	0.295	1.46	4.26	2.27	
0	0.03	0	0.03	0	0	HS Only	0.00		
0.04	0	0	0	0.07	0	0.00	HS Only		
0.14	0.22	0.3	0.22	0.48	0.3	1.57	2.18	1.00	
0	0	0	0.03	0.05	0	HS Only	HS Only		
0	0	0.2	0.72	0.72	0.46	HS Only	HS Only	2.30	
0	0	0	0.25	0.25	0	HS Only	HS Only		
0	0.07	0	0	0.055	0.07		0.79	HS Only	
3.65	4.12	4.23	9.25	9.43	8.2	2.53	2.29	1.94	1.09
0.5	1.14	0.23	0.365	0.675	0.5	0.73	0.59	2.17	0.38
0.35	0.61	0.565	0.35	0.28	0.445	1.00	0.46	0.79	0.29
0.02	0.02	0	0	0.02	0	0.00	1.00		
0.04	0.09	0	0.04	0.04	0.04	1.00	0.44	HS Only	
0.16	0.19	0.075	0.19	0.145	0.15	1.19	0.76	2.00	0.05
0.185	0.28	0.055	0.08	0.125	0.145	0.43	0.45	2.64	0.05
0	0.06	0	0	0	0		0.00		
0	0	0	0.24	0.33	0.33	HS Only	HS Only	HS Only	
0	0	0	0.27	0.13	0	HS Only	HS Only		
0	0.03	0.07	0.03	0	0	HS Only	0.00	0.00	
0	0	0	0	0	0.18			HS Only	
0	0	0	0.14	0.14	0.14	HS Only	HS Only	HS Only	
0	0.06	0.06	0.06	0	0.12	HS Only	0.00	2.00	
0.05	0	0.05	0.075	0	0.1	1.50		2.00	
0	0	0	0.08	0	0.08	HS Only		HS Only	
0.24	0.635	0.24	0.315	0.18	0	1.31	0.28	0.00	
0	0	0.54	0	0	0.39			0.72	

0.11	0.11	0.165	0.22	0.22	0.285	2.00	2.00	1.73	
0	0.09	0	0.14	0.09	0.14	HS Only	1.00	HS Only	
0.17	0.17	0.17	1.33	1.42	0.365	7.82	8.35	2.15	
0	0	0	0	0.26	0		HS Only		
0	0	0	0.05	0.05	0.05	HS Only	HS Only	HS Only	
0.2	0.2	0.1	0.875	1.2	0.875	4.38	6.00	8.75	
0.21	0.21	0.1	1.435	1.09	0.895	6.83	5.19	8.95	
0	0	0	0.09	0.09	0.09	HS Only	HS Only	HS Only	
0	0	0	0.835	0.52	0.15	HS Only	HS Only	HS Only	
0.07	0	0	0	0	0.07	0.00		HS Only	
0	0	0.1	0	0	0			0.00	
0.32	0.58	0.32	0.58	0.32	0.2	1.81	0.55	0.63	1.84
0	0.22	0	0	0.22	0.355		1.00	HS Only	
0	0	0	0	0.08	0		HS Only		
0.02	0	0	0	0	0	0.00			
0.115	0.21	0.055	0.21	0.09	0.135	1.83	0.43	2.45	3.36
0.08	0.08	0.04	0.6	0.595	0.53	7.50	7.44	13.25	
0	0	0	0.545	0.54	0.24	HS Only	HS Only	HS Only	
0	0	0.15	0.62	0.62	0.41	HS Only	HS Only	2.73	
0	0	0	0.13	0.13	0.13	HS Only	HS Only	HS Only	
0	0	0.08	0.08	0	0	HS Only		0.00	
0	0	0	0.15	0.155	0.15	HS Only	HS Only	HS Only	
0	0	0	0.11	0.11	0	HS Only	HS Only		
0	0	0	0.42	0.43	0.6	HS Only	HS Only	HS Only	
0.04	0.04	0.08	0	0	0.04	0.00	0.00	0.50	
0	0	0	0	0	0.06			HS Only	
0	0	0.64	0	0	0			0.00	
0.735	0.43	1.065	0.43	0.7	0.93	0.59	1.63	0.87	0.41
0	0	0	0.33	0	0	HS Only			
0	0	0	0	0.08	0		HS Only		
0	0	0	0.65	0.64	0.49	HS Only	HS Only	HS Only	
0	0	0	0	0.04	0.04		HS Only	HS Only	
0.04	0.04	0.04	0	0	0.06	0.00	0.00	1.50	
0	0	0	0	0.39	0.39		HS Only	HS Only	
0.35	0.475	0.235	0.62	0.43	0.545	1.77	0.91	2.32	0.60
0.08	0.125	0	0.08	0.08	0.08	1.00	0.64	HS Only	
0.02	0.02	0.055	0.02	0.015	0.02	1.00	0.75	0.36	
0	0	0	0	0	0.06			HS Only	
0.1	0	0	0	0	0.1	0.00		HS Only	
0	0	0	0.06	0.05	0.09	HS Only	HS Only	HS Only	
0.425	1.18	0.97	0.56	0.415	0.545	1.32	0.35	0.56	0.66
0	0	0	0.26	0.26	0.26	HS Only	HS Only	HS Only	
0.04	0.1	0.04	0.06	0.04	0.04	1.50	0.40	1.00	0.71
0.09	0.04	0.04	0.065	0.04	0.065	0.72	1.00	1.63	
0	0	0.06	0.06	0.06	0.06	HS Only	HS Only	1.00	
0.05	0.05	0	0.1	0.075	0.1	2.00	1.50	HS Only	
0.125	0.15	0.13	0.42	0.235	0.13	3.36	1.57	1.00	0.19

0.29	0.6	0.55	0.365	0.55	0.38	1.26	0.92	0.69	0.08
0.03	0.08	0.025	0.03	0.15	0.09	1.00	1.88	3.60	0.00
0	0	0	0.03	0.03	0	HS Only	HS Only		
0.105	0.305	0.14	0.395	0.305	0.265	3.76	1.00	1.89	0.56
0.08	0.16	0	0	0.08	0.08	0.00	0.50	HS Only	
0.08	0.26	0.12	0.12	0.08	0.31	1.50	0.31	2.58	0.71
0.095	0.225	0.115	0.17	0.195	0.115	1.79	0.87	1.00	0.01
1.735	2.845	1.735	3.87	3.23	1.97	2.23	1.14	1.14	0.15
1.135	1.99	2.27	2.695	2.58	2.195	2.37	1.30	0.97	0.34
0	0.31	0.14	0.555	0.515	0.43	HS Only	1.66	3.07	
0.105	0.245	0.105	0.225	0.145	0.115	2.14	0.59	1.10	1.84
0	0	0.06	0.06	0.06	0.06	HS Only	HS Only	1.00	
0	0.14	0	0.14	0.14	0.14	HS Only	1.00	HS Only	
0	0	0	0	0	0.05			HS Only	
0.2	0.08	0.155	0.12	0.075	0.2	0.60	0.94	1.29	
0.04	0.06	0.04	0.06	0.08	0.06	1.50	1.33	1.50	0.71
0	0.07	0.055	0.07	0	0.07	HS Only	0.00	1.27	
0.045	0.13	0.075	0.11	0.06	0.095	2.44	0.46	1.27	0.59
0	0	0	0	0.03	0		HS Only		
0.05	0.05	0.035	0.035	0.02	0.05	0.70	0.40	1.43	
0.02	0.035	0.02	0.02	0	0.05	1.00	0.00	2.50	
0.055	0.07	0.055	0.03	0.03	0.055	0.55	0.43	1.00	1.26
0	0.06	0.02	0.065	0.03	0.065	HS Only	0.50	3.25	
0.02	0.02	0.02	0.02	0.02	0.06	1.00	1.00	3.00	
0	0.02	0.02	0.03	0.04	0.04	HS Only	2.00	2.00	
0	0.05	0	0	0	0.09		0.00	HS Only	
0.07	0	0	0	0	0	0.00			
0.06	0.06	0.06	0.06	0.095	0.13	1.00	1.58	2.17	0.00
0.06	0.06	0.06	0.06	0.06	0.06	1.00	1.00	1.00	
0.09	0.065	0.09	0.04	0.04	0.24	0.44	0.62	2.67	0.51
0.06	0.175	0.15	0.11	0.15	0.085	1.83	0.86	0.57	2.69
0.165	0.165	0.23	0.165	0.11	0.11	1.00	0.67	0.48	1.06
0.14	0.09	0.19	0.19	0.36	0.19	1.36	4.00	1.00	0.79
1.66	1.07	1.07	1.66	1.515	1.705	1.00	1.42	1.59	
0	0	0	0.07	0.07	0	HS Only	HS Only		
0	0	0	0	0.05	0.05		HS Only	HS Only	
0.22	0.54	0.64	0.355	0.29	0.275	1.61	0.54	0.43	0.39
0	0	0	0.185	0.12	0.25	HS Only	HS Only	HS Only	
0	0	0	0.3	0.4	0.25	HS Only	HS Only	HS Only	
0	0	0.06	0	0	0.06			1.00	
0.06	0.125	0.14	0.085	0.09	0.2	1.42	0.72	1.43	0.02
0.045	0.095	0.06	0.06	0.06	0.06	1.33	0.63	1.00	0.71
0.07	0.18	0.07	0.07	0.105	0.105	1.00	0.58	1.50	
0.09	0.22	0.14	0.12	0.3	0.12	1.33	1.36	0.86	
0	0	0	0.205	0.16	0.08	HS Only	HS Only	HS Only	
0	0	0	0	0	0.05			HS Only	
0	0	0	0.08	0	0	HS Only			

0.11	0	0	0.23	0.23	0	2.09	HS Only		
0.08	0.02	0	0.095	0.14	0.085	1.19	7.00	HS Only	
0	0	0	0	0.17	0.17		HS Only	HS Only	
0	0	0.08	0	0	0			0.00	
0.135	0.185	0.23	0.45	0.335	0.51	3.33	1.81	2.22	1.06
0.19	0.19	0.19	0.19	0.19	0.42	1.00	1.00	2.21	
0.34	0.97	0.625	3.68	3.27	4.035	10.82	3.37	6.46	6.85
0	0	0	0	0.16	0.16		HS Only	HS Only	
0.11	0	0.06	0	0.11	0	0.00	HS Only	0.00	
0.07	0.07	0.07	0.09	0.03	0.11	1.29	0.43	1.57	
0.15	0	0.15	0.15	0.15	0.15	1.00	HS Only	1.00	
0	0	0.2	0	0	0			0.00	
0.74	0.74	0.17	0.74	1.225	0.9	1.00	1.66	5.29	0.00
0	0	0.17	0.485	0.6	0.87	HS Only	HS Only	5.12	
0.42	0.19	0.19	0.56	0.61	0.725	1.33	3.21	3.82	
0	0	0.12	0	0	0.39			3.25	
0.09	0	0.09	0.19	0.09	0.14	2.11	HS Only	1.56	
0	0	0	0.05	0.05	0.05	HS Only	HS Only	HS Only	
0	0	0	0	0	0.04			HS Only	
0	0	0	0.16	0	0	HS Only			
0	0	0	0	0	0.14			HS Only	
0	0	0	0.05	0.05	0	HS Only	HS Only		
0.12	0.37	0.37	0.37	0.295	0.295	3.08	0.80	0.80	0.47
0	0.06	0	0	0	0		0.00		
0.075	0.16	0.05	0.105	0.1	0.135	1.40	0.63	2.70	0.42
0.29	0.29	0.14	0.29	0.14	0	1.00	0.48	0.00	
0	0	0	0.13	0	0.095	HS Only		HS Only	
0.05	0.05	0	0.17	0.44	0.17	3.40	8.80	HS Only	
0.07	0.285	0.245	0	0.07	0	0.00	0.25	0.00	
0	0	0.03	0.03	0	0.06	HS Only		2.00	
0	0.04	0	0	0	0		0.00		
3.375	5.625	2.78	3.18	4.22	3.51	0.94	0.75	1.26	0.35
0	0	0	0	0	0.04			HS Only	
0.115	0.195	0.09	0.115	0.09	0.18	1.00	0.46	2.00	0.65
0	0.075	0	0	0	0		0.00		
0	0	0	0	0.03	0		HS Only		
0.02	0.02	0.02	0.02	0.03	0.03	1.00	1.50	1.50	
0	0	0	0.08	0.08	0.08	HS Only	HS Only	HS Only	
0.09	0	0.09	0	0.09	0.09	0.00	HS Only	1.00	
0	0	0	0	0.09	0		HS Only		
0	0	0	0	0.09	0.09		HS Only	HS Only	
0	0	0	0.19	0.09	0	HS Only	HS Only		
0	0	0	0	0.1	0.05		HS Only	HS Only	
0	0	0	0	0.25	0.12		HS Only	HS Only	
0.06	0.12	0.06	0.555	0.64	0.41	9.25	5.33	6.83	
7.04	8.785	11.03	8.725	4.905	14.255	1.24	0.56	1.29	0.23
3.71	2.24	3.34	33.39	62.045	16.035	9.00	27.70	4.80	10.20

0	0	0	0.21	0.1	0.1	HS Only	HS Only	HS Only	
0.05	0.05	0.075	0.05	0	0.1	1.00	0.00	1.33	
0	0.02	0.02	0	0	0.02		0.00	1.00	
0.27	0.435	0.27	4.33	5.195	5.285	16.04	11.94	19.57	6.44
0	0.06	0.12	0.06	0.09	0	HS Only	1.50	0.00	
0	0	0	0.02	0.02	0	HS Only	HS Only		
0	0	0	0.05	0.05	0	HS Only	HS Only		
0.05	0.05	0.05	0.235	0.075	0.1	4.70	1.50	2.00	
6.145	7.435	16.56	8.845	10.965	12.485	1.44	1.47	0.75	0.06
0	0	0.08	0	0	0			0.00	
1.815	2.285	3.655	1.76	2.185	1.92	0.97	0.96	0.53	0.13
0	0.03	0	0	0	0		0.00		
0	0	0	0.39	0.39	0.39	HS Only	HS Only	HS Only	
0	0	0	0	0	0.06			HS Only	
0.07	0.07	0	0.11	0.07	0.15	1.57	1.00	HS Only	
0.17	0.08	0.11	0.05	0.08	0.05	0.29	1.00	0.45	
0.665	1.315	1.35	1.435	1.02	1.175	2.16	0.78	0.87	2.47
0.59	0.17	0.36	1.8	1.27	1.185	3.05	7.47	3.29	
0	0	0	0.06	0.13	0	HS Only	HS Only		
0.085	0.145	0.24	0.11	0.12	0.18	1.29	0.83	0.75	0.59
0	0	0	0.08	0.11	0.14	HS Only	HS Only	HS Only	
0	0.11	0.11	0.11	0.11	0.11	HS Only	1.00	1.00	
0	0.05	0	0	0	0.05		0.00	HS Only	
0.13	0	0	0	0	0	0.00			
0	0	0	0.1	0.155	0.1	HS Only	HS Only	HS Only	
0.2	0.28	0.28	1.735	1.82	1.91	8.68	6.50	6.82	
0	0	0	0.16	0	0	HS Only			
0	0	0	0.25	0.25	0	HS Only	HS Only		
0	0.2	0	0.2	0	0.2	HS Only	0.00	HS Only	
0	0	0	0.15	0	0	HS Only			
0	0.09	0.09	0	0	0		0.00	0.00	
0.06	0.06	0.06	0	0	0	0.00	0.00	0.00	
0	0.06	0	0	0	0.06		0.00	HS Only	
0	0	0	0	0	0.03			HS Only	
0.35	0.55	0.345	0.345	0.43	0.34	0.99	0.78	0.99	0.23
0	0	0.07	0	0	0			0.00	
0	0	0	0.13	0	0	HS Only			
0	0.31	0	0.31	0	0	HS Only	0.00		
0	0.07	0	0	0	0		0.00		
0	0.05	0	0.1	0.05	0.21	HS Only	1.00	HS Only	
0	0.25	0.12	0.12	0.12	0.12	HS Only	0.48	1.00	
0	0.04	0	0.04	0.04	0.04	HS Only	1.00	HS Only	
0	0	0	0.25	0.12	0.205	HS Only	HS Only	HS Only	
0.36	0.36	0.32	0.13	0.13	0.13	0.36	0.36	0.41	0.00
0.11	0.165	0.235	0.11	0.22	0.165	1.00	1.33	0.70	
0	0	0	0.15	0.15	0	HS Only	HS Only		
0	0	0	0.14	0.14	0	HS Only	HS Only		

0	0.06	0	0.06	0	0.06	HS Only	0.00	HS Only	
0	0	0	0.06	0.06	0.13	HS Only	HS Only	HS Only	
0	0	0	0.11	0	0	HS Only			
0	0	0	0.06	0.06	0.06	HS Only	HS Only	HS Only	
0	0	0	0	0.05	0.05		HS Only	HS Only	
0.08	0.08	0.08	0.08	0.08	0.08	1.00	1.00	1.00	
0	0.08	0.08	0	0.08	0.08		1.00	1.00	
0.06	0.13	0.06	0.075	0.1	0.045	1.25	0.77	0.75	3.18
0.065	0.065	0	0	0.04	0.04	0.00	0.62	HS Only	
0	0	0	0.04	0.065	0.04	HS Only	HS Only	HS Only	
0	0.03	0	0	0	0		0.00		
0	0	0	0.265	0.155	0.155	HS Only	HS Only	HS Only	
0.27	0	0	0.52	0.43	0.61	1.93	HS Only	HS Only	
0	0	0.05	0.05	0.1	0.075	HS Only	HS Only	1.50	
0	0	0	0.14	0.09	0.09	HS Only	HS Only	HS Only	
0.07	0.07	0	0	0	0	0.00	0.00		
0	0	0	0	0.22	0		HS Only		
0	0	0	0	0	0.11			HS Only	
0.285	0.44	0.28	2.105	2.14	1.58	7.39	4.86	5.64	7.40
0.2	0.32	0.2	0.63	0.45	0	3.15	1.41	0.00	
0	0	0.06	0	0	0			0.00	
0.12	0	0.16	0	0.08	0.08	0.00	HS Only	0.50	
0.05	0.08	0	0.05	0.05	0.08	1.00	0.63	HS Only	
0.21	0.1	0.1	0	0	0.1	0.00	0.00	1.00	
0	0	0	0	0	0.06			HS Only	
0	0.04	0.04	0	0	0		0.00	0.00	
0	0.04	0.04	0	0.04	0		1.00	0.00	
0.03	0.07	0.1	0.04	0	0.02	1.33	0.00	0.20	
0	0	0	0.05	0	0.11	HS Only		HS Only	
0	0.1	0	0.1	0	0.1	HS Only	0.00	HS Only	
0	0.04	0.02	0	0	0		0.00	0.00	
0	0	0.04	0	0	0			0.00	
0	0	0	0	0.06	0		HS Only		
0	0	0	0.05	0	0	HS Only			
0	0	0.04	0	0	0			0.00	
0	0	0	0.06	0.045	0.03	HS Only	HS Only	HS Only	
0	0.06	0	0.03	0	0.06	HS Only	0.00	HS Only	
0	0	0	0	0	0.06			HS Only	
0.07	0	0	0	0	0	0.00			
0.03	0.07	0.03	0.05	0	0.03	1.67	0.00	1.00	
0	0.05	0.05	0	0	0		0.00	0.00	
0.395	0.555	0.55	1.27	0.47	0.635	3.22	0.85	1.15	2.62
0.16	0.295	0.42	0.735	0.355	0.46	4.59	1.20	1.10	3.71
0.05	0.17	0.11	0	0	0.05	0.00	0.00	0.45	
0	0	0.13	0	0	0			0.00	
0	0	0	0.12	0.12	0.12	HS Only	HS Only	HS Only	
0	0	0	0.12	0	0	HS Only			

0	0.11	0	0.39	0.69	0.315	HS Only	6.27	HS Only	
0	0	0	0.16	0.255	0.255	HS Only	HS Only	HS Only	
0	0	0	0.375	0.475	0.29	HS Only	HS Only	HS Only	
0.13	0.13	0	1.42	1.83	0.455	10.92	14.08	HS Only	
0.24	0.11	0	1.515	1.435	0.325	6.31	13.05	HS Only	
0	0	0	0.435	0.47	0.35	HS Only	HS Only	HS Only	
0.12	0.12	0.12	0.12	0.26	0	1.00	2.17	0.00	
0.315	0.315	0.315	1.22	1.54	1.38	3.87	4.89	4.38	4.40
0.27	0.27	0.13	0.445	0.525	0.28	1.65	1.94	2.15	
0	0	0	0.13	0.13	0	HS Only	HS Only		
0	0	0	0.715	0.82	0.13	HS Only	HS Only	HS Only	
0.35	0.35	0.35	0.46	0.695	0.82	1.31	1.99	2.34	
0.13	0.13	0	0.43	0.61	0.28	3.31	4.69	HS Only	
0	0	0	0.995	0.885	0.705	HS Only	HS Only	HS Only	
0	0.18	0	0.18	0.08	0.18	HS Only	0.44	HS Only	
0.05	0.05	0.05	0.05	0.05	0.05	1.00	1.00	1.00	
0	0	0	0.13	0.13	0	HS Only	HS Only		
0	0.09	0	0.09	0	0	HS Only	0.00		
0.1	0.1	0	0.1	0.28	0.21	1.00	2.80	HS Only	
0.08	0.08	0	0.04	0	0.06	0.50	0.00	HS Only	
0.03	0.03	0.03	0.045	0	0.15	1.50	0.00	5.00	
0.07	0.15	0.24	0.195	0.195	0.24	2.79	1.30	1.00	
0	0	0	0	0	0.07			HS Only	
0	0	0.1	0	0	0			0.00	
0	0	0	0	0	0.05			HS Only	
0	0	0	0	0	0.04			HS Only	
0	0	0	0.375	0.37	0	HS Only	HS Only		
0.06	0.06	0.06	0.09	0.06	0.06	1.50	1.00	1.00	
0	0	0	0	0.2	0		HS Only		
0.12	0.515	0.335	0.78	0.12	0.59	6.50	0.23	1.76	
0.185	0.55	0	0.73	0.39	0.4	3.95	0.71	HS Only	
0	0.03	0.02	0.05	0	0.03	HS Only	0.00	1.50	
0.03	0.085	0.065	0.05	0.065	0.085	1.67	0.76	1.31	
0	0.03	0	0.06	0	0.03	HS Only	0.00	HS Only	
0.06	0.11	0.06	0.085	0	0.115	1.42	0.00	1.92	0.59
0	0	0	0.865	0.8	0.62	HS Only	HS Only	HS Only	
0	0	0.08	0	0	0			0.00	
0.05	0.05	0.05	0.05	0.05	0.1	1.00	1.00	2.00	
0	0	0	0	0	0.03			HS Only	
0	0	0	0.08	0	0	HS Only			
0.19	0.09	0.14	0.09	0.09	0.09	0.47	1.00	0.64	
0	0	0	0.955	0.41	0.39	HS Only	HS Only	HS Only	
0.17	0.17	0.295	0.36	0.17	0.36	2.12	1.00	1.22	1.21
0	0	0	0	0.02	0		HS Only		
0.03	0	0	0	0	0	0.00			
0.09	0	0	0.4	0.405	0.53	4.44	HS Only	HS Only	
0.33	0.21	0.155	0.945	0.67	0.35	2.86	3.19	2.26	

0.02	0.04	0.02	0.06	0.05	0.055	3.00	1.25	2.75	
0	0	0	0	0.06	0.06		HS Only	HS Only	
0	0	0.05	0	0	0.05			1.00	
0	0.055	0	0	0	0		0.00		
0	0	0	0.02	0.02	0.02	HS Only	HS Only	HS Only	
0.06	0.04	0.04	0.06	0.06	0.08	1.00	1.50	2.00	1.06
0	0.09	0	0	0	0		0.00		
0	0	0	0.1	0.1	0	HS Only	HS Only		
0	0.02	0	0	0	0.02		0.00	HS Only	
0	0	0	0.72	0.23	0.435	HS Only	HS Only	HS Only	
0	0	0	0	0	0.06			HS Only	
0.04	0.04	0.04	0.065	0.04	0.09	1.63	1.00	2.25	
0.22	0.1	0.22	0.22	0.22	0.425	1.00	2.20	1.93	
0	0	0	0	0	0.06			HS Only	
0	0	0	0.765	0.765	0.27	HS Only	HS Only	HS Only	
0	0	0	0.17	0.17	0	HS Only	HS Only		
0	0	0	0	0	0.06			HS Only	
0	0	0	0.17	0	0.17	HS Only		HS Only	
0	0	0	0.04	0	0	HS Only			
0	0	0	0.07	0	0	HS Only			
0	0.2	0.2	0	0	0		0.00	0.00	
0	0.23	0.15	0.15	0	0.15	HS Only	0.00	1.00	
0	0	0.26	0	0	0			0.00	
0	0	0	0	0	0.09			HS Only	
0.34	0.34	0.34	0	0.34	0.34	0.00	1.00	1.00	
0	0	0	0.07	0	0	HS Only			
0	0.07	0	0.15	0.235	0.23	HS Only	3.36	HS Only	
0.03	0.07	0.03	0.08	0.03	0.08	2.67	0.43	2.67	
0.435	0.49	0.33	0.685	0.51	0.7	1.57	1.04	2.12	0.50
0	0.04	0	0	0	0.04		0.00	HS Only	
0.05	0.05	0.05	0.08	0.05	0.05	1.60	1.00	1.00	
0	0	0	0	0	0.13			HS Only	
0.08	0.04	0.08	0.04	0.04	0.08	0.50	1.00	1.00	
0.37	0.61	0.61	2.195	1.405	1.895	5.93	2.30	3.11	
0	0	0	0	0	0.07			HS Only	
0	0	0	0	0	0.07			HS Only	
0	0	0	0.1	0.34	0.34	HS Only	HS Only	HS Only	
0	0	0	0	0.08	0.08		HS Only	HS Only	
0.06	0.08	0.04	0.34	0.475	0.32	5.67	5.94	8.00	1.68
0	0	0.02	0	0	0			0.00	
0	0.045	0	0.02	0	0.02	HS Only	0.00	HS Only	
0	0.38	1.33	0.88	1.375	1.715	HS Only	3.62	1.29	
0.02	0.04	0.02	0	0	0	0.00	0.00	0.00	
0.615	0.955	1.175	0.775	0.775	0.78	1.26	0.81	0.66	0.07
0	0	0	0.14	0.14	0	HS Only	HS Only		
0	0	0	0.25	0	0	HS Only			
0	0	0	0.12	0	0	HS Only			

0	0.05	0.05	0.05	0	0.05	HS Only	0.00	1.00	
0	0	0	0	0	0.07			HS Only	
0	0	0	0	0	0.06			HS Only	
0	0.06	0.06	0.06	0	0	HS Only	0.00	0.00	
0	0.04	0	0	0.04	0.04		1.00	HS Only	
0.12	0.27	0.12	0.12	0.12	0.19	1.00	0.44	1.58	
0	0	0	0	0	0.08			HS Only	
0.03	0.03	0.03	0	0.03	0	0.00	1.00	0.00	
0	0.11	0	0	0	0		0.00		
0	0	0	0.07	0.07	0.07	HS Only	HS Only	HS Only	
0.04	0.08	0.04	0	0	0.04	0.00	0.00	1.00	
0.06	0.485	0.27	0.1	0.06	0.21	1.67	0.12	0.78	0.00
0	0.09	0	0.09	0.135	0.09	HS Only	1.50	HS Only	
0	0.1	0	0.1	0	0.1	HS Only	0.00	HS Only	
0.04	0.06	0.04	0	0.08	0.04	0.00	1.33	1.00	
0.11	0.24	0.11	0.11	0.175	0.11	1.00	0.73	1.00	
0.19	1.34	0.58	0.41	0.67	0.97	2.16	0.50	1.67	
0	0	0	0	0	0.05			HS Only	
0	0.03	0	0	0	0		0.00		
0	0	0.1	0.1	0.22	0.22	HS Only	HS Only	2.20	
0	0	0	0.245	0.3	0.195	HS Only	HS Only	HS Only	
0	0	0	0.11	0.11	0	HS Only	HS Only		
0	0	0	0	0	0.07			HS Only	
0	0	0	0.06	0.06	0.06	HS Only	HS Only	HS Only	
0.05	0.11	0.05	0.05	0	0.17	1.00	0.00	3.40	0.00
0.18	0.47	0.39	0.47	0.55	0.12	2.61	1.17	0.31	0.68
0	0	0.39	0	0.24	0.12		HS Only	0.31	
0.16	0.16	0	0.16	0	0	1.00	0.00		
0.04	0.04	0	0.04	0.04	0.04	1.00	1.00	HS Only	
0	0.09	0	0	0	0.09		0.00	HS Only	
0.49	0.61	0.34	0.245	0.17	0.165	0.50	0.28	0.49	0.37
0.085	0.15	0.105	0.15	0.175	0.2	1.76	1.17	1.90	0.22
0.06	0	0	0	0	0	0.00			
0	0	0	0	0.06	0		HS Only		
0	0	0.14	0.09	0	0.09	HS Only		0.64	
0	0	0.02	0	0	0			0.00	
0	0	0	0	0.06	0		HS Only		
0.655	1.2	1.08	2.78	2.45	2.535	4.24	2.04	2.35	0.32
0	0	0	0	0	0.03			HS Only	
0	0.09	0	0	0.09	0		1.00		
0.12	0.25	0.12	0	0.03	0.385	0.00	0.12	3.21	
0	0	0	0	0.2	0		HS Only		
0.03	0	0	0.03	0	0	1.00			
0.31	0.55	0.665	0.325	0.285	0.16	1.05	0.52	0.24	0.08
0.06	0.13	0	0.13	0.095	0.13	2.17	0.73	HS Only	
0.075	0.125	0.09	0.045	0.02	0.055	0.60	0.16	0.61	1.11
0	0	0	0.09	0.2	0.09	HS Only	HS Only	HS Only	

0	0	0.09	0.09	0	0.09	HS Only		1.00	
0	0	0	0	0.15	0.15		HS Only	HS Only	
0.03	0	0	0.03	0	0.05	1.00		HS Only	
0	0	0.11	0	0	0			0.00	
0	0	0	0	0	0.11			HS Only	
0.09	0.19	0.09	0.09	0.115	0	1.00	0.61	0.00	
0	0	0	0	0	0.04			HS Only	
0.22	0.29	0.29	0.29	0.165	0.165	1.32	0.57	0.57	0.45
0	0	0	0	0	0.08			HS Only	
0.33	0.15	0	0.15	0.15	0.15	0.45	1.00	HS Only	
0.13	0.14	0.24	0.06	0.045	0.16	0.46	0.32	0.67	0.04
0	0.15	0.33	0.15	0.15	0.15	HS Only	1.00	0.45	
0	0	0	0	0.14	0.14		HS Only	HS Only	
0.04	0.205	0.09	0.18	0.085	0.16	4.50	0.41	1.78	1.77
0.52	0.23	0.395	0.435	0.685	0.61	0.84	2.98	1.54	0.63
0.26	0.28	0.255	0.415	0.595	0.365	1.60	2.13	1.43	1.32
0.225	0.4	0.225	0.375	0.355	0.27	1.67	0.89	1.20	0.86
0.285	0.29	0.15	0.25	0.39	0.31	0.88	1.34	2.07	0.30
0.43	0.43	0.43	0.43	0.43	0.43	1.00	1.00	1.00	0.00
0	0	0	0.18	0	0	HS Only			
0.3	0.41	0.47	0.35	0.335	0.35	1.17	0.82	0.74	0.59
0	0	0	0.09	0.09	0	HS Only	HS Only		
0	0	0	0	0	0.24			HS Only	
0	0.05	0	0.05	0.1	0.1	HS Only	2.00	HS Only	
0	0	0.1	0.1	0.1	0.075	HS Only	HS Only	0.75	
0	0	0	0	0	0.1			HS Only	
0	0.18	0.18	0	0.18	0.18		1.00	1.00	
0	0.25	0.37	0.435	0.43	0.645	HS Only	1.72	1.74	
0.19	0.23	0.23	0.15	0.15	0.31	0.79	0.65	1.35	0.25
0	0.035	0.02	0	0	0		0.00	0.00	
0	0.13	0.13	0	0	0		0.00	0.00	
0.38	0.18	0.5	1.24	1.67	1.125	3.26	9.28	2.25	
0.06	0	0	0	0	0	0.00			
0	0	0	0	0.05	0.05		HS Only	HS Only	
0	0.05	0.05	0.05	0	0.05	HS Only	0.00	1.00	
0	0	0	0.17	0.17	0.11	HS Only	HS Only	HS Only	
0	0	0	0.71	0.71	0.73	HS Only	HS Only	HS Only	
0.12	0	0.09	0.12	0	0.185	1.00		2.06	
0	0	0	0.35	0.35	0.16	HS Only	HS Only	HS Only	
0	0	0	0.09	0	0	HS Only			
0.05	0	0.05	0	0.05	0	0.00	HS Only	0.00	
0.06	0.06	0.03	0.03	0.045	0.06	0.50	0.75	2.00	
0	0.04	0	0	0.07	0.055		1.75	HS Only	
0	0	0	0	0.12	0		HS Only		
0.05	0.05	0	0	0	0	0.00	0.00		
0	0	0	0	0.08	0.08		HS Only	HS Only	
0	0	0	0	0.02	0.02		HS Only	HS Only	

0	0	0	0.02	0.02	0	HS Only	HS Only		
0	0	0	0	0	0.14			HS Only	
0	0	0	0.06	0	0	HS Only			
0.04	0.08	0.1	0.04	0.04	0.04	1.00	0.50	0.40	
0	0	0	0.76	0.695	0.555	HS Only	HS Only	HS Only	
0	0	0	0.13	0.13	0	HS Only	HS Only		
0	0.08	0.08	0.08	0.08	0	HS Only	1.00	0.00	
0	0	0	0	0	0.08			HS Only	
0	0	0	0.18	0.18	0.18	HS Only	HS Only	HS Only	
0.23	0.23	0.23	0.11	0.17	0.23	0.48	0.74	1.00	
0.04	0	0.04	0	0	0	0.00		0.00	
0	0	0.09	0	0	0			0.00	
0.26	0.605	0.315	0.72	0.535	0.39	2.77	0.88	1.24	3.05
0	0.03	0	0	0	0.03		0.00	HS Only	
0	0	0	0	0	0.27			HS Only	
0	0	0	0	0.1	0		HS Only		
0	0	0	0	0	0.19			HS Only	
0	0.24	0.24	0	0	0.24		0.00	1.00	
0	0.1	0	0.1	0.48	0.16	HS Only	4.80	HS Only	
0	0	0	0.05	0.05	0.05	HS Only	HS Only	HS Only	
0.05	0.1	0.1	0.19	0.25	0.19	3.80	2.50	1.90	
0	0.05	0	0	0	0		0.00		
0	0	0	0.23	0.23	0.22	HS Only	HS Only	HS Only	
0	0.03	0	0	0	0		0.00		
0	0	0	0.14	0.14	0.14	HS Only	HS Only	HS Only	
0	0	0	0.73	0.98	0.44	HS Only	HS Only	HS Only	
0	0	0	0.43	0.43	0.255	HS Only	HS Only	HS Only	
0	0	0	0.385	0.385	0.145	HS Only	HS Only	HS Only	
0	0	0.3	0	0.3	0.3		HS Only	1.00	
0	0	0.28	0	0	0			0.00	
0	0	0	0.26	0	0	HS Only			
0	0	0	0	0.43	0		HS Only		
0.33	0	0.33	0	0	0	0.00		0.00	
0	0	0	0.29	0.47	0	HS Only	HS Only		
0.04	0.065	0.065	0.135	0.16	0.155	3.38	2.46	2.38	1.59
0.05	0.095	0	0.145	0.095	0.09	2.90	1.00	HS Only	
0	0	0	0	0.1	0		HS Only		
0	0	0	0	0.14	0		HS Only		
0	0	0	0	0.12	0		HS Only		
0	0	0	0.03	0	0	HS Only			
0.555	0.665	1.125	1.825	2.975	2.475	3.29	4.47	2.20	1.38
0	0	0.4	0	0	0			0.00	
0.08	0.08	0.16	0.22	0.16	0.26	2.75	2.00	1.63	
1.23	0.76	1.755	1.4	1.56	1.84	1.14	2.05	1.05	0.03
1.37	1.28	1.485	2.79	2.19	1.725	2.04	1.71	1.16	0.60
6.675	8.905	12.985	59.2	52.45	31.755	8.87	5.89	2.45	7.80
0	0	0	0.33	0.33	0.37	HS Only	HS Only	HS Only	

0.09	0.19	0.155	0.12	0.09	0.16	1.33	0.47	1.03	0.71
0	0.07	0	0.14	0.105	0.14	HS Only	1.50	HS Only	
0	0.16	0	0.16	0	0.16	HS Only	0.00	HS Only	
0	0	0.1	0.1	0	0.35	HS Only		3.50	
0.25	0.325	0.26	0.25	0.185	0.185	1.00	0.57	0.71	
0.08	0.08	0.17	0.31	0.26	0.26	3.88	3.25	1.53	
0	0	0	0.14	0	0.14	HS Only		HS Only	
0	0	0.04	0	0	0			0.00	
0.12	0.185	0.25	0.185	0.26	0.44	1.54	1.41	1.76	
0.07	0.105	0	0.105	0.105	0.23	1.50	1.00	HS Only	0.71
0	0	0	0	0.07	0		HS Only		
0	0.08	0	0	0	0		0.00		
0	0	0	0.02	0	0	HS Only			
0	0	0	0	0	0.06			HS Only	
0.03	0.03	0	0	0	0	0.00	0.00		
0.05	0.035	0	0.02	0.02	0.02	0.40	0.57	HS Only	
0	0	0	0.12	0	0	HS Only			
0	0	0	0.62	0.845	0.62	HS Only	HS Only	HS Only	
0.12	0.165	0.06	0.1	0.1	0.12	0.83	0.61	2.00	
0.355	0.685	0.65	1.005	0.49	0.46	2.83	0.72	0.71	1.35
0.09	0.31	0.09	0.09	0	0.31	1.00	0.00	3.44	
0	0.21	0	0.1	0.1	0.1	HS Only	0.48	HS Only	
0.09	0.09	0	0.14	0.09	0.19	1.56	1.00	HS Only	
0.24	0.23	0.23	0.23	0.11	0.23	0.96	0.48	1.00	1.04
0	0	0.17	0.315	0	1.015	HS Only		5.97	
0	0.04	0	0	0	0		0.00		
0	0	0.16	0	0	0			0.00	
0	0	0	0	0	0.05			HS Only	
0	0.02	0.02	0	0.05	0.07		2.50	3.50	
0	0.075	0	0.03	0	0.03	HS Only	0.00	HS Only	
0	0.04	0.04	0.04	0.04	0.04	HS Only	1.00	1.00	
0	0.07	0	0.07	0	0	HS Only	0.00		
0	0	0	0	0	0.15			HS Only	
0	0	0	0.03	0	0.03	HS Only		HS Only	
0.11	0	0	0	0	0.11	0.00		HS Only	
0	0	0	0	0	0.07			HS Only	
0	0	0	0	0.24	0		HS Only		
0	0	0	0	0.04	0		HS Only		
0	0	0	0.205	0.205	0.16	HS Only	HS Only	HS Only	
0	0	0	0	0.09	0		HS Only		
0	0	0	0.32	0.32	0	HS Only	HS Only		
0.08	0.08	0.08	0.165	0.16	0.08	2.06	2.00	1.00	
0.1	0.1	0.41	0.16	0.22	0.1	1.60	2.20	0.24	
0	0	0	0.14	0.105	0.07	HS Only	HS Only	HS Only	
0	0	0	0	0.05	0		HS Only		
0	0	0	0.15	0.06	0	HS Only	HS Only		
0	0	0	0.08	0	0	HS Only			

0.59	0.32	0.32	0.26	0.45	0.32	0.44	1.41	1.00	
0.11	0.11	0	0.11	0.11	0.11	1.00	1.00	HS Only	
0.05	0.04	0.03	0.11	0.055	0.095	2.20	1.38	3.17	
0	0.13	0	0	0	0.13		0.00	HS Only	
0	0	0.1	0.1	0.1	0.1	HS Only	HS Only	1.00	
0	0.08	0	0	0.08	0		1.00		
0.05	0.05	0.05	0.08	0.08	0.05	1.60	1.60	1.00	
0.15	0.15	0	0.32	0.15	0.32	2.13	1.00	HS Only	
0.35	0.06	0.06	0	0.06	0	0.00	1.00	0.00	
0	0	0	0.08	0.08	0	HS Only	HS Only		
0	0	0	0.08	0.12	0.08	HS Only	HS Only	HS Only	
0.14	0.14	0.31	0.225	0.225	0.315	1.61	1.61	1.02	
0	0	0	0	0.19	0		HS Only		
0.065	0.155	0.03	0.055	0.05	0.03	0.85	0.32	1.00	0.87
0.11	0.17	0.11	0.295	0.295	0.295	2.68	1.74	2.68	0.84
0.04	0	0.04	0	0.065	0	0.00	HS Only	0.00	
0.04	0.12	0.08	0.14	0.08	0.12	3.50	0.67	1.50	0.71
0.03	0.075	0.06	0.06	0.09	0.06	2.00	1.20	1.00	
0	0	0	0.14	0.14	0.105	HS Only	HS Only	HS Only	
0	0.19	0	0.12	0	0	HS Only	0.00		
0.15	0.24	0.15	0.24	0.15	0.15	1.60	0.63	1.00	
0	0	0	0.1	0.1	0	HS Only	HS Only		
0	0	0	0	0.15	0		HS Only		
0	0	0.07	0	0	0			0.00	
0	0	0	0	0.11	0.11		HS Only	HS Only	
0	0	0	0.07	0.07	0	HS Only	HS Only		
0	0.13	0	0	0	0		0.00		
0.1	0.22	0.1	0.35	0.16	0.22	3.50	0.73	2.20	
0.2	0.61	0.35	0.31	0.405	0.28	1.55	0.66	0.80	0.55
0	0.14	0	0.14	0.14	0.14	HS Only	1.00	HS Only	
0	0	0	0.27	0	0	HS Only			
0.19	0.09	0.19	0	0.29	0.09	0.00	3.22	0.47	
5.31	7.94	5.31	6.235	8.505	9.535	1.17	1.07	1.80	0.27
0.11	0.11	0.11	0.11	0.11	0.11	1.00	1.00	1.00	
0	0	0	0	0.06	0		HS Only		
0	0	0	0	0.16	0		HS Only		
0.09	0	0	0	0	0.09	0.00		HS Only	
0	0	0	0.045	0.03	0.03	HS Only	HS Only	HS Only	
0.07	0.11	0.155	0.15	0.11	0.195	2.14	1.00	1.26	0.00
0	0	0.06	0.06	0.06	0.2	HS Only	HS Only	3.33	
1.93	3.745	2.585	3.225	2.375	3.46	1.67	0.63	1.34	0.69
0.35	0.57	0.42	0.605	0.585	0.48	1.73	1.03	1.14	0.66
0.07	0.15	0.07	0.11	0.11	0.235	1.57	0.73	3.36	0.81
0.17	0	0	0.17	0.37	0	1.00	HS Only		
0	0	0	0.2	0.2	0	HS Only	HS Only		
0.13	0.13	0	0.2	0.13	0	1.54	1.00		
0.19	0.365	0.15	1.13	1.205	0.82	5.95	3.30	5.47	1.85

0	0.07	0.07	0.225	0.07	0.14	HS Only	1.00	2.00	
0	0	0	0.04	0.04	0.09	HS Only	HS Only	HS Only	
0	0	0.08	0	0	0			0.00	
0.09	0.09	0.18	0.09	0.09	0.24	1.00	1.00	1.33	
0.06	0	0	0	0	0	0.00			
0.09	0.285	0.135	0.335	0.46	0.24	3.72	1.61	1.78	
0.12	0	0	0	0.26	0	0.00	HS Only		
0	0	0	0.685	1.055	0.53	HS Only	HS Only	HS Only	
0.1	0	0	0.56	0.28	0.28	5.60	HS Only	HS Only	
0	0	0	0	0.075	0		HS Only		
0.03	0.05	0.03	0.105	0.11	0.07	3.50	2.20	2.33	
0	0	0	0	0.02	0		HS Only		
0.1	0.1	0.1	0.1	0.1	0.1	1.00	1.00	1.00	
1.535	1.63	4.25	1.37	1.535	1.415	0.89	0.94	0.33	0.14
0	0	0	0.21	0	0.38	HS Only		HS Only	
0	0.06	0	0.06	0	0	HS Only	0.00		
0.03	0.06	0.03	0.03	0.03	0.03	1.00	0.50	1.00	
0.105	0.27	0.15	0.105	0.12	0.16	1.00	0.44	1.07	0.99
0.02	0.02	0.02	0	0	0	0.00	0.00	0.00	
0	0.05	0.05	0.05	0	0	HS Only	0.00	0.00	
0.06	0.04	0.04	0.04	0	0.04	0.67	0.00	1.00	
0	0	0	0.06	0.06	0.06	HS Only	HS Only	HS Only	
0	0.04	0	0	0.04	0		1.00		
0.17	0.11	0.05	0.23	0	0	1.35	0.00	0.00	
0.02	0.04	0.02	0.02	0.03	0.04	1.00	0.75	2.00	
0.175	0.255	0.205	0.07	0.135	0.1	0.40	0.53	0.49	0.55
0	0	0.12	0	0	0.12			1.00	
0.04	0.08	0.08	0.105	0.08	0.11	2.63	1.00	1.38	0.88
0	0.03	0	0.03	0	0.03	HS Only	0.00	HS Only	
0.07	0.175	0.055	0.03	0.045	0.08	0.43	0.26	1.45	0.09
0.04	0.04	0.04	0	0	0	0.00	0.00	0.00	
0	0.03	0.03	0.045	0	0.09	HS Only	0.00	3.00	
0.01	0.01	0.03	0	0.01	0.01	0.00	1.00	0.33	
0	0	0	0	0	0.04			HS Only	
0	0	0	0	0.04	0		HS Only		
0.08	0.08	0	0.08	0.08	0.12	1.00	1.00	HS Only	
0	0	0	0.24	0.285	0.11	HS Only	HS Only	HS Only	
0	0	0	0	0	0.04			HS Only	
0.03	0.03	0.045	0.01	0.04	0.08	0.33	1.33	1.78	
0.02	0.035	0.035	0.035	0.035	0.08	1.75	1.00	2.29	1.18
0	0	0	0	0	0.02			HS Only	
0	0	0	0	0.05	0.05		HS Only	HS Only	
0	0	0	0	0.1	0		HS Only		
0.33	0.61	0.47	1.26	0.785	0.85	3.82	1.29	1.81	0.47
0	0	0	0	0.09	0		HS Only		
0	0	0	0	0.08	0		HS Only		
0	0.115	0	0.09	0.05	0.115	HS Only	0.43	HS Only	

0	0	0	0	0.11	0		HS Only		
0	0.07	0.07	0.395	0.14	0.14	HS Only	2.00	2.00	
0.25	0.47	0.285	0.745	0.515	0.48	2.98	1.10	1.68	1.86
0	0	0	0.36	0.425	0.5	HS Only	HS Only	HS Only	
0.05	0	0	0	0	0.11	0.00		HS Only	
0	0	0	0.09	0.19	0	HS Only	HS Only		
0	0	0	0	0.05	0		HS Only		
0	0	0	0	0	0.05			HS Only	
0.07	0.15	0.07	0.15	0.07	0.11	2.14	0.47	1.57	0.00
0.24	0.24	0.54	0.54	0.54	0.92	2.25	2.25	1.70	
0	0.02	0	0	0	0		0.00		
0	0	0	0.37	0.17	0.17	HS Only	HS Only	HS Only	
0	0	0	0.1	0.1	0	HS Only	HS Only		
0	0	0	0	0.37	0		HS Only		
0	0.23	0	0	0	0		0.00		
0.29	0.29	0.29	0.29	0.29	0.29	1.00	1.00	1.00	
0	0	0.34	0.34	0	0.34	HS Only		1.00	
0	0.16	0	0	0	0		0.00		
0.18	0.18	0	0.29	0.18	0.4	1.61	1.00	HS Only	
0	0.03	0	0.03	0	0	HS Only	0.00		
0	0	0.03	0	0	0			0.00	
0.05	0.105	0.05	0.1	0.075	0.05	2.00	0.71	1.00	
0	0.06	0	0	0	0		0.00		
0	0.13	0.13	0	0	0.13		0.00	1.00	
0	0	0	0	0.06	0		HS Only		
0.2	0.43	0.315	0.315	0.2	0.2	1.58	0.47	0.63	
0	0	0	0.51	0.975	0.515	HS Only	HS Only	HS Only	
0	0	0	0.05	0.05	0	HS Only	HS Only		
0	0	0.05	0	0	0			0.00	
0.2	0.44	0.505	0.8	0.815	1.065	4.00	1.85	2.11	
0.57	0.74	0.905	4.51	4.055	4.22	7.91	5.48	4.66	0.00
0	0	0.05	0	0	0.05			1.00	
0.235	0.51	0.445	0.335	0.23	0.235	1.43	0.45	0.53	2.94
0	0	0	0	0	0.07			HS Only	
0	0	0	0.05	0.05	0.05	HS Only	HS Only	HS Only	
0	0	0	0	0.22	0		HS Only		
0	0	0	0.06	0	0	HS Only			
0.09	0	0	0	0	0	0.00			
0	0.08	0.08	0.17	0.08	0.08	HS Only	1.00	1.00	
0	0.11	0	0	0.11	0.11		1.00	HS Only	
0.03	0.03	0.03	0.05	0.08	0.065	1.67	2.67	2.17	
0	0	0	0.03	0	0.03	HS Only		HS Only	
0.05	0.065	0.02	0.08	0.02	0.08	1.60	0.31	4.00	
0.02	0.04	0.02	0	0	0.02	0.00	0.00	1.00	
0	0	0	0	0	0.03			HS Only	
0	0.08	0	0.08	0.08	0	HS Only	1.00		
0	0.04	0	0.04	0.08	0.08	HS Only	2.00	HS Only	

0	0	0	0	0	0.05			HS Only	
0.05	0.1	0.05	0.22	0.19	0.22	4.40	1.90	4.40	
0.12	0	0	0.185	0.12	0.12	1.54	HS Only	HS Only	
0	0	0	0	0	0.42			HS Only	
0.19	0	0	0	0	0	0.00			
0	0	0	0.105	0.105	0.07	HS Only	HS Only	HS Only	
0	0	0.1	0.995	0.48	0.28	HS Only	HS Only	2.80	
0	0	0	0.165	0	0.08	HS Only		HS Only	
0	0	0	0	0.06	0		HS Only		
0.02	0	0	0.04	0.04	0.02	2.00	HS Only	HS Only	
0.23	0.38	0.23	0.23	0.53	0.53	1.00	1.39	2.30	0.00
0.14	0.14	0.14	0.3	0.22	0.7	2.14	1.57	5.00	
0	0.03	0	0.07	0	0	HS Only	0.00		
0	0	0	0.06	0.03	0.03	HS Only	HS Only	HS Only	
0.16	0.06	0.06	0.04	0.04	0.18	0.25	0.67	3.00	
0	0	0	0.04	0	0	HS Only			
0.135	0.29	0.18	0.29	0.235	0.135	2.15	0.81	0.75	1.14
0.19	0.495	0.26	0.42	0.265	0.62	2.21	0.54	2.38	2.71
0	0	0.165	0.11	0.22	0.59	HS Only	HS Only	3.58	
0.07	0.07	0.07	0.07	0.07	0.145	1.00	1.00	2.07	
0	0	0	0	0	0.03			HS Only	
0	0	0	0.09	0	0	HS Only			
0	0	0	0.05	0	0	HS Only			
0	0	0	0	0	0.095			HS Only	
0.06	0.07	0.08	0.03	0.08	0.04	0.50	1.14	0.50	
0.08	0.12	0.1	0.12	0.06	0.105	1.50	0.50	1.05	
0	0.03	0	0	0	0.03		0.00	HS Only	
0.08	0.08	0.08	0.08	0	0.08	1.00	0.00	1.00	
0.22	0.22	0.165	0.165	0.165	0.11	0.75	0.75	0.67	
0	0	0	0	0	0.02			HS Only	
0.13	0	0	0.13	0.29	0.29	1.00	HS Only	HS Only	
0	0	0	0	0.02	0.02		HS Only	HS Only	
0.13	0.13	0	0.31	0.095	0.2	2.38	0.73	HS Only	
0.13	0.27	0.24	0.2	0.165	0.165	1.54	0.61	0.69	
0	0.06	0	0.12	0.155	0	HS Only	2.58		
0	0.09	0	0.09	0	0	HS Only	0.00		
0.18	0.285	0.09	0.445	0.29	0.26	2.47	1.02	2.89	
0	0.06	0	0.12	0.09	0	HS Only	1.50		
0	0	0.03	0	0	0.03			1.00	
0	0.02	0	0	0	0		0.00		
0	0	0	0	0.18	0		HS Only		
0	0	0	0	0	0.06			HS Only	
0	0.05	0	0	0	0		0.00		
0	0	0.05	0	0	0			0.00	
0.11	0	0	0.355	0.355	0.42	3.23	HS Only	HS Only	
0	0	0	0	0	0.26			HS Only	
0	0	0	0.02	0	0.04	HS Only		HS Only	

0	0	0	0	0	0.1			HS Only	
0.425	1.03	0.675	1.2	1.52	0.885	2.82	1.48	1.31	0.95
0.04	0.04	0	0.23	0.205	0.16	5.75	5.13	HS Only	
0	0	0	0.07	0	0.07	HS Only		HS Only	
0	0	0	0	0.1	0		HS Only		
0	0.04	0.04	0	0	0		0.00	0.00	
0	0	0	0.37	0.27	0.37	HS Only	HS Only	HS Only	
0	0	0	0.45	0.68	1.385	HS Only	HS Only	HS Only	
0	0	0.1	0.26	0.1	0.275	HS Only	HS Only	2.75	
0	0.08	0	0	0	0		0.00		
0.1	0.48	0	0.28	0.1	0.64	2.80	0.21	HS Only	
0.165	0.31	0.145	0.145	0.11	0.145	0.88	0.35	1.00	2.12
0	0.08	0	0	0	0		0.00		
0	0	0	0.03	0.06	0	HS Only	HS Only		
0	0	0	0.03	0	0	HS Only			
0	0	0	0.07	0.15	0.07	HS Only	HS Only	HS Only	
0	0	0	0	0.28	0.28		HS Only	HS Only	
0	0.145	0.09	0	0	0.09		0.00	1.00	
0	0	0.03	0.03	0.03	0.03	HS Only	HS Only	1.00	
0	0	0	0.09	0.09	0	HS Only	HS Only		
0	0	0.08	0	0	0			0.00	
0	0.06	0.13	0.165	0.165	0.06	HS Only	2.75	0.46	
0	0	0	0.21	0.47	0	HS Only	HS Only		
0	0	0	0	0.02	0		HS Only		
0.07	0.07	0.07	0.07	0	0	1.00	0.00	0.00	
0	0.11	0.07	0.19	0.07	0.15	HS Only	0.64	2.14	
0	0	0	0.155	0.11	0.07	HS Only	HS Only	HS Only	
0	0	0	0.07	0	0	HS Only			
0	0	0	0	0.05	0		HS Only		
0.05	0.05	0	0.05	0	0	1.00	0.00		
0	0	0	0.06	0	0.06	HS Only		HS Only	
0	0	0	0.07	0	0	HS Only			
0	0	0	0	0.11	0		HS Only		
0	0	0	0	0.07	0		HS Only		
0	0	0	0	0	0.08			HS Only	
0	0.02	0.01	0.01	0.01	0.02	HS Only	0.50	2.00	
0	0	0	0.69	0.585	0.255	HS Only	HS Only	HS Only	
0	0.05	0	0.18	0.39	0.1	HS Only	7.80	HS Only	
0.05	0	0	0.175	0.23	0.485	3.50	HS Only	HS Only	
0	0	0	0.165	0.11	0.11	HS Only	HS Only	HS Only	
0	0.18	0	0.13	0.08	0.08	HS Only	0.44	HS Only	
0	0	0	0.05	0	0	HS Only			
0	0	0	0	0.05	0.05		HS Only	HS Only	
0.445	0.62	0.635	0.62	0.27	0.75	1.39	0.44	1.18	1.08
0	0	0	0.94	0.39	0	HS Only	HS Only		
0	0.18	0.18	0.18	0.18	0.18	HS Only	1.00	1.00	
0.16	0.16	0.16	0	0	0.16	0.00	0.00	1.00	

0.3	0.14	0.195	0.14	0.19	0.3	0.47	1.36	1.54	
0	0.58	0.58	0.58	1.51	0	HS Only	2.60	0.00	
0	0	0.01	0	0	0.02			2.00	
0.2	0.575	0.46	1.255	0.885	1.09	6.28	1.54	2.37	1.45
0	0.12	0	0.12	0	0.12	HS Only	0.00	HS Only	
0	0	0	0	0.37	0		HS Only		
0	0	0	0	0.05	0		HS Only		
0.02	0.02	0	0.02	0.02	0.02	1.00	1.00	HS Only	
0	0.03	0	0	0	0		0.00		
0	0	0	0.19	0	0.19	HS Only		HS Only	
0.17	0.17	0.17	0.17	0.265	0.17	1.00	1.56	1.00	0.00
0.15	0	0	0.32	0	0.15	2.13		HS Only	
0	0.11	0.175	0.175	0.11	0.24	HS Only	1.00	1.37	
0	0	0	0.12	0	0.12	HS Only		HS Only	
0	3.39	0	0	2.08	0		0.61		
0	0	0.66	0.64	0.7	0	HS Only	HS Only	0.00	
1.87	2.08	0	0	0	3.09	0.00	0.00	HS Only	
0	0	0	1.5	2.115	0	HS Only	HS Only		
0	0.92	0	0	0	0		0.00		
0	0	0.75	0	0	0			0.00	
0	0	0	2.54	0	0	HS Only			
0	0	0	1.21	0	0.55	HS Only		HS Only	
0	0	6.21	0	0	0			0.00	
0.82	1.13	0.79	1.17	0	0	1.43	0.00	0.00	
0	0	5.69	1.87	0	1.87	HS Only		0.33	
0	1.29	0	0	0	1.45		0.00	HS Only	
0	0	0	0	0	0.64			HS Only	
0.92	0	1.08	0	0	0	0.00		0.00	
0	0.75	0	0	0	0.52		0.00	HS Only	
0.58	0.72	0	0.85	0	0.63	1.47	0.00	HS Only	
0	0	0	1.49	2.08	0	HS Only	HS Only		
2.98	3.11	2.32	2.82	0	2.905	0.95	0.00	1.25	
0	0	1.45	0.99	1.025	0	HS Only	HS Only	0.00	
0	0	0	0	0	1.17			HS Only	
0.99	1.33	1.02	0	0	0	0.00	0.00	0.00	
0	0	0	0.15	0.275	0	HS Only	HS Only		
0.17	0	0.23	0.27	0.36	0.23	1.59	HS Only	1.00	
0	0	0	0	0	0.07			HS Only	
0.19	0.15	0.19	0	0	0	0.00	0.00	0.00	
0	0	0	0.37	0	0	HS Only			
0	0	0	0	0.32	0		HS Only		
0	0.02	0	0	0	0		0.00		
0	0	0	0	0.02	0		HS Only		
0	0	0	0.03	0.03	0	HS Only	HS Only		
0.15	0.06	0.03	0.425	0.39	0.58	2.83	6.50	19.33	
0.03	0.03	0.03	0.25	0.23	0.395	8.33	7.67	13.17	
0.04	0.04	0.04	0.05	0.03	0.065	1.25	0.75	1.63	

0.03	0.03	0.03	0.03	0.05	0.05	1.00	1.67	1.67	
0.105	0.265	0.18	0.165	0.14	0.24	1.57	0.53	1.33	0.92
0	0	0.1	0	0	0			0.00	
0.14	0.48	0.215	1.77	1.795	1.165	12.64	3.74	5.42	
0	0	0	0.07	0	0	HS Only			
0	0	0	0	0	0.07			HS Only	
0.14	0	0	0.3	0.31	0.3	2.14	HS Only	HS Only	
0	0	0	0	0	0.06			HS Only	
0.04	0.04	0.04	0	0	0	0.00	0.00	0.00	
0	0	0	0.14	0	0.14	HS Only		HS Only	
0	0	0	0.05	0.05	0.09	HS Only	HS Only	HS Only	
0	0	0	0	0	0.08			HS Only	
0.09	0.05	0	0.28	0.41	0.2	3.11	8.20	HS Only	
0.07	0.07	0	0.325	0.15	0.32	4.64	2.14	HS Only	
0	0	0	0	0.17	0		HS Only		
0.07	0.15	0.11	0	0.07	0.235	0.00	0.47	2.14	
0	0.07	0	0.15	0	0	HS Only	0.00		
0.07	0.11	0.07	0.19	0.15	0.23	2.71	1.36	3.29	0.81
0	0.03	0	0	0.03	0		1.00		
0.06	0.15	0.15	0.12	0.09	0.12	2.00	0.60	0.80	
0	0	0	0	0.09	0.09		HS Only	HS Only	
0	0.08	0	0.27	0.175	0.08	HS Only	2.19	HS Only	
0	0	0	0.06	0	0.06	HS Only		HS Only	
0	0	0	0.03	0.03	0.1	HS Only	HS Only	HS Only	
0.17	0.36	0.265	0.36	0.17	0.36	2.12	0.47	1.36	0.00
0.11	0.11	0.23	0.11	0.17	0.17	1.00	1.55	0.74	0.00
0.07	0.13	0.07	0.14	0.11	0.075	2.00	0.85	1.07	
0	0.19	0.12	0	0	0		0.00	0.00	
0	0.03	0	0	0	0.03		0.00	HS Only	
0.04	0.04	0.08	0.04	0.12	0	1.00	3.00	0.00	
0	0	0.03	0	0.03	0		HS Only	0.00	
0.165	0.095	0.2	0.165	0.165	0.165	1.00	1.74	0.83	0.63
0.11	0.05	0.05	0.05	0.05	0.05	0.45	1.00	1.00	
0	0.02	0	0	0	0.02		0.00	HS Only	
0.07	0.03	0.03	0.07	0.05	0.07	1.00	1.67	2.33	
0.08	0.22	0.19	0.13	0.13	0.125	1.63	0.59	0.66	0.53
0.08	0.08	0.08	0.15	0.125	0.105	1.88	1.56	1.31	
0	0	0	0	0.05	0		HS Only		
0.07	0.105	0.07	0.105	0.07	0.14	1.50	0.67	2.00	
0.12	0.25	0.12	0.285	0.155	0.19	2.38	0.62	1.58	1.69
0.09	0.065	0.04	0.14	0.04	0.04	1.56	0.62	1.00	2.90
0.05	0.14	0.05	0.27	0.11	0.24	5.40	0.79	4.80	
0.17	0.17	0.05	0.235	0.11	0.11	1.38	0.65	2.20	
0	0	0	0.34	0	0	HS Only			
0	0	0	0.39	0.39	0.39	HS Only	HS Only	HS Only	
0.17	0.37	0	0.27	0.17	0	1.59	0.46		
0	0.37	0	0.37	0.37	0.62	HS Only	1.00	HS Only	

0.41	0.99	0.41	1.98	0.99	0.41	4.83	1.00	1.00	
0.29	0.29	0.29	0.29	0.29	0.29	1.00	1.00	1.00	
0	0	0.1	0	0	0			0.00	
0	0	0	0.07	0.07	0	HS Only	HS Only		
0	0.04	0	0	0	0		0.00		
0	0	0	0	0.02	0		HS Only		
0.15	0.25	0.19	0.11	0.15	0.19	0.73	0.60	1.00	0.28
0	0	0	0	0.04	0		HS Only		
0.03	0.03	0.03	0.03	0.03	0	1.00	1.00	0.00	
0	0	0	0.14	0.14	0	HS Only	HS Only		
0.1	0.07	0	0.05	0	0.03	0.50	0.00	HS Only	
0	0.065	0.03	0.1	0.05	0.03	HS Only	0.77	1.00	
3.035	1.615	5.37	3.855	2.815	2.815	1.27	1.74	0.52	2.52
0	0.03	0	0.03	0.06	0.045	HS Only	2.00	HS Only	
0	0	0	0.2	0	0.2	HS Only		HS Only	
0.15	0.15	0.15	0.15	0	0.15	1.00	0.00	1.00	0.00
0	0.33	0	0.77	0.55	0.77	HS Only	1.67	HS Only	
0.05	0	0.05	0	0	0	0.00		0.00	
0.06	0.2	0.06	0.06	0.06	0.35	1.00	0.30	5.83	
0	0	0	0.08	0.08	0.08	HS Only	HS Only	HS Only	
0	0	0	0.08	0.17	0.36	HS Only	HS Only	HS Only	
0	0	0	0	0	0.07			HS Only	
0	0.07	0	0	0	0		0.00		
0	0	0	0.06	0.09	0.12	HS Only	HS Only	HS Only	
0	0.1	0	0.1	0.12	0.095	HS Only	1.20	HS Only	
0	0	0	0	0	0.02			HS Only	
0.03	0	0	0	0	0	0.00			
0	0.04	0.04	0	0	0		0.00	0.00	
0.02	0	0	0	0	0	0.00			
0.3	0.3	0.3	0.3	0.3	0.3	1.00	1.00	1.00	0.00
0	0	0	0	0.06	0.06		HS Only	HS Only	
0	0	0	0.2	0.2	0.13	HS Only	HS Only	HS Only	
0.425	0.98	0.735	4.83	5.02	2.85	11.36	5.12	3.88	0.19
0	0	0	0.475	0.53	0.4	HS Only	HS Only	HS Only	
0	0.08	0	0	0	0.08		0.00	HS Only	
0	0.07	0	0.07	0	0.07	HS Only	0.00	HS Only	
0	0.06	0.06	0.06	0	0	HS Only	0.00	0.00	
0	0	0	0.15	0	0	HS Only			
0	0	0	0.13	0.13	0.13	HS Only	HS Only	HS Only	
0	0.27	0	0.27	0.13	0.43	HS Only	0.48	HS Only	
0	0	0	0	0.13	0		HS Only		
0	0	0	0.16	0	0	HS Only			
0.14	0.14	0.07	0.265	0.41	0.44	1.89	2.93	6.29	
0	0	0	0.13	0	0	HS Only			
0	0	0	0.305	0.37	0.615	HS Only	HS Only	HS Only	
0	0	0	0	0.13	0		HS Only		
0	0	0	1.145	0.91	0.81	HS Only	HS Only	HS Only	

0	0	0	0.06	0.18	0.06	HS Only	HS Only	HS Only	
0.04	0.105	0.06	0.06	0.04	0.085	1.50	0.38	1.42	
0	0	0	0.03	0	0.09	HS Only		HS Only	
0	0	0	0.28	0.29	0.13	HS Only	HS Only	HS Only	
0	0	0	0	0.11	0.22		HS Only	HS Only	
0	0	0	0.05	0	0.11	HS Only		HS Only	
0	0	0	0	0	0.04			HS Only	
0	0	0	0.845	0.64	0.5	HS Only	HS Only	HS Only	
0.03	0.03	0.03	0.03	0	0	1.00	0.00	0.00	
0	0.07	0.07	0	0	0.07		0.00	1.00	
0	0	0	0	0.12	0		HS Only		
0	0.03	0	0	0	0		0.00		
0	0	0	1.49	0	0	HS Only			
0	0	0	0	0.04	0		HS Only		
0	0	0	0	0	0.08			HS Only	
0	0	0	0	0.04	0		HS Only		
0	0	0	0.07	0.07	0	HS Only	HS Only		
0	0	0.11	0	0.11	0		HS Only	0.00	
0	0.31	0	0	0.31	0.31		1.00	HS Only	
0	0	0.09	0.09	0.09	0	HS Only	HS Only	0.00	
0.13	0.095	0.06	0.095	0.06	0.29	0.73	0.63	4.83	
0	0	0	0.3	0.22	0.14	HS Only	HS Only	HS Only	
0.05	0	0	0.05	0	0	1.00			
0	0	0.03	0	0	0			0.00	
0	0	0	0	0	0.22			HS Only	
0	0	0	0	0.04	0		HS Only		
0	0	0	0.05	0.05	0.1	HS Only	HS Only	HS Only	
0	0.08	0.08	0.08	0.08	0.17	HS Only	1.00	2.13	
0	0	0	0	0.07	0		HS Only		
0	0	0	0.07	0.07	0	HS Only	HS Only		
0	0	0	0.1	0.21	0.1	HS Only	HS Only	HS Only	
0	0	0.04	0.04	0	0	HS Only		0.00	
0	0	0.22	0	0.22	0.22		HS Only	1.00	
0	0	0	0.04	0	0.04	HS Only		HS Only	
0	0.255	0	0.09	0	0.09	HS Only	0.00	HS Only	
0	0	0.02	0.02	0	0.02	HS Only		1.00	
0	0.18	0.29	0.29	0.29	0.19	HS Only	1.61	0.66	
0.21	0.895	0.56	0.88	0.77	0.88	4.19	0.86	1.57	2.64
0	0.07	0.07	0	0.07	0.07		1.00	1.00	
0	0	0	0.11	0.11	0.23	HS Only	HS Only	HS Only	
0.04	0.11	0.04	0	0.04	0.04	0.00	0.36	1.00	
0	0	0	0.15	0	0	HS Only			
0.05	0.175	0.125	0	0	0.2	0.00	0.00	1.60	
0	0.51	0.51	0.51	0.51	0.51	HS Only	1.00	1.00	
0.17	0.08	0.17	0.08	0.125	0.08	0.47	1.56	0.47	
0	0	0	0.17	0	0	HS Only			
0.05	0	0.05	0.05	0.05	0.05	1.00	HS Only	1.00	

0	0.11	0	0	0	0.11		0.00	HS Only	
0	0	0	0.09	0.14	0	HS Only	HS Only		
0.065	0.04	0.04	0	0.04	0	0.00	1.00	0.00	
0	0	0.19	0	0	0			0.00	
0	0.08	0	0.12	0.08	0.08	HS Only	1.00	HS Only	
0	0	0	0.09	0	0.09	HS Only		HS Only	
0	0.03	0.03	0	0.03	0.03		1.00	1.00	
0	0.11	0	0	0.17	0.11		1.55	HS Only	
0	0	0	0.13	0	0	HS Only			
0	0	0	0.1	0.1	0.1	HS Only	HS Only	HS Only	
0	0	0	0.05	0.03	0.08	HS Only	HS Only	HS Only	
0	0	0	0.135	0.18	0.09	HS Only	HS Only	HS Only	
0	0	0.06	0.06	0	0	HS Only		0.00	
0	0	0	0.25	0.56	0.12	HS Only	HS Only	HS Only	
0.09	0.09	0.09	0.09	0.09	0.19	1.00	1.00	2.11	
0	0.25	0	0.41	0.25	0.25	HS Only	1.00	HS Only	
0	0	0	0.04	0	0	HS Only			
0.05	0	0	0.05	0	0	1.00			
0	0	0	0	0	0.17			HS Only	
0	0	0	0.915	1.575	0.57	HS Only	HS Only	HS Only	
0.35	0	0.35	0	0	0.35	0.00		1.00	
0	0	0	0	0	0.06			HS Only	
0	0	0	0.18	0.09	0	HS Only	HS Only		
0	0	0	0.05	0	0	HS Only			
0	0.1	0	0	0	0		0.00		
0	0	0	0	0	0.16			HS Only	
0.09	0.19	0.09	0.14	0	0	1.56	0.00	0.00	
0	0.35	0.16	0.16	0.16	0	HS Only	0.46	0.00	
0.04	0.16	0.1	0.185	0.1	0.185	4.63	0.63	1.85	0.88
0.05	0.085	0.07	0.07	0.07	0.065	1.40	0.82	0.93	0.94
0	0	0	0	0	0.05			HS Only	
0	0	0	0	0	0.03			HS Only	
0	0	0	0.09	0.09	0.09	HS Only	HS Only	HS Only	
0	0	0.12	0	0	0			0.00	
0	0	0.12	0.12	0.12	0.12	HS Only	HS Only	1.00	
0	0.03	0	0.03	0.03	0.03	HS Only	1.00	HS Only	
0	0	0	0.31	0	0	HS Only			
0	0	0	0	0	0.06			HS Only	
0	0	0	0.1	0	0.1	HS Only		HS Only	
0.21	0.1	0.21	0.27	0.155	0.1	1.29	1.55	0.48	
0.09	0.145	0.145	0.5	0.815	0.33	5.56	5.62	2.28	1.10
0	0	0.03	0	0	0			0.00	
0.06	0.06	0	0.06	0	0	1.00	0.00		
0	0	0	0.25	0.325	0.12	HS Only	HS Only	HS Only	
0	0	0	0.235	0.19	0.135	HS Only	HS Only	HS Only	
0	0	0	0.08	0	0	HS Only			
0	0	0	0.06	0	0	HS Only			

0.13	0	0.13	0.13	0.13	0.13	1.00	HS Only	1.00	
0.29	0.42	0.53	0.53	0.4	0.29	1.83	0.95	0.55	0.40
0	0	0	0.03	0.05	0.11	HS Only	HS Only	HS Only	
0	0	0	0.405	0.31	0.16	HS Only	HS Only	HS Only	
0	0	0	0	0	0.08			HS Only	
0	0	0	0	0.36	0		HS Only		
0.16	0.16	0.08	0.25	0.3	0.12	1.56	1.88	1.50	
0	0	0.04	0	0	0			0.00	
0.03	0.055	0.03	0.03	0	0.055	1.00	0.00	1.83	
0	0	0	0.12	0.12	0.12	HS Only	HS Only	HS Only	
0.45	0	0	0	0	0.45	0.00		HS Only	
0.5	0.5	0.5	0.5	0.5	0.5	1.00	1.00	1.00	
0	0	0	0	0.2	0		HS Only		
0	0.07	0	0.14	0	0	HS Only	0.00		
0	0	0	0.58	0	0	HS Only			
0.04	0.04	0	0.105	0.125	0.04	2.63	3.13	HS Only	
0.05	0	0	0.135	0.16	0.16	2.70	HS Only	HS Only	
0	0	0	0	0	0.03			HS Only	
0.03	0	0.03	0.03	0	0.03	1.00		1.00	0.00
0	0.05	0	0	0	0		0.00		
0	0	0	0	0	0.03			HS Only	
0	0	0	0	0	0.05			HS Only	
0	0	0	0	0.19	0		HS Only		
0	0.11	0	0	0	0		0.00		
0	0	0	0	0.09	0		HS Only		
0	0.11	0.11	0.11	0	0.175	HS Only	0.00	1.59	
0	0.11	0.11	0.17	0.11	0.11	HS Only	1.00	1.00	
0	0	0	0.09	0	0	HS Only			
0.105	0.265	0.14	0.175	0.09	0.095	1.67	0.34	0.68	1.10
0	0	0	0.18	0.285	0.285	HS Only	HS Only	HS Only	
0	0	0.37	0	0	0.37			1.00	
0	0	0	0	0.47	0.21		HS Only	HS Only	
0	0.1	0	0	0	0		0.00		
0	0	0	0.18	0	0	HS Only			
0.31	0.31	0	0.31	0	0.31	1.00	0.00	HS Only	
0	0	0	0	0	0.13			HS Only	
0	0	0	0	0.12	0		HS Only		
0	0	0	0	0.09	0		HS Only		
0	0	0	0.23	0.49	0	HS Only	HS Only		
0	0	0	0	0.07	0		HS Only		
0	0	0	0.095	0.165	0.13	HS Only	HS Only	HS Only	
0	0.12	0	0.08	0.08	0.08	HS Only	0.67	HS Only	
0	0.03	0	0	0	0		0.00		
0.335	0.795	0.46	0.46	0.335	0.335	1.37	0.42	0.73	0.84
0.15	0.15	0.15	0.235	0.445	0.235	1.57	2.97	1.57	
0	0	0	0	0.09	0		HS Only		
0	0	0	0.185	0.255	0.12	HS Only	HS Only	HS Only	

1.455	0.915	1.695	3.86	4	4.02	2.65	4.37	2.37	0.63
0.03	0.03	0.05	0.03	0	0.03	1.00	0.00	0.60	
0	0.06	0.06	0.53	0.4	0.2	HS Only	6.67	3.33	
0	0	0	0.17	0	0	HS Only			
0	0	0	0.07	0.03	0	HS Only	HS Only		
0	0	0	0	0	0.07			HS Only	
0.03	0.045	0.045	0.11	0.045	0.16	3.67	1.00	3.56	0.94
0	0	0.02	0	0.02	0.02		HS Only	1.00	
0.1	0	0	0	0	0	0.00			
0	0.15	0.215	0.06	0.06	0.25	HS Only	0.40	1.16	
0.42	0.79	0.735	1.29	0.825	1.25	3.07	1.04	1.70	1.18
0	0	0	0	0.01	0.02		HS Only	HS Only	
0	0	0.14	0.14	0.3	0	HS Only	HS Only	0.00	
0	0	0	0.16	0	0	HS Only			
0	0	0.08	0	0.08	0.08		HS Only	1.00	
0.12	0.12	0.12	0.185	0.185	0.12	1.54	1.54	1.00	
0.03	0	0	0	0	0.03	0.00		HS Only	
0.06	0	0	0	0	0	0.00			
0	0.04	0	0.04	0.04	0	HS Only	1.00		
0	0.03	0	0.03	0.07	0.05	HS Only	2.33	HS Only	
0.03	0.03	0	0	0	0	0.00	0.00		
0	0	0	0.05	0	0	HS Only			
0	0	0.03	0	0	0.03			1.00	
0	0	0	0	0.11	0		HS Only		
0	0.16	0	0.16	0.16	0.16	HS Only	1.00	HS Only	
0.04	0.04	0.04	0.04	0.04	0	1.00	1.00	0.00	
0.13	0.13	0.13	0.13	0.13	0.13	1.00	1.00	1.00	
0	0	0	0	0.13	0		HS Only		
0.05	0.135	0.105	0.11	0.08	0	2.20	0.59	0.00	0.00
0	0	0	0.03	0.045	0.06	HS Only	HS Only	HS Only	
0.04	0.04	0.04	0	0	0.04	0.00	0.00	1.00	
0	0	0	0.05	0	0	HS Only			
0.215	0.29	0.215	0.14	0.215	0.4	0.65	0.74	1.86	0.37
0.39	0.515	0.575	0.155	0.16	0.34	0.40	0.31	0.59	
0.21	0.16	0.155	0.7	0.555	0.635	3.33	3.47	4.10	0.11
0.08	0.04	0.06	0.08	0	0.24	1.00	0.00	4.00	
0.475	0.765	0.545	2.98	3.34	3.55	6.27	4.37	6.51	12.13
0	0	0	0.08	0.08	0.08	HS Only	HS Only	HS Only	
0	0	0	0.475	0.475	0.385	HS Only	HS Only	HS Only	
0	0.26	0.12	0.19	0.12	0.12	HS Only	0.46	1.00	
0	0	0	0	0.14	0		HS Only		
0	0	0	0	0	0.3			HS Only	
0.03	0.03	0.03	0.03	0.03	0	1.00	1.00	0.00	
0	0	0	0	0	0.06			HS Only	
0	0.04	0.04	0.04	0.04	0.06	HS Only	1.00	1.50	
0	0	0	0	0.06	0.06		HS Only	HS Only	
0	0	0	0	0.16	0		HS Only		

0	0.04	0	0	0	0		0.00		
0	0	0.025	0	0	0			0.00	
0	0	0	0	0.05	0		HS Only		
0.51	0.51	0.51	0.48	0.84	1.72	0.94	1.65	3.37	1.12
0	0	0	0	0.11	0		HS Only		
0	0	0	0	0.13	0.13		HS Only	HS Only	
0	0.05	0	0.05	0	0	HS Only	0.00		
0	0.1	0	0.1	0	0.1	HS Only	0.00	HS Only	
0	0.03	0	0	0	0		0.00		
0.07	0.07	0.15	0.07	0.07	0.24	1.00	1.00	1.60	

‹			Reproducibility between replicate experiments					
ıdard Deviation			Standard Deviation					
Knockout	**Mutant**	**Protein**	**WT-GR**	**KO-GR**	**MU-GR**	**WT-HS**	**KO-HS**	**MU-HS**
3.15	3.05	GPP1_YEAST	0.00	0.11	0.00	0.41	0.00	0.40
		GPP2_YEAST						
		BDH1_YEAST				0.00		0.06
0.09	0.09	NEW1_YEAST	0.21	0.03	0.16	0.10	0.08	0.21
2.84	3.68	RNQ1_YEAST		0.21	0.14	0.25	0.07	0.56
	0.31	FKS1_YEAST	0.00	0.01	0.06	0.01		0.06
		FKS2_YEAST						
0.22	0.09	GAS1_YEAST	0.06	0.06	0.12	0.11	0.05	0.11
0.02	0.20	GAS5_YEAST	0.11	0.13	0.13	0.00	0.05	0.00
	13.40	GLGB_YEAST			0.04	0.13	0.16	0.48
0.40		CH10_YEAST		0.32		0.32	0.00	0.00
		HSP12_YEAST					0.00	
0.79	1.48	SNU13_YEAST	0.74	0.33	0.00	0.93	0.00	0.93
		NOB1_YEAST				0.00		
		PRS4_YEAST						
		PRS6A_YEAST				0.00	0.12	
		PRS6B_YEAST				0.06		
		PRS7_YEAST	0.00			0.12	0.14	0.48
		PRS8_YEAST				0.07	0.14	0.00
		PRS10_YEAST				0.00	0.00	
		RPN1_YEAST					0.00	0.00
		RPN11_YEAST				0.09	0.11	0.00
		RPN13_YEAST					0.00	
		RPN2_YEAST						
		RPN7_YEAST						
		RPN8_YEAST				0.00	0.08	
		PANE_YEAST				0.00	0.00	
		DOG2_YEAST						
		LEU9_YEAST					0.04	
		LEU1_YEAST				0.04		
		ODO1_YEAST					0.05	0.05
		RIB3_YEAST					0.00	0.00
		PDE1_YEAST				0.00	0.06	0.06
		HSP30_YEAST				0.10	0.00	0.23
	1.56	RT01_YEAST			0.00	0.08	0.08	0.16
		RT13_YEAST						
		RT06_YEAST	0.00			0.22	0.22	0.22
		RT02_YEAST				0.25	0.00	
		RT04_YEAST				0.00	0.00	0.00
		RT51_YEAST		0.00		0.00		
		NAM9_YEAST				0.00		0.05
		RTPT_YEAST				0.00	0.00	
		RSM28_YEAST						

		RT10_YEAST				0.00	0.13	
		RT12_YEAST						
		RT17_YEAST				0.23	0.00	0.11
		RT18_YEAST				0.00	0.26	
		RT19_YEAST					0.00	
		RT23_YEAST		0.00				
		RT24_YEAST						
		RT25_YEAS7						
		RT26_YEAST				0.00	0.09	
		RT28_YEAST				0.08	0.08	
		RT35_YEAST						
		RT05_YEAST				0.00	0.08	
		RT07_YEAST				0.11		
		RT08_YEAST				0.49	0.00	
		RT09_YEAST				0.00	0.00	
		SWS2_YEAST				0.00		
		HMDH1_YEAST						
		HMDH2_YEAST						
		3HAO_YEAST						
		HIBCH_YEAST						
		LEUC_YEAST				0.00		
4.58	5.38	LEU3_YEAST		0.07	0.08		0.62	0.84
		MKAR_YEAST						
		ERG27_YEAST	0.00	0.00				
		RSSA1_YEAS1			0.28			
0.77		RSSA2_YEAS1		0.28		0.00	0.22	
1.58	0.43	RS10A_YEAST	1.08	0.77	2.96	1.36	6.13	0.00
0.08	0.17	RS11_YEAST	1.79	0.00	6.45	1.23	0.68	4.67
1.69	0.47	RS12_YEAST	0.41	0.00	0.91	0.00	2.33	1.87
0.01	0.08	RS13_YEAST	2.29	0.75	0.00	0.50	0.62	0.62
		RS14A_YEAST				2.86	3.60	15.08
		RS14B_YEAST		13.40	6.92			
0.01	0.37	RS15_YEAST	4.12	3.74	5.08	1.77	1.74	1.77
0.00	0.00	RS16_YEAST	1.11	2.01	1.11	2.48	2.01	1.11
0.93	0.43	RS17A_YEAST	2.65	2.65	0.00	2.14	12.13	12.34
0.13	0.51	RS18_YEAST	2.48	5.05	2.02	9.55	5.06	8.63
0.29	0.41	RS19A_YEAST	0.70	2.01	0.73	0.00	0.59	1.07
0.17	0.32	RS3A1_YEAS1	9.60	4.67	2.50	0.67	0.76	10.08
0.39	0.16	RS3A2_YEAS1	8.53	11.14	5.96	0.60	2.03	6.72
0.35	0.18	RS2_YEAST	1.46	0.33	0.00	0.25	1.14	1.14
0.63	0.12	RS20_YEAST	1.30	0.00	3.78	4.00	4.80	1.30
		RS21A_YEAST	1.82		4.97	0.00	9.69	
		RS21B_YEAST					9.69	8.83
0.17	0.37	RS22A_YEAST	3.98	0.00	72.18	3.17	3.17	10.67
0.00	0.07	RS23_YEAST	0.56	0.00	0.38	0.00	0.00	0.21
0.30	0.47	RS24_YEAST	0.00	1.53	1.53	2.22	1.79	2.76
0.37	0.00	RS25A_YEAST	1.17	0.89	2.06	2.06	0.67	2.06

8.40		RS26A_YEAST		1.51		0.52	2.18	
		RS26B_YEAST						1.22
0.15	0.35	RS27A_YEAST	6.03	1.92	0.00	3.26	0.00	4.19
0.60		RS28A_YEAST	1.32	0.00		11.16	11.00	28.04
		RS28B_YEAST			22.92		11.00	
1.56		RS29A_YEAST	1.77	0.69	1.11		0.69	
		RS29B_YEAST		0.00				
0.18	0.25	RS3_YEAST	1.56	1.96	0.66	0.40	0.31	1.20
0.09	0.25	RS30_YEAST	14.95	23.38	14.26	5.83	3.73	14.44
0.15	0.28	RS37_YEAST	0.47	5.07	1.65	5.14	0.00	0.67
0.47	0.33	RS4_YEAST	0.00	1.06	5.15	1.81	2.84	0.00
0.63	0.48	RS5_YEAST	0.18	0.18	0.23	0.18	0.23	0.79
0.22	0.12	RS6_YEAST	6.90	3.73	4.81	2.47	5.92	7.23
0.20	0.63	RS7A_YEAST	0.49	1.46	2.03	0.00	2.16	1.24
0.02	0.46	RS7B_YEAST	0.36	2.78	6.75	0.00	0.78	0.57
0.35	0.28	RS8_YEAST	1.17	0.33	2.14	1.70	1.17	2.45
		RS9A_YEAST	0.62	1.17	1.58	0.00		
		RS9B_YEAST						
		GATA_YEAST				0.16	0.31	0.12
		PNPP_YEAST						
0.45	0.12	XRN1_YEAST	0.01	0.04	0.04	0.04	0.05	0.08
		XRN2_YEAST		0.02				
	0.59	IMG1_YEAST			0.41	0.00	0.18	1.00
		RM01_YEAST				0.09		
		RM11_YEAST						
0.00	0.00	MNP1_YEAST	0.00	0.00	0.00	0.00	0.00	0.00
		RM13_YEAST						
		RM15_YEAST						
		RM17_YEAST				0.00		
		RM19_YEAST				0.23	0.20	0.43
		RM02_YEAST					0.21	0.06
		RM23_YEAST						
		RM24_YEAST						
		RM28_YEAST				0.00	0.18	
		RM03_YEAST				0.00		
		RM33_YEAST			0.00	0.40	0.40	
		RM34_YEAST						
		RM35_YEAST	0.06			0.00	0.06	0.13
		RM36_YEAST						
0.00		RM38_YEAST	0.00	0.00	0.23		0.00	
		RM04_YEAS7						
		RM40_YEAST						
0.96		RM44_YEAST		0.00	0.00		0.32	
		RN49_YEAST						
		RM51_YEAST						
		RM06_YEAST						
	0.39	RM08_YEAST			0.11	0.00		0.00

		RM09_YEAST						
		RL4P_YEAST						
		FTHC_YEAST						
		METE_YEAST				0.07	0.11	0.16
		RIB4_YEAST						0.00
0.43	1.31	RLA0_YEAST	0.34	0.14	0.47	0.30	0.27	0.99
		RLA3_YEAST	0.00		0.00			
0.00	1.58	RLA2_YEAST		0.80	2.28	0.80	0.80	0.34
		RLA4_YEAST		0.00				
		NMD3_YEAST				0.04		
0.60	2.88	RL1_YEAST	0.52	0.00	0.40	0.28	0.60	1.85
0.21	0.10	RL10_YEAST	1.53	0.43	1.54	0.87	0.74	1.13
		RL11A_YEAST	0.31	0.66		0.22		1.50
		RL11B_YEAST			1.32			
1.15	0.85	RL12_YEAST	1.71	2.07	1.69	2.50	0.55	1.01
		RL13A_YEAST		0.00		0.00		0.45
		RL13B_YEAST	0.54				0.00	
		RL14A_YEAST	1.46	0.52		3.41		0.94
		RL14B_YEAST						
0.12	0.18	RL15A_YEAST	2.13	0.45	1.22	0.52	1.12	0.98
0.23	0.18	RL16A_YEAST	0.22	0.29	0.76	0.00	0.22	0.18
0.15		RL16B_YEAST	0.25	0.00	0.54	0.56	0.22	
0.47	0.31	RL17A_YEAST	4.70	2.35	1.50	1.44	0.66	3.21
0.58	0.31	RL17B_YEAST		2.91	1.50	1.44	0.00	3.21
0.19	0.00	RL18_YEAST	1.48	0.29	1.08	0.29	0.54	1.08
0.56	0.10	RL19_YEAST	0.78	0.00	1.24	0.19	0.49	0.93
0.09	0.29	RL2_YEAST	1.14	0.37	0.86	0.00	0.48	0.00
0.65	0.21	RL20_YEAST	4.78	0.78	4.78	2.91	4.53	4.19
0.21	0.64	RL21A_YEAST	0.37	0.96	1.59	1.96	0.53	2.89
0.87	0.47	RL21B_YEAST		0.36	0.43	0.79	0.95	1.29
	0.39	RL22A_YEAST		0.25	0.00	0.25		0.25
0.43	1.11	RL23_YEAST	22.67	21.14	248.63	21.70	17.22	174.26
0.38	0.26	RL24A_YEAST	0.83	0.00	2.21	0.57	1.71	2.93
0.02	0.30	RL24B_YEAST	2.11	0.47	0.00		0.57	1.76
0.14	1.29	RL25_YEAST	0.00	0.92	1.65	0.92	1.34	3.87
1.14	0.18	RL26A_YEAST	5.68	4.72	22.78	7.18	3.49	0.00
	0.36	RL27A_YEAST			0.95	0.00	0.76	2.90
		RL27B_YEAST						
0.22	0.33	RL28_YEAST	2.37	0.52	0.00	0.52	0.00	1.29
0.15	0.16	RL3_YEAST	0.23	0.14	0.42	0.14	0.12	0.16
0.00	5.60	RL30_YEAST	0.98	0.00	1.73	1.31	0.00	3.63
1.33	0.30	RL31A_YEAST	0.00	0.27	0.34	0.00	0.27	0.00
0.82	0.79	RL32_YEAST	1.70	0.80	1.25	0.45	0.00	1.35
0.30	0.03	RL33A_YEAST	1.53	0.87	1.15	1.53	0.00	0.50
		RL33B_YEAST		1.51				
0.00		RL34A_YEAST	1.17	0.40		0.40	0.40	1.24
		RL34B_YEAST						

0.41	0.56	RL35_YEAST	1.84	2.33	0.00	1.03	0.00	4.28
		RL36A_YEAST	3.31		1.44	3.38	1.07	
		RL36B_YEAST						
0.15	0.43	RL38_YEAST	21.80	8.72	30.82	39.54	0.00	37.77
		RL39_YEAST	0.00		0.75			
		RL40_YEAST						
1.47	1.21	RL44_YEAST	0.00	0.66	0.00	0.00	0.29	0.87
0.00	0.04	RL43_YEAST	0.71	0.52	0.98	0.89	0.52	0.52
0.01	0.31	RL4B_YEAST	0.66	0.43	0.21	0.30	0.36	0.86
1.26	1.61	RL5_YEAST	0.00	0.18	0.00	0.00	0.08	0.18
		RL6A_YEAST						
		RL6B_YEAST	0.56	0.51	0.78	0.00		
0.43		RL7A_YEAST	0.37	0.18	0.66	0.42	0.19	
		RL7B_YEAST						0.00
0.37	0.30	RL8A_YEAST	0.00	0.31	1.05	1.04	0.73	1.36
0.27	0.40	RL8B_YEAST	0.00	0.74	0.00	0.82	0.31	1.78
0.62	1.33	RL9A_YEAST		0.93	3.12		0.00	0.93
		RL9B_YEAST	0.30		2.41	0.00		
		LOC1_YEAS7				0.00	0.12	
0.00		NIP7_YEAST	0.00	0.18		0.18	0.18	0.00
		NOP8_YEAST				0.05		
4.04	0.98	K6PF1_YEAST	0.00	0.05	0.03	0.03	0.16	0.21
2.11	0.96	K6PF2_YEAST		0.11	0.08	0.11	0.08	0.38
		6PGD1_YEAST				0.24	0.18	0.43
		6PGD2_YEAST						
		SOL4_YEAST				0.00	0.45	0.63
		SOL2_YEAST					0.00	
0.06	1.71	GRP78_YEAST	0.12	0.09	0.04	0.06	0.16	0.51
0.29	0.62	ARB1_YEAST	0.09	0.05	0.00	0.06	0.06	0.10
		ADY4_YEAST						
0.17	0.82	ILVB_YEAST	0.08	0.00	0.15	0.00	0.10	0.27
0.75	0.87	ILV6_YEAST		0.00	0.20	0.23	0.26	0.88
1.18		THIL_YEAST		0.00		0.33	0.21	0.25
0.13	0.41	ACAC_YEAST	0.41	0.37	0.15	0.04	0.02	0.49
		ACH1_YEAST						0.05
0.35	0.71	ACS2_YEAST	0.04	0.04	0.04	0.00	0.04	0.00
		ARGD_YEAST						
0.88	1.02	ACON_YEAST		0.00	0.00	0.07	0.04	0.18
		END3_YEAS7	0.07		0.00			
		END3_YEAST						
		PAN1_YEAS7						
		PAN1_YEAST	0.02	0.01	0.05			
0.32		SLA1_YEAS7	0.02	0.11	0.04		0.00	
0.37	2.24	ACT_YEAST	0.00	1.00	0.23	0.09	0.00	1.97
		APD1_YEAST				0.00	0.00	
		ABP1_YEAST				0.00	0.00	
		AIP1_YEAST				0.04	0.00	

0.00		ARP9_YEAST		0.00		0.05	0.00	
		PRK1_YEAST						0.09
0.00	0.20	ARP2_YEAST	0.21	0.18	0.16	0.00	0.18	0.38
		ARPC1_YEAST						
0.13	4.71	ARPC2_YEAST	0.00	0.08	0.07	0.08	0.08	0.35
0.00		ARPC3_YEAST		0.15		0.00	0.15	0.33
0.71	0.32	ARPC4_YEAST	0.18	0.00	0.34	0.00	0.47	0.55
0.00	2.25	ARPC5_YEAST	0.18	0.00	0.18	0.00	0.00	0.41
0.42	0.45	ARP3_YEAST	0.06	0.00	0.19	0.06	0.18	0.22
		ARP5_YEAST						
		ACK1_YEAST						
		ACPM_YEAST				0.00	0.24	
		ACO1_YEAST						
		AHC2_YEAST						
		APT1_YEAST						
		ADA_YEAST					0.00	
		ADK_YEAST				0.00		
1.65	3.25	SAHH_YEAST		0.00	0.00	0.38	0.25	0.49
		KAD1_YEAS1		0.42				
		KAD2_YEAST						
		PUR8_YEAST				0.00	0.16	0.00
		PURA_YEAST				0.00		
		CAP_YEAST		0.00				
		UBA4_YEAS1				0.00		
		UBA4_YEAS7						
		SPB1_YEAST				0.00	0.00	0.02
0.05	0.81	ADT2_YEAST	0.63	0.25	1.71	0.22	0.00	2.97
		ADPP_YEAST				0.13	0.11	
		ARF1_YEAST		0.00				
		AGE1_YEAST						
		AGE2_YEAST		0.18	0.00	0.00		
		GCS1_YEAST						
		GLO3_YEAST		0.05		0.05		
		GGA1_YEAST						0.00
0.03	0.04	GGA2_YEAST	0.04	0.11	0.16	0.05	0.04	0.09
		AAP1_YEAST						
		SYAC_YEAST				0.03		
1.40	2.55	ADH1_YEAST	0.81	0.59	0.19	0.00	3.00	5.62
2.99	2.83	ADH3_YEAST	0.00	0.00	0.31	0.00	0.27	0.08
		ADH4_YEAS7						
		ADH5_YEAST				0.10		
		ATF2_YEAST						
		ALDH2_YEAST				0.09	0.00	0.33
		ALDH3_YEAST				0.00	0.91	0.85
		ALDH5_YEAS7				0.00		
		LEM3_YEAST	0.00	0.00	0.00			
	7.20	TPS1_YEAST			0.05	0.12	0.13	0.33

		KTR1_YEAST		0.00	0.00	0.00		
		ADD37_YEAST						
		MPH3_YEAS8						
		MAN1_YEAST						0.00
		AIM38_YEAST		0.12				
		GCST_YEAST				0.06	0.00	
		APE2_YEAST						
		ATO3_YEAST	0.00	0.10	0.00	0.00		
		AMPD_YEAST						0.00
		YNP5_YEAST				0.20	0.09	0.00
		YO052_YEAST				0.00		
		CDC23_YEAST						
		YCU1_YEAST					0.00	
		TRPD_YEAST						
		TRPE_YEAST				0.00	0.10	
		TRPG_YEAST				0.00		
		SLH1_YEAST		0.01		0.01		
		AP1B1_YEAST						
		AP1M1_YEAST						
		AP1S1_YEAST						
0.35	0.71	AP2A_YEAST		0.02	0.00	0.00	0.00	0.02
		AP2M_YEAST						
		AP2S_YEAST			0.00	0.00	0.00	
		AIF1_YEAST						
		SYT1_YEAST						
		GEA1_YEAST						
		GEA2_YEAST						
		ARGI_YEAST				0.11	0.09	0.08
		ARGJ_YEAST						
		RMT2_YEAST				0.00	0.00	
		ARLY_YEAST					0.05	
		ASSY_YEAST				0.00		
		SYRC_YEAST				0.00		
		SYRM_YEAST						
		ARO8_YEAST				0.00	0.07	0.28
0.83	0.00	ABF2_YEAST	0.14	0.00	0.00	0.16	0.14	0.00
		ASNS2_YEAST				0.00	0.05	0.00
		SYNC_YEAST					0.00	
		AATC_YEAST				0.18	0.00	0.16
		AATM_YEAST		0.00		0.05		
		DHAS_YEAST				0.10	0.30	0.07
		MKC7_YEAST						
		SYDC_YEAST				0.04	0.00	0.08
		SYDM_YEAST					0.00	
		HIS1_YEAST				0.11	0.00	0.09
		ATPF_YEAST						0.00
		ATPO_YEAST						0.00

0.06	1.53	ATPA_YEAST	0.04	0.17	0.00	0.08	0.29	0.78
1.51	2.45	ATPB_YEAST	0.00	0.26	0.30	0.22	0.41	2.24
		ATP7_YEAST						
		ATPD_YEAST				0.00		
		ATPJ_YEAST						
		ATPK_YEAST		0.00	0.00			
0.00		ATPN_YEAST	0.00	0.00	0.00	0.00	0.00	
0.00	2.76	ATPG_YEAST		0.00	0.00	0.19	0.00	0.30
		ATP14_YEAST				0.00		
		ATP18_YEAST						
		STF2_YEAST						0.40
		HMI1_YEAST						
		KU70_YEAST						
		NAM7_YEAST				0.03	0.05	
		ULS1_YEAST						
1.56	2.24	HSC82_YEAST	0.04	0.22	0.00	0.24	0.12	0.54
		HSP82_YEAST				0.17	0.18	0.48
		MDL1_YEAST		0.00				
0.01	0.69	PDR12_YEAST	0.02	0.09	0.22	0.17	0.06	0.31
	0.28	PDR15_YEAST			0.01	0.03	0.04	0.09
		CHL1_YEAS7						
		DBP1_YEAS7						
		DBP10_YEAS7						
		DBP10_YEAST		0.00		0.00		
0.21	0.40	DBP2_YEAS7	0.57	0.21	0.09	0.33	0.58	0.57
	0.48	DBP3_YEAS7	0.00		0.11			0.00
		DBP3_YEAST					0.07	
0.00		DBP4_YEAS7		0.04		0.00	0.04	
0.35		DBP5_YEAS7		0.00	0.05	0.05	0.05	
		DBP6_YEAS7		0.00		0.00		
		DBP6_YEAST					0.00	
0.36	0.00	DBP8_YEAS7	0.12	0.00	0.18	0.00	0.12	0.18
0.47	2.20	DBP9_YEAS7	0.08	0.00	0.17	0.04	0.17	0.14
0.60	1.25	DED1_YEAS7	1.02	1.99	1.40	0.23	0.45	3.54
0.38	0.58	DHH1_YEAS7	0.10	0.06	0.00	0.00	0.11	0.25
		MTR4_YEAST		0.08		0.00		
0.06	0.54	DRS1_YEAS7		0.07	0.06	0.00	0.06	0.13
0.07	0.47	IF4A_YEAS7	0.20	0.19	0.08	0.00	0.15	0.33
		FAL1_YEAS7		0.07		0.00		
0.02	0.09	HAS1_YEAST	0.34	0.17	0.48	0.18	0.15	0.70
0.71		MAK5_YEAS7		0.00			0.03	0.09
		MAK5_YEAST						
0.07	0.69	MS116_YEAST	0.18	0.05	0.05	0.19	0.00	0.37
		ROK1_YEAS7						
	1.23	SUB2_YEAS7	0.06	0.13	0.06	0.06		0.24
		SUV3_YEAST						
		RRP3_YEAS7						

		RRP3_YEAST		0.06	0.13	0.21		
		SPB4_YEAS7				0.00		
		ATG14_YEAST						
		ATG16_YEAS7						
		ATG19_YEAS7						
		ATG2_YEAS7						
		ATG21_YEAS7				0.00		
		ATG29_YEAS7						
		ATG29_YEAST						
		CIS1_YEAST						
		BAR1_YEAST						
		PUR91_YEAST				0.00	0.16	0.00
		PUR92_YEAST				0.05	0.00	0.09
		PUR2_YEAST				0.00	0.11	
		BCA2_YEAST				0.00	0.12	0.09
		BCA1_YEAST				0.09		0.07
		BDF2_YEAST		0.00	0.00	0.00		
0.37		BEM1_YEAST	0.08	0.05	0.00	0.05	0.04	
0.00		BEM4_YEAST	0.00	0.00	0.00		0.00	
		BUD4_YEAS7		0.00				
		BUD6_YEAST						
		RAX1_YEAST		0.06	0.06			
0.00	1.20	C1TC_YEAST	0.03	0.06	0.06	0.03	0.06	0.00
0.00	0.13	C1TM_YEAST	0.23	0.06	0.16	0.04	0.07	0.24
		ERG2_YEAST						
		CANB_YEAST		0.00				
		KCC2_YEAST				0.00	0.06	
		NCS1_YEAST				0.00		
		CALM_YEAST		0.00				
0.14	0.96	KAPR_YEAST	0.12	0.00	0.06	0.07	0.08	0.39
		KAPA_YEAST						
		KAPB_YEAST						
		KAPC_YEAST						
		CAN_YEAST				0.00		0.12
		CBPS_YEAST						
		CPYI_YEAST				0.95	0.22	0.70
		YPP1_YEAS7						
		YPP1_YEAST						
		YAT2_YEAST						
		YMC1_YEAST		0.00				
		KC11_YEAST						
0.35	0.47	KC12_YEAST	0.04	0.00	0.08	0.04	0.04	0.00
		KC13_YEAST		0.00				
0.38		HRR25_YEAST	0.00	0.05	0.00	0.05	0.00	
		CSK2B_YEAST				0.00	0.00	
		CSK2C_YEAST				0.00	0.00	0.00
1.90	1.48	STDH_YEAST	0.10	0.46	0.54	0.00	0.51	0.86

		CAT5_YEAST						
		CATT_YEAST				0.39	0.22	0.10
		CHAC_YEAST				0.24		
0.00	1.61	MOB2_YEAST		0.00	0.00	0.08	0.00	0.18
0.58		DBF2_YEAST		0.00		0.05	0.10	0.18
1.20	0.00	CDC10_YEAST	0.00	0.42	0.12	0.11	0.11	0.12
0.38	0.83	CDC11_YEAST	0.21	0.00	0.09	0.27	0.30	0.60
0.46	0.24	CDC12_YEAST	0.41	0.13	0.77	0.14	0.55	1.03
		CDC24_YEAST				0.00		
		CDC28_YEAST				0.11	0.00	0.17
0.68	0.72	CDC3_YEAST	0.06	0.33	0.16	0.17	0.33	0.93
		CDC42_YEAST						
0.84	3.15	CDC48_YEAST	0.00	0.06	0.03	0.04	0.08	0.23
		CDC53_YEAST		0.03	0.03	0.03		
		CDC54_YEAST						
		CDC7_YEAST						
0.22		YL413_YEAST	0.00	0.04	0.04	0.04	0.07	
0.00		TAO3_YEAST		0.00	0.01	0.00	0.00	
		WSC2_YEAST						
		HS150_YEAS6				0.09		0.00
		PST1_YEAS7						0.00
		CWP1_YEAST						
0.35	0.42	ECM33_YEAS2	0.33	0.12	0.12	0.09	0.47	0.54
		CHL4_YEAST						
		CBF3A_YEAST						
		PRTB_YEAST				0.08	0.04	0.04
		CNM67_YEAST						
		CHS5_YEAST						
		CHS3_YEAST						
0.11	0.37	AROC_YEAST	0.24	0.24	0.16	0.31	0.00	0.10
		RLF2_YEAST						
		EAF3_YEAST					0.00	
		EAF7_YEAST						
		RSC30_YEAST			0.00	0.00	0.00	
		RSC58_YEAST					0.00	
		RSC8_YEAST						
		RSC4_YEAST						
		RSC7_YEAST				0.06	0.00	0.06
		RSC9_YEAST				0.00		
		SFH1_YEAST				0.06	0.00	
2.47		CHD1_YEAST		0.00		0.05	0.05	0.12
		CSM3_YEAST						
		CST9_YEAST						
		CTF8_YEAST						
0.72	4.15	CISY1_YEAST	0.38	0.12	0.06	0.23	0.00	1.16
		AP18B_YEAST						
2.24	4.36	CLH_YEAST	0.01	0.06	0.00	0.07	0.08	0.26

		CLC1_YEAST		0.00				
2.73	1.50	COPA_YEAST	0.00	0.01	0.00	0.02	0.04	0.12
		COPB_YEAST				0.05	0.07	0.03
		COPB2_YEAST				0.00		
		COPD_YEAST					0.00	
		COPE_YEAST				0.28	0.10	0.11
		COPG_YEAST						
		COPZ_YEAST				0.00		
		COFI_YEAST		0.21				0.46
		SWD2_YEAST				0.00		
		COG4_YEAST						
		COG5_YEAST						
		COG7_YEAST				0.00		
		CSN10_YEAST						
		CSN9_YEAST						
2.12		SEC16_YEAST		0.01		0.02	0.01	0.06
		CTR1_YEAST			0.00			
	6.22	CORO_YEAST	0.04	0.08	0.00			0.31
		CCW12_YEAST						0.00
		YKJ1_YEAST				0.08	0.16	
		CTK1_YEAST						
		CTK3_YEAST						
0.55	1.57	URA7_YEAST		0.00	0.09	0.15	0.17	0.00
		URA8_YEAS7				0.04	0.04	0.04
		PHO85_YEAST	0.08					
		DUG1_YEAST				0.08	0.00	0.44
		STR3_YEAST						
2.21		CBS_YEAST		0.05		0.10	0.06	
		CYS3_YEAST				0.07	0.07	
0.35		NFS1_YEAST		0.05		0.05	0.05	0.16
		BLH1_YEAST					0.05	
		SYC_YEAST						
0.37	0.16	CDD_YEAST	0.90	6.80	2.34	0.40	0.49	1.39
		MBI2_YEAST						
		CBP2_YEAST						
		CBP6_YEAST						
		QCR1_YEAST				0.35	0.13	0.25
		QCR2_YEAST				0.10	0.10	0.27
		QCR6_YEAST						
		QCR7_YEAST				0.29	0.23	0.00
	0.80	UCRI_YEAST			0.00	0.00	0.00	0.13
		CCHL_YEAST				0.00		
0.44	0.71	CYC1_YEAST	20.72	39.24	7.42	7.62	13.29	20.72
		COX5A_YEAST				0.00		
		COX8_YEAST						
		COX4_YEAST						
		COX6_YEAST				0.00	0.27	0.41

		COX9_YEAST						
		CY1_YEAST				0.00	0.00	0.08
		ERG5_YEAST						
		CYK2_YEAST						
		CYK3_YEAST						
		CTU1_YEAS1						
		NAR1_YEAS7						
		NBP35_YEAST						
		SER33_YEAST					0.00	
		ARA2_YEAST	0.00	0.00		0.00		
		ARA1_YEAST				0.17	0.28	0.15
		DAD3_YEAST				0.00		
		MOB1_YEAST			0.08		0.00	
		ERG4_YEAST						
		PUT2_YEAST						
		HEM2_YEAST				0.08	0.27	
		DCTD_YEAST		0.09	0.17	0.17		
		DOHH_YEAST				0.18	0.25	0.08
		DHYS_YEAST				0.00	0.00	
		DFM1_YEAST			0.00	0.00		
		DIP5_YEAST						
0.00	1.24	DLDH_YEAST	0.25	0.00	0.30	0.30	0.00	0.45
0.28	0.87	ODP2_YEAST	0.00	0.08	0.15	0.08	0.08	0.36
		ODO2_YEAST				0.00	0.06	0.06
		PYRD_YEAST					0.00	
		DAK1_YEAST				0.05		
		DAK2_YEAST						
0.00	1.24	ILV3_YEAST	0.13	0.00	0.00	0.00	0.00	0.15
		DIM1_YEAST				0.08	0.00	
		ERG19_YEAST						
		DLD1_YEAST						
		DLD2_YEAST				0.14	0.04	
		DLD3_YEAST				0.00	0.06	
		RAD17_YEAST		0.00				
		LCD1_YEAST						
		DUN1_YEAST						
		RPH1_YEAST						
		MSH1_YEAST						
		DPOA_YEAST						
		HCS1_YEAST						
		DPOD2_YEAST						
		DPOE_YEAST						
		DPO5_YEAST						
		DPOZ_YEAST						
		PRI1_YEAST				0.00	0.06	
		RAD52_YEAST						
		RDH54_YEAST	0.00	0.03		0.03		

		RAD16_YEAST						
		RAD2_YEAST						
		RAD50_YEAST						
		RAD51_YEAST				0.00	0.00	
		RAD9_YEAST						
		DNA2_YEAST	0.00					
		CDC47_YEAST						
		MCM2_YEAST						
		MCM6_YEAST				0.00	0.02	
		TOP1_YEAST				0.00		
		TOP2_YEAST				0.04		
		PAT1_YEAST						
		APN1_YEAST						
		MAG_YEAST						
		RAP1_YEAST						
0.30		RPA1_YEAST	0.10	0.00		0.00	0.04	0.04
		RPA12_YEAST		0.00				
0.53	3.30	RPA2_YEAST	0.04	0.08	0.00	0.02	0.04	0.10
		RPA34_YEAST	0.00	0.00				
		RPA43_YEAST		0.00				
		RPA49_YEAST	0.06	0.06		0.00		0.06
3.30		RPB1_YEAST	0.00	0.03		0.01	0.03	0.11
		RPB11_YEAST				0.25		
1.18		RPB2_YEAST		0.00		0.01	0.04	
		RPB3_YEAST						
		RPB4_YEAST						
		RPC10_YEAST						
		RPC2_YEAST					0.02	0.00
		RPC6_YEAST				0.00		
		RPC9_YEAST						
0.16	0.88	RPAC1_YEAST	0.27	0.00	0.10	0.00	0.15	0.64
	0.39	RPAC2_YEAST	0.00	0.21	0.21	0.00		0.00
0.75		RPAB1_YEAST	0.00	0.00		0.00	0.11	
		RPAB3_YEAST					0.00	
	0.00	RPAB4_YEAST		0.00	0.00	0.56		0.00
0.44		RPAB5_YEAST		0.49		0.49	0.72	
0.03	8.06	MDJ1_YEAST	0.06	0.05	0.06	0.00	0.17	0.95
		XDJ1_YEAST						
		JEM1_YEAST						
0.51	0.22	SCJ1_YEAST	0.00	0.00	0.00	0.07	0.26	0.08
		DID4_YEAST			0.00			
		YL422_YEAST		0.00		0.00		
0.37		DPM1_YEAST		0.09			0.00	
		OST3_YEAST						
		OST2_YEAST		0.00		0.00		
		OSTB_YEAST		0.00				0.06
		PMT2_YEAST						

		PMT4_YEAST						
		MRE11_YEAST						
		MGM1_YEAST				0.02		
0.20		BRE1_YEAST		0.04	0.11	0.04	0.07	
		DMA1_YEAST						
0.21	0.98	RSP5_YEAST	0.10	0.03	0.04	0.00	0.04	0.27
		EMI1_YEAST					0.00	
		EDE1_YEAST		0.02				0.06
0.54	0.58	EF1A_YEAST	16.13	9.64	14.61	33.74	24.31	75.02
0.00	0.38	EF1B_YEAST	0.00	0.00	0.00	0.00	0.00	0.13
0.80		EF1G1_YEAST	0.13	0.06		0.06	0.18	0.39
	1.21	EF1G2_YEAST	0.07		0.07	0.08	0.53	0.35
0.46	0.48	EF2_YEAST	0.00	0.33	0.28	0.41	0.29	1.46
0.43	0.50	EF3A_YEAST	0.04	0.25	0.37	0.04	0.00	0.13
0.27	0.90	EFTU_YEAST		0.06	0.00	0.06	0.13	0.13
0.00		ELO2_YEAST		0.00			0.00	
		ELP1_YEAST				0.00		
		ELP3_YEAST				0.00		
		ELP4_YEAST						
		ELP5_YEAST		0.00	0.00	0.00		
		ELP6_YEAST				0.09		
		PPN1_YEAST						
0.88	1.65	EDC3_YEAST	0.04	0.00	0.04	0.05	0.11	0.24
		ENO1_YEAST				3.61	8.52	5.21
7.00	23.49	ENO2_YEAST	1.20	0.28	1.37	4.62	6.19	10.92
		ERR1_YEAST						
		ERR3_YEAST						
		TSC13_YEAST						
		ETR1_YEAST				0.10	0.30	0.08
		ENT1_YEAST						0.05
0.00		ENT2_YEAST	0.08	0.00	0.16		0.00	
		ENT3_YEAST						
		ENT4_YEAST		0.10				
	0.71	ENT5_YEAST			0.00		0.00	0.06
	0.39	ERV29_YEAST		0.00	0.08			0.00
		ERV46_YEAST				0.00		
		ERG28_YEAST						
		ERJ5_YEAST					0.09	
0.25	1.69	EMG1_YEAST		0.11	0.11	0.11	0.29	0.11
0.00		ENP1_YEAST		0.00			0.00	
		IF4F2_YEAST						
		IF4F1_YEAST		0.00				
0.08	0.18	ERF3_YEAST	0.11	0.05	0.13	0.04	0.00	0.04
0.54	1.00	ERF1_YEAST	0.33	0.31	0.00	0.11	0.13	0.89
		IF1A_YEAST				0.00		
		IF2A_YEAST	0.00	0.00				0.00
0.47	1.11	IF2B_YEAST	0.30	0.30	0.11	0.30	0.23	0.71

0.00	0.49	IF2G_YEAST	0.16	0.00	0.18	0.00	0.00	0.34
		EIF2A_YEAST				0.04	0.04	
0.00	0.35	EIF3A_YEAST	0.11	0.16	0.21	0.03	0.05	0.25
0.16	0.45	EIF3B_YEAS7	0.16	0.07	0.16	0.10	0.06	0.21
		EIF3C_YEAS7		0.00				
		EIF3C_YEAST						
2.35		EIF3G_YEAS7	0.00	0.20	0.00	0.00	0.00	
		EIF3G_YEAST						
0.79		EIF3I_YEAS7		0.07		0.00	0.00	0.00
		EIF3J_YEAST		0.00				
		IF4B_YEAST				0.00	0.00	
0.24		IF4E_YEAST		0.14	0.83	0.26	0.35	
0.27		IF5_YEAST	0.00	0.13	0.00	0.00	0.06	
0.00	0.20	IF5A2_YEAST	0.00	0.33	0.91	0.74	0.33	1.24
0.35	0.71	IF2P_YEAST	0.00	0.02	0.02	0.03	0.05	0.05
		IF6_YEAST				0.11	0.11	
1.22		SUI1_YEAST	0.28	0.37		0.00	0.49	0.37
		EXO70_YEAST						
		SEC10_YEAST					0.00	
		SEC15_YEAST				0.00		
		SEC3_YEAST						0.00
		SEC5_YEAST						
		SEC6_YEAST						
1.06		SEC8_YEAST		0.00		0.00	0.06	
		EXO1_YEAST						
		CSL4_YEAST						
		RRP40_YEAST						0.11
		RRP43_YEAST						
		RRP45_YEAST						
		RRP46_YEAST						
		RRP44_YEAST						
		POB3_YEAST				0.04	0.00	0.18
2.00	2.99	SPT16_YEAST		0.04	0.04	0.05	0.08	0.31
		CAPZB_YEAST					0.00	
		FSH1_YEAST				0.11	0.11	
		FSH3_YEAST				0.00		
		FPPS_YEAST						
1.07	1.40	FAS2_YEAST	0.04	0.08	0.03	0.04	0.01	0.20
0.26	0.11	FAS1_YEAST	0.05	0.04	0.06	0.04	0.02	0.10
		YL352_YEAST						
		FRE1_YEAST						
		HEMH_YEAST					0.13	
		FIMB_YEAST						
1.12	1.38	FKBP3_YEAST	0.12	0.06	0.07	0.09	0.46	0.25
		FKBP_YEAST						
0.71		FKBP4_YEAST		0.07		0.00	0.36	0.25
		FLC1_YEAST		0.00				

		FHP_YEAST				0.06	0.00	
		YCP4_YEAST		0.00				0.00
		F26_YEAST						
1.34	6.46	ALF_YEAST		0.30	0.16	0.71	0.77	0.42
		FUMH_YEAST	0.00			0.11	0.18	0.13
		FRDS_YEAST				0.06	0.35	0.17
		NOT1_YEAST				0.02	0.01	0.04
		NOT2_YEAST						
		NOT4_YEAST						
		NOT5_YEAST						
		GIP2_YEAST						
		GIP4_YEAST				0.00		
0.35		EXG1_YEAST	0.00	0.05	0.00	0.11	0.00	
		BGL2_YEAST						
		HXKG_YEAST				0.29	0.35	0.42
		GFA1_YEAST				0.00	0.04	0.07
		G6PD_YEAST				0.10	0.05	0.10
		YMY9_YEAST					0.09	
		G6PI_YEAST				0.05	0.12	0.26
		GID8_YEAST					0.00	
		CCR4_YEAST						
0.21		PROB_YEAST		0.07	0.13	0.15	0.13	
		DCE_YEAST				0.00	0.00	0.33
		GLT1_YEAST				0.01		
		GSH1_YEAST						
		GLNA_YEAST				0.19	0.63	0.39
		SYEC_YEAST		0.04		0.00		
1.08	0.92	GLRX2_YEAST		0.00	0.00	0.21	0.25	0.21
		GPX2_YEAST						
	0.71	GSHR_YEAST			0.00	0.00	0.13	0.05
		GST1_YEAST				0.00	0.11	0.23
		GST2_YEAST						
		GSHB_YEAST						
		G3P1_YEAST				1.15	0.00	0.42
		G3P2_YEAST				1.27		
0.36	0.30	G3P3_YEAST	0.00	1.25	0.75	1.84	1.10	0.00
		GPD1_YEAST			0.00	0.00	0.06	
0.38		GPD2_YEAST		0.06			0.00	
		GPT1_YEAST						
		GDE1_YEAST			0.00	0.00	0.01	
		GCSH_YEAST						
		GCSP_YEAST						
		GYS1_YEAST				0.00	0.00	
14.67	1.31	GYS2_YEAST		0.14	0.13	0.05	0.27	1.04
	0.88	GDE_YEAST			0.00	0.03		0.07
		PHSG_YEAST				0.15	0.14	0.66
		KRE2_YEAST						

		SYG_YEAST				0.00	0.13	0.29
		SYG2_YEAST						
		GUAA_YEAST				0.10	0.15	
		IMH1_YEAST						
		YSP2_YEAST	0.00	0.04	0.01			
		GRH1_YEAST						
		WHI2_YEAST				0.11		
		GCH1_YEAST					0.25	0.11
		RIB1_YEAST						
		MTG2_YEAST				0.00	0.00	
0.02	1.31	BEM2_YEAST	0.02	0.05	0.04	0.01	0.04	0.16
		GYP1_YEAST						
		GYP3_YEAST						
		GYP8_YEAST						
		SAC7_YEAST						
		GSP1_YEAST						
		GSP2_YEAST				0.11		
		GTR2_YEAST						
0.33	1.64	RBG1_YEAST		0.11	0.09	0.00	0.11	0.57
0.32	0.13	RHO1_YEAST	0.33	0.00	1.02	0.15	0.18	0.15
		RHO3_YEAST				0.00	0.00	
1.15		RHO5_YEAST	0.00	0.08	0.16	0.08	0.08	
		YPT1_YEAST				0.00	0.13	
		YPT7_YEAST					0.13	
		G4P1_YEAST				0.00		
		LTE1_YEAST						
		GPB1_YEAST				0.00		
0.88	0.24	GBLP_YEAST	0.59	0.21	0.90	0.30	1.27	0.54
		GBG_YEAST				0.00		
		KGUA_YEAST						
0.37	1.11	GAR1_YEAST	0.14	0.14	0.31	0.17	0.17	0.00
0.04	0.00	NHP2_YEAST	0.28	0.41	0.00	0.00	0.28	0.00
0.35	2.24	NOP10_YEAST	0.69	1.11	0.69	1.77	0.00	0.00
0.40	1.34	CBF5_YEAST	0.24	0.30	0.23	0.09	0.19	0.61
		YB92_YEAST						
		YGK1_YEAST				0.12	0.00	
6.36	39.63	HS104_YEAST		0.00	0.03	0.09	0.19	1.10
		HSP26_YEAST				0.00	0.80	1.95
		HSP42_YEAST				0.27	0.71	0.21
1.92	6.74	HSP60_YEAST		0.11	0.06	0.64	0.32	2.04
		HSP78_YEAST				0.11	0.04	0.44
1.68	3.12	HSP7F_YEAST	0.14	0.21	0.11	0.34	0.00	0.11
		HSP79_YEAST				0.15	0.04	0.10
0.53	2.30	HSP71_YEAST	0.69	0.47	0.21	0.21	0.00	3.87
0.06	2.39	HSP72_YEAST	0.45	0.23	0.21	0.00	0.47	4.08
		HSP73_YEAST						
		HSP74_YEAST				0.23	0.23	1.43

	0.59	HSP75_YEAST		0.23	0.00	0.39		2.51
0.24	0.61	HSP76_YEAST	1.08	0.48	0.20	0.41	0.95	2.89
0.48	1.84	HSP77_YEAST	0.17	0.06	0.15	0.24	0.50	2.35
		STI1_YEAST				0.10	0.04	0.09
		SEN1_YEAST	0.02	0.00		0.00		0.04
		HOT13_YEAST						
		HAP1W_YEAST				0.00	0.02	
		GPG1_YEAST						
		COQ1_YEAST				0.00		
		COQ3_YEAST						
		HXKA_YEAST				0.00	0.15	0.20
		HXKB_YEAST				0.05	0.00	
0.00	0.00	HMO1_YEAST		0.00	0.00	0.00	0.00	0.00
		GNP1_YEAST		0.04	0.04			
1.53	1.13	HXT7_YEAST		0.00	0.10	0.05	0.09	0.22
		TRK1_YEAST		0.00				0.00
		HOT1_YEAST						
		HIS2_YEAST				0.00	0.00	
		SYH_YEAST				0.04		
		GCN5_YEAST			0.05			
		SAS3_YEAST						
		ASF1_YEAST						
		CTI6_YEAST						
		HDA1_YEAST						
0.37	0.31	HOS3_YEAST	0.07	0.07	0.11	0.04	0.00	0.04
		RPD3_YEAST					0.06	0.18
0.40	1.44	H1_YEAST	0.12	0.15	0.00	0.13	0.40	0.40
0.37	0.59	H2A1_YEAST	0.00	0.30	0.88	0.69	0.69	0.00
0.37	0.55	H2AZ_YEAST	0.00	0.37	0.00	0.47	0.00	0.84
		H2B1_YEAST				0.00		
0.52		H2B2_YEAST		0.96	0.96	0.00	1.22	
1.54		H3_YEAST	0.00	0.22		0.00	0.00	0.22
0.41	3.80	H4_YEAST	75.89	58.40	18.68	58.40	18.68	285.88
		SET1_YEAST						
		HNT1_YEAST						
		HMT1_YEAST						
		LYS4_YEAST					0.00	
0.31	0.58	HOSC_YEAST	0.06	0.00	0.00	0.07	0.13	0.39
		DHOM_YEAST					0.08	
		KHSE_YEAST				0.00	0.07	
		SNL1_YEAST		0.00				
		AHA1_YEAST		0.00		0.00		
2.71		HMCS_YEAST		0.00		0.00	0.16	0.00
		HPRT_YEAST					0.00	
1.89		IMA1_YEAST		0.04			0.09	0.04
		IMB1_YEAST		0.00		0.00		
		IMB4_YEAST						

		ISN1_YEAST						
2.21		IST2_YEAST		0.08	0.00	0.00	0.05	
		I23O_YEAST						
		BUD2_YEAST						
		IRA1_YEAST						
		SLI15_YEAST		0.04		0.00		
		IES5_YEAST						
0.00		PHO88_YEAST		0.00	0.15	0.15	0.00	
		PHO86_YEAST		0.00	0.00			
1.67	1.67	IPYR_YEAST		0.00	0.00	0.00	0.18	0.18
		IPYR2_YEAST						
3.08		IMDH2_YEAST		0.00		0.00	0.62	
		VIP1_YEAST						
		ISC1_YEAST		0.00		0.05		
		INP52_YEAST						
		INP53_YEAST	0.06	0.06		0.02		
		INV1_YEAST				0.00		
		ISU1_YEAST						
		ISU2_YEAST						
		AFT1_YEAST						
		IAH1_YEAST				0.11		
1.37	1.34	IDH1_YEAST	0.00	0.15	0.08	0.00	0.08	0.18
0.36	1.00	IDH2_YEAST	0.16	0.10	0.00	0.15	0.46	0.83
		IDHH_YEAST		0.00				
0.16	0.46	IDHP_YEAST	0.21	0.37	0.69	0.21	0.00	0.78
		SYIC_YEAST				0.00		
		IDI1_YEAST				0.00	0.08	
		ISW1_YEAST						
		ISW2_YEAST						
		IOC3_YEAST				0.00		
		IOC4_YEAST				0.00		
		APJ1_YEAST				0.00	0.11	
		KAR4_YEAST						
		KEL1_YEAST		0.06		0.00		
0.13	1.22	ILV5_YEAST		0.25	0.00	0.08	0.08	0.45
		YBD2_YEAST	0.00	0.00		0.13		
		YL032_YEAST						
		KRE5_YEAST						
		CIN8_YEAST		0.00				
		KAR3_YEAST						
		KIP2_YEAST						
		SMY1_YEAST						
		NUF2_YEAST						
		KYNU_YEAST				0.00	0.06	
		LAH1_YEAST						
		LGUL_YEAST				0.11	0.50	0.50
		LRE1_YEAST						

		LYS5_YEAST						
		CP51_YEAST				0.04		
1.06		LSG1_YEAST		0.04			0.04	
		LSB1_YEAST						
0.03	0.37	LSB3_YEAS7	0.19	0.07	0.07	0.06	0.06	0.21
		ASPG1_YEAST						
		LCMT2_YEAST				0.00		
		SOG2_YEAST						
		SYLC_YEAST				0.00	0.06	0.04
	2.26	YD266_YEAST		0.04	0.00			0.11
		TGL3_YEAST						
		TGL5_YEAST						
		LIP5_YEAST						
1.27	0.35	LCF1_YEAST	0.00	0.06	0.06	0.04	0.00	0.21
		LCF3_YEAST						
0.99		LCF4_YEAST		0.00		0.05	0.05	
		PPAL_YEAST						
		GLY1_YEAST				0.08	0.52	0.08
0.23	0.27	HXT1_YEAST	0.05	0.05	0.06	0.00	0.08	0.18
0.22	0.22	HXT3_YEAST	0.16	0.11	0.00	0.04	0.04	0.14
		PLB1_YEAST						
		NTE1_YEAST				0.01	0.00	
		SYKC_YEAST					0.04	
		SYKM_YEAST						
		YO111_YEAST						
		ALR1_YEAST						
		ALR2_YEAST						
17.72		ALDH6_YEAST		0.16		0.11	0.38	0.81
		MDHM_YEAST				0.08	0.09	0.11
0.28	0.25	MDHP_YEAST	0.21	0.00	0.52	0.00	0.43	0.19
		MASY_YEAST						
		FABD_YEAST						
		MNR2_YEAST						
0.00		DCW1_YEAST		0.00		0.00	0.00	0.00
0.00		MNN9_YEAST		0.00	0.00	0.00	0.00	
		VAN1_YEAST						
0.27	0.95	MPG1_YEAST	0.21	0.00	0.25	0.13	0.33	0.65
		MPI_YEAST				0.06		
		MKK2_YEAST						
		PBS2_YEAST						
		MHP1_YEAST		0.04		0.02		0.05
		MATA1_YEAST					0.00	
		MRC1_YEAST				0.00		
		MED11_YEAST						
		MED15_YEAST						
		MED20_YEAST				0.00	0.00	
		MED22_YEAST				0.00	0.25	

		MED5_YEAST						
		MED8_YEAST						
		RIM4_YEAST						
		MSC3_YEAST	0.00	0.00		0.00		0.00
		MSC6_YEAST						
		MCA1_YEAS7				0.06		
8.84	1.77	AMPM1_YEAST	0.06	0.00	0.00	0.00	0.71	0.14
		AMPM2_YEAST				0.00	0.06	0.00
0.88		SYMC_YEAST	0.00	0.00		0.11	0.04	0.10
		MMS1_YEAST						
		YB9H_YEAST					0.00	
		MDN1_YEAST						
		MCM10_YEAST						
		MCM5_YEAST				0.00	0.03	
0.38	1.54	FIS1_YEAST	0.00	0.00	0.22	0.18	0.18	0.65
		ACEB_YEAST						
		ODC2_YEAST		0.00	0.08			
		MAM33_YEAST						
		ATP10_YEAST	0.00					
		RIM2_YEAST		0.06	0.06	0.00		
		TCM62_YEAST						
		MCX1_YEAST						0.00
		NTG1_YEAST						
0.71	0.39	YHM2_YEAST	0.08	0.08	0.27	0.00	0.00	0.08
		YME2_YEAS7						
		ERV1_YEAST						
		MG101_YEAST				0.10		
		MTG1_YEAST				0.00		
		TIM10_YEAST						
		TIM14_YEAST						
		TIM16_YEAST			0.00	0.00		
		TIM21_YEAST						
0.59	0.24	TIM44_YEAST	0.06	0.24	0.14	0.24	0.14	0.19
		TOM20_YEAST						
		TOM40_YEAST						
		TOM6_YEAST						
		TOM70_YEAS7	0.00		0.04	0.04		
		PMIP_YEAST						
		MMT1_YEAST						
		NUC1_YEAST			0.00			
		IML2_YEAS7				0.00		
		OM45_YEAST						0.21
2.47	3.11	VDAC1_YEAST	0.57	0.56	0.57	1.10	0.96	0.26
		YKR18_YEAS7						
		OAC1_YEAST						
		MPM1_YEAS7				0.00		
1.00	3.45	PRX1_YEAST		0.00	0.10	0.00	0.12	0.25

0.48	1.07	MPCP_YEAST	0.12	0.00	0.54	0.15	0.62	1.05
		FMP38_YEAST						
0.49	1.90	MAS5_YEAST	0.49	0.72	0.52	0.43	0.00	1.39
		AFG3_YEAST						
		RCA1_YEAST		0.00	0.00			
		GEM1_YEAST						
		MPPA_YEAST						
		MPPB_YEAST				0.00	0.00	0.00
		FUS3_YEAST	0.06	0.00		0.00		
		HOG1_YEAST				0.06	0.06	
		KSS1_YEAST						
		SLT2_YEAST						
		CSM1_YEAST						
		GLRX5_YEAST				0.23	0.19	
		MSB1_YEAST			0.00			
		RNA15_YEAST						
		YTH1_YEAST				0.00		
		CTH1_YEAST				0.00	0.00	
0.04	0.64	MEX67_YEAST	0.17	0.08	0.04	0.00	0.04	0.13
		GFD1_YEAST						
		MTR2_YEAST						
0.83		MRT4_YEAST		0.11		0.30	0.33	0.23
		PUF2_YEAST						
		PUF3_YEAST	0.00					
		DCP1_YEAST		0.11		0.11		
		DCP2_YEAS7					0.03	
		MEU1_YEAST				0.00	0.00	0.37
		TR112_YEAST					0.00	
		MRD1_YEAST					0.02	
2.41	2.51	MBF1_YEAST	0.66	0.00	1.48	5.61	9.93	7.10
1.00		MLC1_YEAST	0.00	0.91		0.19	0.25	
0.08	0.01	BBC1_YEAST	0.10	0.10	0.09	0.00	0.00	0.08
		MYO1_YEAST						
		MYO2_YEAST	0.03	0.07				
0.29	0.41	MYO3_YEAST	0.04	0.04	0.08	0.04	0.02	0.14
0.11	1.59	MYO5_YEAS7	0.02	0.11	0.04	0.00	0.02	0.16
		TRM1_YEAST						
		TRPF_YEAST				0.13	0.00	
		AML1_YEAST						
		NAH1_YEAST		0.00	0.00			
		HPA3_YEAST						
		HST2_YEAST				0.07	0.07	0.07
		SIR2_YEAST		0.00				
		MAOM_YEAST				0.04		0.00
		NPY1_YEAST				0.00		
0.08		NCB5R_YEAS7		0.12		0.11	0.08	
		NCB5R_YEAST						

	0.29	MCR1_YEAS7			0.08			0.09
		ADH6_YEAST				0.07	0.00	0.07
0.75		OYE2_YEAST		0.00		0.25	0.13	0.15
		OYE3_YEAST						
		NCPR_YEAST						
		GRE3_YEAST				0.60	0.14	0.60
		KAR_YEAST				0.66	0.42	0.39
		GRE2_YEAST						
		DHE4_YEAST				0.45	0.00	
		DHE5_YEAST						
		NBP1_YEAST						
0.11		NACA_YEAST	0.17	0.20	0.17	0.20	0.17	
		NACB1_YEAS7						0.19
		RPI1_YEAST						
		PMD1_YEAST						
0.08	1.62	UTP17_YEAST	0.11	0.03	0.02	0.03	0.03	0.13
		TREA_YEAST				0.23	0.05	0.04
		NIF3_YEAST				0.23	0.00	
		PNC1_YEAST				0.16	0.16	0.14
		NRK1_YEAST				0.00		0.00
		NMA1_YEAST						
		NPT1_YEAST				0.00	0.12	
		NADC_YEAST				0.00	0.00	
		NFU1_YEAST				0.00	0.24	
		NPR1_YEAST	0.00	0.00				
		SNG1_YEAST						
		NCE1_YEAST						
0.00	0.27	NCE2_YEAST	0.43	0.00	0.52	0.00	0.00	0.71
		NHP6B_YEAST				0.00		
		UPF3_YEAST						
		ARD1_YEAST				0.28	0.00	0.51
		NAT1_YEAST						
		MDM20_YEAST	0.00					0.03
		MAK3_YEAST						
0.12	1.19	NUG1_YEAST	0.11	0.06	0.05	0.00	0.00	0.39
		NSR1_YEAST		0.06				
0.35	0.05	NUM1_YEAST		0.00	0.01		0.01	0.00
		NAB2_YEAST						
		SNF4_YEAST						
		STH1_YEAST				0.01		
0.26	0.26	BFR1_YEAST	0.19	0.58	0.44	0.00	0.06	0.47
		NTF2_YEAST						
0.12	0.00	NOP14_YEAST	0.00	0.03	0.00	0.03	0.00	0.00
		NOC2_YEAST				0.04	0.00	0.04
		NOC4_YEAST						
		NOC3_YEAST				0.00	0.04	
0.24	0.00	NOG1_YEAST	0.04	0.00	0.11	0.14	0.04	0.11

0.13	0.27	NOG2_YEAST	0.11	0.07	0.14	0.12	0.14	0.24
		URB1_YEAST	0.00	0.01	0.01	0.00		
		URB2_YEAST						
0.85	1.26	NOP12_YEAST	0.05	0.12	0.00	0.13	0.12	0.18
		NOP13_YEAST					0.00	
	0.62	NOP3_YEAST	0.00	0.00	0.06	0.06		0.21
0.21	0.00	NOP4_YEAST	0.06	0.04	0.04	0.11	0.08	0.04
0.06	0.43	NOP56_YEAST	0.12	0.66	0.12	0.00	0.91	0.88
0.17	0.59	NOP58_YEAS7	0.09	0.25	0.14	0.16	0.00	1.21
0.94		NOP6_YEAST		0.00		0.59	0.29	0.41
0.33	1.30	NET1_YEAST	0.06	0.05	0.11	0.02	0.05	0.05
		NUP59_YEAST				0.00		
0.00		GLE2_YEAST		0.07		0.07	0.07	0.07
		NDC1_YEAST						
0.62		NIC96_YEAST		0.00	0.06	0.06	0.05	
		NSP1_YEAST	0.00	0.03		0.03		0.03
		NU100_YEAST		0.00	0.02			
	0.90	NU116_YEAST	0.02	0.00	0.02	0.03		0.09
		NU133_YEAST						
0.00		NU145_YEAST		0.00	0.02	0.02	0.00	
		NU157_YEAST	0.00	0.02				
0.20	0.00	NU159_YEAST	0.05	0.00	0.02	0.01	0.01	0.02
0.24		NU170_YEAST		0.00		0.04	0.01	0.04
		NU188_YEAST		0.00				
		NU192_YEAST		0.00	0.00	0.01		
		NUP2_YEAST						
		NUP49_YEAST						
0.82		NUP57_YEAST	0.00	0.00	0.00	0.00	0.05	
		NUP60_YEAST		0.00				
0.39		NUP82_YEAST	0.07	0.04	0.07	0.00	0.00	
0.18	0.61	PO152_YEAST	0.06	0.04	0.00	0.01	0.00	0.09
		POM34_YEAST	0.08	0.08	0.17	0.08		
0.94		SEH1_YEAST	0.07	0.00		0.00	0.08	
0.23	0.54	NDK_YEAST		0.83	0.83	0.00	1.01	1.73
		NAP1_YEAST						
		MALX3_YEAST						
0.28	0.61	YOR1_YEAST	0.01	0.07	0.17	0.06	0.11	0.30
		ORN_YEAST				0.09	0.00	
		OAT_YEAST				0.07	0.07	
		OSM1_YEAST						
0.26	0.57	OSH2_YEAST	0.01	0.04	0.01	0.02	0.06	0.10
		OSH3_YEAST	0.02	0.05		0.00		
0.48	0.71	OSH6_YEAST		0.06	0.00	0.00	0.05	0.05
		PBP1_YEAST		0.04		0.10		0.10
		PBP2_YEAST				0.06		
		PAN3_YEAST						
		REP1_YEAST				0.00		

		REP2_YEAST						
		ARO1_YEAST				0.08	0.01	0.09
		MSRA_YEAST					0.00	
		PTR2_YEAST			0.04			
2.36	0.06	PPID_YEAST	0.06	0.13	0.07	0.08	0.08	0.17
		ESS1_YEAST				0.00		
0.35	2.06	CYPH_YEAST	0.18	0.27	0.22	0.00	0.58	2.62
		PTH2_YEAST						
		PWP1_YEAST						
0.51		PWP2_YEAST		0.06		0.03	0.00	
		DOT5_YEAST			0.00			
		GPX3_YEAST						
0.22		TSA1_YEAST	0.20	0.20		0.20	0.49	0.42
		TSA2_YEAST				0.16		
3.13		AHP1_YEAST		0.00		0.20	0.59	0.43
		SPS19_YEAST						
	0.79	PTE1_YEAST			0.00			0.07
		PEX8_YEAST						
		FOX2_YEAST						
		PEX17_YEAST						
		PEX11_YEAST						
		PEX5_YEAST						
0.26	0.01	FAT2_YEAST	0.00	0.06	0.06	0.06	0.05	0.05
		PIP2_YEAST						
0.39		PESC_YEAST	0.04	0.08		0.08	0.00	0.12
		PAD1_YEAST		0.00				
		SYFA_YEAST						0.05
4.24		SYFB_YEAST		0.00		0.08	0.21	
		STE2_YEAST	0.00	0.06	0.12			
		PHM7_YEAST						
		PEM1_YEAST						
0.13	0.01	NPC2_YEAST	2.10	2.43	0.47	1.03	2.50	0.57
		VPS34_YEAST						
0.20	2.04	SLM1_YEAST	0.04	0.08	0.00	0.04	0.00	0.18
		SLM2_YEAST		0.04				
		PIK1_YEAST						
		STT4_YEAST		0.00				
		CSR1_YEAST				0.00		
		PDR16_YEAST						
		PDR17_YEAST						
		AROF_YEAST						
		AROG_YEAST					0.00	
		PGM3_YEAST						
		PGM1_YEAST						
		PGM2_YEAST				0.12	0.13	0.33
0.03	0.25	PGK_YEAST	0.88	1.59	5.67	0.53	0.64	4.90
17.75	7.00	PMG1_YEAST	2.36	0.28	1.84	8.91	31.61	11.02

		PMG2_YEAST					0.00	
		SAC1_YEAST		0.00	0.04			
		SPO14_YEAST			0.00			
8.87		PMM_YEAST	0.00	0.23		1.74	0.52	4.31
0.71		PUR6_YEAST		0.00			0.04	
		PUR4_YEAST				0.00		
		PALA_YEAST				0.00	0.00	
		TPA1_YEAST				0.12	0.04	0.00
0.16	0.46	PMA1_YEAST	1.41	0.42	0.00	2.41	0.59	7.56
		FTR1_YEAST						
0.32	0.33	PDR5_YEAST	0.21	0.09	0.13	0.04	0.64	1.12
		SNI1_YEAST						
		PCC1_YEAST				0.00	0.00	
		PAP_YEAST						
0.00		POP2_YEAST		0.00		0.06	0.00	
0.00		PAP2_YEAST		0.04	0.08		0.04	
0.28	0.10	PABP_YEAST	0.50	0.26	0.62	0.09	0.16	0.66
		PAA1_YEAST				0.91	0.96	0.47
		FMS1_YEAST						
0.92		TPO1_YEAST	0.04	0.05	0.00	0.00	0.08	
		TPO2_YEAST				0.04		0.04
		TPO3_YEAST		0.00	0.08	0.00		
		TPO4_YEAST						
		TPP1_YEAST						
		HEM3_YEAST				0.00	0.08	
	3.50	ALDH4_YEAST			0.11	0.12	0.00	0.13
		PFD3_YEAST						
		PFD4_YEAST						
		PFD5_YEAST				0.00		
		PML1_YEAST						
		PML39_YEAST						
		PRP19_YEAST						
		PRP16_YEAST						
		PRP22_YEAST						
0.28	0.97	PRP43_YEAST	0.11	0.08	0.04	0.04	0.08	0.30
		PRP2_YEAST						
		ISY1_YEAST						
		RDS3_YEAST						
		URN1_YEAST						
0.00		ESF1_YEAST		0.00		0.00	0.00	
		PNO1_YEAST		0.00				
		RIX1_YEAS7					0.00	
		BDH2_YEAST				0.00	0.06	0.06
		GAS3_YEAST	0.00	0.00	0.06	0.00		
	1.20	PLSC_YEAST	0.00	0.08	0.18			0.08
		PSMD9_YEAST						
		PSD10_YEAST				0.00		

		PRPD_YEAST						
		ACON2_YEAST				0.03	0.03	
		YMX7_YEAST				0.00		
		ALAT_YEAST				0.00		
		ALAM_YEAST						
		MNN10_YEAST				0.00		
		MNN11_YEAST						
	0.42	DHR1_YEAST	0.06	0.04	0.01	0.04		0.04
		DHR2_YEAST	0.04	0.04				
		DPP3_YEAST					0.04	
		SNT1_YEAST						
		ETFA_YEAST				0.08	0.08	0.08
		ETFB_YEAST				0.13		
		ETFD_YEAST						0.04
		SCW4_YEAST				0.07		
		CRH2_YEAST		0.00				
		HOS2_YEAST						
		NIT3_YEAST						
	3.24	IMDH3_YEAST	0.22		0.11	0.13	0.68	1.47
		IMDH4_YEAST		0.06				
		ALG9_YEAST						
		KTR3_YEAST	0.06					
		ARX1_YEAST		0.04		0.00		0.04
		FSF1_YEAST		0.00	0.00			
		ADRO_YEAST						
		MSS4_YEAST						
		ATC5_YEAST						
		ATC4_YEAST	0.01	0.01	0.03			
		SYPM_YEAST				0.00		
		QOR_YEAST				0.00		
		HSL1_YEAST						
		KKQ8_YEAST						
		KBN8_YEAST						
		KD025_YEAST						
		KN8R_YEAST						
		KOE5_YEAST				0.04	0.02	
		KOK0_YEAST						
		BIT2_YEAST						
		HMS1_YEAST						
		STB4_YEAST		0.00		0.03		0.00
		AQR1_YEAST		0.00	0.00			
0.17	1.32	PHB1_YEAST	0.22	0.23	0.00	0.17	0.11	0.73
0.85	1.51	PHB2_YEAST	0.08	0.28	0.10	0.12	0.19	0.51
		LAS17_YEAST	0.00	0.08				
		ADY1_YEAST						
		POC1_YEAST				0.00		
		POC2_YEAST						

		PSA3_YEAST				0.00	0.64	0.11
		PSB2_YEAST					0.13	0.13
		PSB1_YEAST				0.12	0.26	0.00
1.85		PSA6_YEAST		0.00		0.82	0.24	0.25
		PSB5_YEAST				0.19	0.73	0.30
		PSB6_YEAST				0.15	0.44	0.27
		PSB4_YEAST						
5.56	3.94	PSA1_YEAST	0.25	0.25	0.25	0.00	0.00	0.23
0.50	1.63	PSA7_YEAST		0.00	0.00	0.25	0.13	0.21
		PSB7_YEAST						
		PSA5_YEAST				0.15	0.00	0.00
		PSB3_YEAST				0.16	0.18	0.00
		PSA4_YEAST				0.00	0.00	0.21
		PSA2_YEAST				0.18	0.33	0.59
		CIC1_YEAST					0.00	
		AFR1_YEAST		0.00	0.00			
		AIM2_YEAST						
		AIR2_YEAST						
		APA1_YEAST				0.00	0.25	0.00
		ARG56_YEAST						0.03
		ASK10_YEAST		0.00		0.02		
0.42		AST1_YEAST		0.00		0.06	0.06	
		AST2_YEAST						
		ATP11_YEAST						
		ATP13_YEAST						
		BCH2_YEAST						
		BCP1_YEAST				0.21	0.00	
0.00		BFR2_YEAST		0.00	0.00	0.04	0.00	
		BIM1_YEAST						
	0.21	BMH1_YEAST		0.36	0.11	0.28		0.25
		BMH2_YEAST	0.09					0.21
		BNI1_YEAST		0.00				
0.80	0.28	BOB1_YEAST		0.02	0.05	0.03	0.05	0.08
		BOI2_YEAST				0.04		
		BSP1_YEAST	0.00	0.00		0.04		0.08
		BTN2_YEAST				0.09	0.18	0.25
		BUR2_YEAST						
		BZZ1_YEAST						
		CF130_YEAST						
		CAJ1_YEAST						
		CBP3_YEAST			0.07	0.00		
		CG121_YEAST				0.45	0.33	
0.00	0.40	CMS1_YEAST	0.08	0.08	0.09	0.00	0.08	0.00
		CSF1_YEAST						
		CWH43_YEAST						
		DCS2_YEAST				0.00	0.16	0.18
3.10	1.31	MPD1_YEAST		0.00	0.08	0.26	0.65	0.35

0.35	2.47	DOP1_YEAST		0.00	0.00	0.00	0.01	0.05
		DSE1_YEAST						
		EAP1_YEAST						
		EBS1_YEAST		0.02				
		ECM30_YEAST						
0.71	1.41	EFR3_YEAST	0.03	0.00	0.00	0.03	0.03	0.06
		FAF1_YEAST						
		FNTA_YEAST				0.00		
		FMP27_YEAST		0.00				
		FMP52_YEAST				0.00	0.11	0.40
		FYV10_YEAST						
0.00		GCN20_YEAST		0.00	0.00	0.04	0.00	
		GCY_YEAST				0.17	0.17	0.29
		GDS1_YEAST						
		GVP36_YEAST				0.23	0.23	0.08
		HAM1_YEAST				0.00	0.00	
		HBT1_YEAST						
		HGH1_YEAST						
		HIR1_YEAST						
		HIR2_YEAST						
		HIT1_YEAST						
		HLJ1_YEAST		0.11				
		IGO2_YEAST						
		PIH1_YEAST						
		ISD11_YEAST	0.00		0.00			
		IVY1_YEAST				0.00		
		KES1_YEAST				0.00	0.12	
		KPC1_YEAST		0.06		0.04		
0.69	1.07	MCK1_YEAST	0.08	0.00	0.23	0.09	0.34	0.75
		SCY1_YEAST						
		KRI1_YEAST		0.00		0.04		0.00
		LDB16_YEAST						
		LDB19_YEAST		0.00				
0.45	2.98	LSM12_YEAST		0.00	0.00	1.39	0.28	1.82
		LTV1_YEAST						
		MAK11_YEAST						
		MAK16_YEAST					0.00	
		MIDA_YEAST						
0.44		MKT1_YEAST	0.03	0.00		0.07	0.04	0.10
		MLP1_YEAST						
		MLP2_YEAST		0.04				0.00
4.58	0.89	MMF1_YEAST		0.21	0.00	0.00	0.70	1.18
		MON2_YEAST						
0.48	0.41	MRH1_YEAST	0.22	0.26	0.57	0.23	0.23	0.81
		MSF1_YEAST						
		MSO1_YEAST				0.13		
		MSS18_YEAST						

		MUK1_YEAST		0.00				
		NAM1_YEAST						
		NAM8_YEAST						
		NBA1_YEAST		0.00		0.00		
		NIP80_YEAST						
	0.82	NIP29_YEAST		0.21	0.00	0.00		0.10
		NIS1_YEAST						
		NNF2_YEAST		0.00				
		NSG1_YEAST						
		NTA1_YEAST				0.00	0.00	
		NUD1_YEAST			0.00			
0.07		NUF1_YEAST	0.00	0.23	0.14	0.00	0.00	
		OCA4_YEAST					0.06	
		OPY1_YEAST		0.00				
		PAM1_YEAST		0.03				
		PAR32_YEAST			0.00	0.00	0.09	
		PBP4_YEAST	0.00	0.00	0.55			
		PCF11_YEAST						
		PDC2_YEAST						
		PET54_YEAST				0.00		
		SDS22_YEAST				0.08	0.00	0.15
		PP2C1_YEAST						
		PP2C2_YEAST						
		2ABA_YEAST						
		PSP2_YEAST	0.00			0.00		
		PXR1_YEAS7	0.08	0.11		0.11		
		PXR1_YEAST						
		RFS1_YEAST						
		ROD1_YEAST						
		SCD6_YEAST						
0.03	0.29	SC160_YEAST	0.33	0.35	0.24	0.02	0.08	0.19
1.53	1.68	SDA1_YEAST	0.06	0.10	0.04	0.10	0.06	0.10
		SDS23_YEAS7	0.00					
		SDS23_YEAST						
		SFK1_YEAST			0.07			
		SIP3_YEAST						
		SIP5_YEAST						
0.97	1.04	SIS1_YEAST	0.11	0.42	0.00	0.24	0.23	1.12
		SKG3_YEAST						
		SKT5_YEAST		0.00				
	1.34	SLA2_YEAST	0.03	0.00	0.03			0.25
		SLM4_YEAST						
		SNI2_YEAST						
0.25	0.26	SNQ2_YEAST	0.04	0.18	0.12	0.02	0.04	0.14
0.38		DCA13_YEAST		0.00		0.00	0.05	
	0.10	SPA2_YEAST	0.05	0.02	0.07	0.04		0.05
		SPT2_YEAST					0.00	

		SPT3_YEAST						
		SRN2_YEAST						
		SSD1_YEAST						
		SSO1_YEAST						
		SSO2_YEAST						
0.19		SST2_YEAST		0.00			0.04	
		STB6_YEAST						
0.49	0.49	SUR7_YEAST	0.00	0.10	0.10	0.10	0.08	0.08
		TEX1_YEAST						
		THO1_YEAST		0.00		0.00		
0.13	0.44	TIF31_YEAST	0.04	0.06	0.08	0.01	0.04	0.16
		TMA23_YEAST		0.00				
		GOS1_YEAST						
0.39		SEC1_YEAST	0.00	0.04		0.07	0.06	0.17
1.08	1.42	SEC13_YEAST	0.23	0.00	0.40	0.11	0.25	0.35
0.74	0.56	SEC23_YEAST	0.18	0.07	0.04	0.04	0.05	0.19
0.32	0.21	SEC24_YEAST	0.12	0.07	0.12	0.04	0.06	0.18
0.34	0.06	SEC31_YEAST	0.09	0.00	0.10	0.00	0.10	0.21
0.00		SC61G_YEAST	0.00	0.00	0.00	0.00	0.00	
		UPS1_YEAST						
0.27	0.48	PYR1_YEAST	0.16	0.03	0.00	0.03	0.13	0.23
		URE2_YEAST				0.00		
		VAB2_YEAS7						
		WHI3_YEAST						
		WHI4_YEAST					0.00	0.04
		YGP1_YEAST						
		YOP1_YEAST		0.00				
0.62	1.25	YRO2_YEAST		0.08	0.08	0.18	0.00	0.30
		YSC84_YEAST	0.06	0.00		0.00		
		YSP1_YEAST		0.02				
		ZPS1_YEAST						
3.38	0.71	PST2_YEAST		0.00	0.17	0.00	0.61	0.71
		PPOX_YEAST						
		YJB0_YEAST						
		PUF6_YEAST				0.00		0.00
		PNPH_YEAST				0.08	0.08	
		YN14_YEAST				0.21	0.21	0.42
	0.06	YEC0_YEAST			0.04			0.09
		KAD6_YEAST						
		YP088_YEAST				0.00		
		IRC3_YEAST						
		ECM32_YEAST			0.00		0.02	
		YL419_YEAST						0.02
		DLHH_YEAST					0.00	
		METX_YEAST						
		CYSK_YEAST						0.00
		INO80_YEAS7						

		INO80_YEAST						
		YG4D_YEAST						
		HFD1_YEAST						
0.47	0.12	FLC3_YEAST		0.06	0.03	0.00	0.00	0.00
		EMI2_YEAST				0.31	0.08	0.28
		YL126_YEAST						
		HOC1_YEAST		0.00	0.00			
		YLF2_YEAST						
		MGDP1_YEAST						
0.37	0.00	YHM1_YEAST		0.00	0.00		0.08	0.00
		PT127_YEAST						
		DET1_YEAST						
0.15	0.56	YHI0_YEAST	0.24	0.05	0.16	0.21	0.05	0.35
		AXL1_YEAST		0.00				
		PHS_YEAST						
		BUD16_YEAST						
		PLR1_YEAST						
		FMP46_YEAST						
		YPR1_YEAST				0.00		0.08
		YL143_YEAST				0.00		0.00
0.42		NOP2_YEAST		0.00		0.04	0.04	0.13
		THIX_YEAST		0.00				
		THTR_YEAST				0.17	0.17	
		SEF1_YEAST						
		YKD3A_YEAST				0.00	0.00	
		YOR31_YEAST				0.00	0.00	0.41
		YGD9_YEAST				0.00	0.00	0.08
		YGP7_YEAST				0.26	0.26	0.08
		API2_YEAST						
		YCE2_YEAST						
		YG3E_YEAST						
		YI20A_YEAST						
		YO318_YEAST						
		YD020_YEAST				0.00		
3.36	0.88	XPP_YEAST	0.00	0.04	0.04	0.06	0.10	0.04
1.73		YIK8_YEAST		0.06		0.08	0.06	0.00
		YL455_YEAST						
		PDX3_YEAST						
		P5CR_YEAST						
		PYC1_YEAST						
6.87	5.36	PDC1_YEAST	0.43	0.59	1.12	0.88	0.16	0.54
		PDC6_YEAST						
	0.00	ODPX_YEAST			0.00	0.20	0.00	0.00
2.30	0.80	ODPA_YEAST	0.58	0.28	0.43	0.62	1.05	1.81
0.74	1.27	ODPB_YEAST	0.28	0.41	0.45	0.23	0.20	1.28
4.33	2.38	KPYK1_YEAST	3.94	3.90	1.87	8.08	11.89	26.00
		KPYK2_YEAST				0.06	0.06	

0.22	1.31	QDR2_YEAST	0.04	0.00	0.05	0.00	0.04	0.14
		GDI1_YEAST				0.00	0.05	0.00
		YRB1_YEAST				0.00		0.00
	0.00	RAS2_YEAST			0.00			0.00
0.10	0.27	RSR1_YEAST		0.11	0.20	0.00	0.09	0.09
		DOM3Z_YEAST		0.00		0.07		
		RMI1_YEAST						
		RCY1_YEAST						
0.42		RV161_YEAST		0.09		0.09	0.20	0.45
1.06		RV167_YEAST	0.00	0.05		0.05	0.05	0.23
		RCC1_YEAST						
		RT103_YEAST						
		ADR1_YEAST						
		PHO2_YEAST						
		SIR3_YEAST						
		SIR4_YEAST		0.02		0.00		
		RFA2_YEAST						
		RFA3_YEAST				0.00	0.32	
0.83	1.06	RFC1_YEAST		0.12	0.03	0.08	0.03	0.11
0.63	0.37	RFC2_YEAST	0.08	0.21	0.49	0.25	0.27	0.52
		RFC3_YEAST		0.00				
		RFC4_YEAST				0.00		
0.00		RFC5_YEAST		0.00		0.07	0.00	0.00
0.00	0.00	RTN1_YEAST	0.18	0.00	0.00	0.00	0.00	0.00
		RTN2_YEAST				0.08		0.76
		RFX1_YEAST						
		RHEB_YEAST						
		RGD1_YEAST						
		ROM2_YEAST		0.00				
		LRG1_YEAST		0.02				
		RGD2_YEAST		0.00		0.00		
		RNT1_YEAST						
		RMP1_YEAST						
		RPM2_YEAST						
		RPP1_YEAST						
		RNY1_YEAST						
		POP8_YEAST						
		RIR1_YEAST						
		RIR2_YEAST				0.06	0.06	0.00
		RIR4_YEAST						
		SML1_YEAST						
		KPR1_YEAST				0.12	0.00	
	0.06	KPR3_YEAST			0.10	0.08	0.17	0.00
		KPR5_YEAST					0.05	
		RKM1_YEAST						
		RKM3_YEAST				0.04		
		RMAR_YEAST				0.00		

		KRR1_YEAST		0.00		0.08		
		RRP1_YEAST						
0.42	3.06	RRP12_YEAST		0.01	0.00	0.00	0.04	0.09
		RRP15_YEAST						
		RRP7_YEAST						
		RRP8_YEAST						
0.85	0.00	RRP9_YEAST		0.00	0.00	0.04	0.04	0.00
		RSA3_YEAST						
		RRB1_YEAST					0.00	
		SQT1_YEAST					0.00	
		RIX7_YEAST					0.00	
0.86		NOP15_YEAST		0.00		0.12	0.12	0.25
		ALB1_YEAS7						
		BMS1_YEAST	0.02	0.02	0.00	0.04		
0.37	0.84	BRX1_YEAST	0.00	0.08	0.00	0.09	0.09	0.09
		NOL10_YEAST					0.04	
0.47		ERB1_YEAS7	0.00	0.00	0.06	0.03	0.06	
0.35		MAK21_YEAST		0.02		0.04	0.00	0.04
		NOP53_YEAST				0.00	0.00	0.05
		NSA2_YEAS7		0.10		0.00		
		RLP24_YEAST		0.13	0.00	0.13		
		RLP7_YEAST						
		SLX9_YEAST					0.00	
		SSF2_YEAST						
		RL1D1_YEAST						
		YTM1_YEAS7						
		SDO1_YEAST						
0.39		RPF1_YEAST		0.00		0.18	0.08	
0.48	0.61	SSZ1_YEAST	0.10	0.00	0.00	0.06	0.29	0.21
		RRF1_YEAST						
		RBX1_YEAST				0.00		
		RCL1_YEAST						0.00
0.35	0.96	YRA1_YEAST	0.61	1.71	0.61	0.70	0.91	3.97
		REXO4_YEAST	0.00	0.00				
		NGL2_YEAST						
		SSU72_YEAST						
		TFB3_YEAST						
		NAB6_YEAST				0.02		
0.00	0.81	SRO9_YEAST	0.00	0.06	0.12	0.00	0.06	0.06
		NDI1_YEAST				0.00		0.00
0.09	0.72	FBRL_YEAST	1.57	1.00	1.24	1.73	0.94	0.00
0.04	0.17	RRP5_YEAST	0.01	0.00	0.34	0.21	0.02	0.34
0.25	1.72	EBP2_YEAST	0.00	0.11	0.00	0.06	0.06	0.12
		FCF1_YEAST						
		FYV7_YEAST						
		UTP23_YEAST		0.00		0.10		
0.88	9.85	RUVB1_YEAST	0.06	0.06	0.11	0.00	0.11	0.44

0.00		RUVB2_YEAST		0.00		0.12	0.00	
		PRTD_YEAST				0.00	0.00	
		CARP_YEAST						
		LYS1_YEAST		0.00				0.21
		SAM3_YEAST						
0.06	2.71	METK1_YEAST		0.15	0.06	0.08	0.25	0.21
		SGF29_YEAST						
		DCPS_YEAST				0.40	0.12	0.18
		SEC14_YEAST				0.11	0.08	0.08
		SFB2_YEAST					0.05	
		SFB3_YEAST		0.03		0.05		0.06
		ESP1_YEAST						
		YJU3_YEAST		0.00		0.00		
0.36	0.20	GLYC_YEAST	0.23	0.37	0.49	0.00	0.23	0.67
		GLYM_YEAST						
		LCB1_YEAST		0.00				
		KIN1_YEAST		0.00		0.00		
0.28	1.59	AKL1_YEAST	0.06	0.07	0.04	0.02	0.04	0.18
		BCK1_YEAST						
		BUR1_YEAST		0.00				
		CBK1_YEAST	0.03	0.00				
		CHK1_YEAST						
		CLA4_YEAST						
		DBF20_YEAST						
0.24		GCN2_YEAST		0.03			0.01	
0.46	0.29	GIN4_YEAST	0.13	0.02	0.09	0.01	0.11	0.10
		HAL5_YEAST						
0.00	1.24	HRK1_YEAST	0.00	0.00	0.00	0.04	0.00	0.10
		KIC1_YEAST						
0.02		KIN2_YEAST	0.01	0.09	0.04	0.00	0.02	
		KIN4_YEAST		0.00				
		KSP1_YEAST			0.00	0.02		
		ATR_YEAST						
		PKH1_YEAST						
		PKH3_YEAST						
		PTK2_YEAST		0.06				0.06
		RIO2_YEAST				0.00	0.06	0.06
		SCH9_YEAST						
		TOR1_YEAST			0.01			
0.00		TOR2_YEAST	0.01	0.01	0.01	0.01	0.01	
		VPS15_YEAST						
		YPK1_YEAST						
		PP11_YEAST						
0.41	2.55	PP12_YEAST	0.00	0.00	0.20	0.16	0.25	0.74
		PP2A1_YEAST						
		PP2A2_YEAST						
		PPZ1_YEAST		0.04		0.00		0.04

		TYE7_YEAST						
1.41	0.00	SYSC_YEAST		0.00	0.00	0.26	0.10	0.00
0.14	1.05	SHS1_YEAST	0.10	0.00	0.15	0.13	0.06	0.51
		SFGH_YEAST				0.20	0.11	
		SRPR_YEAST						
		SRP54_YEAST				0.04		
		SRP68_YEAST						
		SRP72_YEAST						
		GBP2_YEAST	0.00			0.00	0.00	0.06
		RIM1_YEAST				0.00	0.00	
		PDS5_YEAST						
		SAR1_YEAST					0.00	
		SGT2_YEAST						
		RUXE_YEAST						
		SMD1_YEAST						
		SMD2_YEAST			0.00	0.00		
		SMD3_YEAST			0.00	0.00		
		RSMB_YEAST		0.00				
		LSM1_YEAST		0.00		0.16		
		ATN1_YEAST						
		ATN2_YEAST						
1.19		SAS10_YEAST		0.08			0.04	
		SAS4_YEAST		0.00				
		SAS5_YEAST		0.00				
		MVP1_YEAST						
		SNX3_YEAST		0.00	0.16	0.16		
		SPEE_YEAST				0.00	0.43	0.22
		LCB4_YEAST				0.00	0.00	
		LCB5_YEAST						
1.71	0.92	LSP1_YEAST		0.18	0.09	0.11	0.35	0.26
4.99	0.35	PIL1_YEAST	0.00	0.44	0.47	0.00	0.64	1.94
		SGPL_YEAST						
0.31	0.41	SPC42_YEAST	0.22	0.17	0.08	0.08	0.07	0.22
		RMD1_YEAST						
		RMD8_YEAST						
		SPO73_YEAST						
		SPO77_YEAST						
		SPG5_YEAST						
		ERG6_YEAST					0.00	
		SUT1_YEAST						
0.00	0.71	SMC1_YEAST		0.00	0.00	0.00	0.00	0.02
		SMC2_YEAST						
0.11		SMC3_YEAST		0.02		0.00	0.00	
		SMC4_YEAST						
		SMC6_YEAST						
		RAD27_YEAST						
		SVL3_YEAST		0.00		0.00		0.06

		DHSX_YEAST						
		DHSA_YEAST				0.00	0.04	
		DHSB_YEAST				0.09		
		SDHF1_YEAS7						
		SDHF2_YEAS1						
		UGA2_YEAST				0.05	0.05	
		SUCA_YEAST				0.28	0.00	0.08
		SUCB_YEAST				0.12		
		MET3_YEAST						
		SKI3_YEAST						
		SODC_YEAST	0.00	0.21	0.00	0.00		
		SODM_YEAST				0.00	0.11	0.00
		SGD1_YEAST						
		SUM1_YEAST				0.04		
	1.06	SYP1_YEAST		0.03	0.03			0.03
		MPT5_YEAST				0.00		
0.27		SRP40_YEAST	0.06	0.00		0.00	0.08	0.06
0.56	1.96	STM1_YEAST	0.10	0.12	0.00	0.23	0.21	0.51
	4.21	FMP45_YEAST			0.08	0.00		0.34
0.00	1.52	HSV2_YEAST		0.00	0.00	0.00	0.00	0.11
		SNF5_YEAST						
		YO338_YEAST						
		SWC3_YEAST						
		SWC4_YEAST						0.05
0.18		KOG1_YEAST		0.01	0.00	0.01	0.03	
0.24	0.65	TCO89_YEAST		0.00	0.03		0.03	0.09
		AVO1_YEAST		0.00				
		AVO2_YEAST			0.00			
0.35	0.35	LST8_YEAST		0.00	0.08	0.08	0.08	0.00
		MOT1_YEAST						0.00
		TBP_YEAST						
		TBP7_YEAST						
		TCPB_YEAST				0.06	0.05	
0.18	0.83	TCPD_YEAST		0.00	0.16	0.10	0.05	0.05
		TCPE_YEAST				0.00	0.13	
		TCPG_YEAST		0.04		0.04		
0.37	0.94	TCPQ_YEAST		0.05	0.04	0.18	0.16	0.20
		TCPZ_YEAST					0.04	
		TERT_YEAST						
		RIF1_YEAST						
		TIP1_YEAST						
		THI6_YEAST						
		THI7_YEAST						
		THI72_YEAST						
		TRXB1_YEAST				0.19	0.19	0.10
		TRX3_YEAST						0.00
		THO2_YEAST						

		SRY1_YEAST						
0.23	0.92	THDH_YEAST	0.16	0.16	0.06	0.08	0.00	0.70
		SYTC_YEAST				0.07	0.04	0.10
		SYTM_YEAST						
		TYSY_YEAST					0.00	
		TOF2_YEAST						
		RAF_YEAST				0.00	0.14	
		TAL2_YEAST				0.00	0.33	0.91
	2.47	TAL1_YEAST			0.00	0.08	0.00	0.25
		MIG3_YEAST						
		TFS2_YEAST		0.00		0.08		
0.09	0.00	SPT5_YEAST	0.15	0.00	0.12	0.08	0.03	0.12
		IWS1_YEAST						
		PDR1_YEAST						
		TFC3_YEAST						
		TFC7_YEAST						
		TOA2_YEAST						0.00
		TF2B_YEAST		0.08	0.00			
		TAF1_YEAST						
		TAF11_YEAST						
		TAF4_YEAS7						
0.82		TAF6_YEAST		0.00		0.05	0.05	
		TAF9_YEAST				0.00		
		SNF2_YEAST						
		MOT3_YEAST		0.00				
0.38		ADA2_YEAST		0.06		0.06	0.00	
		WTM1_YEAST				0.12	0.06	0.00
		WTM2_YEAST						
		ASH1_YEAST						
		DOT6_YEAST						
		GAT1_YEAST						
		RXT2_YEAST						
		RXT3_YEAST						
		UME1_YEAST						
		OPI1_YEAST						
		TRA1_YEAST		0.00				
		SCP1_YEAST				0.18	0.33	0.13
		TKT1_YEAST				0.04	0.00	0.07
		TKT2_YEAST				0.04	0.04	0.05
		EI2BA_YEAST				0.08	0.00	
		EI2BB_YEAST				0.07		
		EI2BD_YEAST				0.00		
		EI2BG_YEAST						
0.41		RLI1_YEAST	0.30	0.06	0.29	0.06	0.23	
		TMA10_YEAST						
		TMA20_YEAST					0.00	
		DENR_YEAST						

		TMA46_YEAST		0.07	0.15	0.07		
		TMA7_YEAST				0.00		
		GCN1_YEAST						
1.02	4.45	TCTP_YEAST	0.00	0.21	0.37	0.29	0.23	0.52
		SEC62_YEAST						
		SEC72_YEAST						
		TMN2_YEAST						
		TR120_YEAST		0.00		0.00		
		TR130_YEAST						
		TRS20_YEAST						
0.79		BET3_YEAST	0.00	0.00	0.00	0.00	0.13	
		TRS23_YEAST						
		TRS31_YEAST		0.00	0.09	0.09		
		TRS33_YEAST						
		YA11A_YEAST						
		YB11B_YEAST					0.17	
		YB12A_YEAST		0.00				
		YD11A_YEAST					0.62	
		YD11B_YEAST						
		YD17A_YEAST						
		YD12A_YEAST						
		YD12B_YEAST						
		YD15A_YEAST						
		YG12B_YEAST						
		YJ12A_YEAST						
		YJ12B_YEAST						
		YM11B_YEAST						
		YM14B_YEAST			0.13			
		YN11A_YEAST						
		YN11B_YEAST	0.04					
		YN12A_YEAST						
		YO11A_YEAST	0.59	0.41				1.15
		YO11B_YEAST					0.15	
		YP13B_YEAST						
		YP14B_YEAST		0.11				
		YB21A_YEAST					0.06	
		YB21B_YEAST						
		YD21A_YEAST						
		YD23B_YEAST		0.03				
		YF21B_YEAST						
		YG21B_YEAST						
		YI31B_YEAST						
		YJ41B_YEAST						
		TPS3_YEAST					0.00	
	6.13	TSL1_YEAST			0.00	0.04	0.14	0.18
		TPS2_YEAST				0.03	0.00	0.30
	0.05	TCB1_YEAST	0.01	0.01	0.01			0.02

		TCB2_YEAST		0.00				
0.01	0.47	TCB3_YEAST	0.06	0.02	0.00	0.02	0.01	0.08
		TGS1_YEAST						
3.72	0.98	TPIS_YEAST		0.27	0.11	0.00	0.50	0.39
		TRM82_YEAS1						
		TRM82_YEAS7						
		TPT1_YEAST				0.00	0.24	
		RIT1_YEAST						
		TYW1_YEAST			0.00			
		TYW2_YEAST						
		DUS3_YEAS7					0.00	
		TAD1_YEAST						
		TRP_YEAST				0.04	0.23	0.16
		SYWC_YEAST				0.13		
		SYWM_YEAST						
	2.53	TBA1_YEAST			0.06		0.00	0.12
		TBA3_YEAST				0.00		
1.99		TBB_YEAST	0.00	0.06	0.00	0.06	0.11	
		PTP3_YEAST						
0.12	0.82	CDC14_YEAST		0.04	0.04	0.00	0.04	0.08
		PVH1_YEAST						0.00
		SYYC_YEAST				0.14	0.13	
		SYYM_YEAST						
		SF3B1_YEAST						
0.00		IMP3_YEAST	0.00	0.00	0.13	0.00	0.00	
0.77		IMP4_YEAST	0.00	0.00		0.00	0.08	0.08
0.26	0.74	UTP10_YEAST		0.03	0.03	0.01	0.06	0.08
		UTP11_YEAS6		0.10				
		UTP12_YEAST						
		UTP13_YEAST	0.00	0.00				
		UTP14_YEAST						
0.44	0.25	UTP15_YEAST	0.05	0.05	0.00	0.05	0.05	0.05
	0.00	UTP18_YEAST			0.00	0.00		0.00
		UTP20_YEAST						
		UTP21_YEAST			0.00		0.03	
0.12	0.71	UTP22_YEAST	0.00	0.04	0.00	0.04	0.00	0.13
		UTP4_YEAST				0.10	0.06	0.04
		UTP5_YEAST						
		UTP6_YEAST		0.05	0.00	0.05		
0.54		UTP7_YEAST	0.08	0.00		0.05	0.13	0.18
0.39		UTP8_YEAST	0.07	0.04	0.00	0.07	0.00	
		UTP9_YEAST		0.04		0.04		
0.00	1.70	MPP10_YEAST		0.00	0.00	0.09	0.00	0.08
		LSM2_YEAST				0.00		
		LSM3_YEAST				0.00		
		LSM4_YEAST				0.14	0.00	
0.00		LSM5_YEAST		0.00		0.00	0.00	0.35

		LSM6_YEAS7				1.40		
		LSM7_YEAST			0.00	0.00		
		COQ5_YEAST						
		COQ6_YEAST						
		UBP10_YEAST						
		UBP15_YEAST						
0.26	0.31	UBP3_YEAST	0.11	0.08	0.06	0.11	0.11	0.11
		UBP5_YEAST						
0.00		UBP7_YEAST		0.00	0.00		0.00	
		UBL1_YEAST				0.00	0.00	
		BUL1_YEAST		0.00		0.03		0.00
0.21		BUL2_YEAST		0.05	0.00	0.00	0.03	
1.50	1.02	UBIQ_YEAST	3.64	0.69	4.62	2.48	1.01	1.01
		UBA1_YEAST						0.02
		UBC7_YEAST						
		MDY2_YEAST	0.00			0.00		
		SMT3_YEAST				0.00	0.31	0.00
		ULP1_YEAST						
		BRE5_YEAST			0.00		0.00	
		UBX4_YEAST				0.00		
		UBX6_YEAST						
		UAP1_YEAST						
		GPT_YEAST						
		YD061_YEAST					0.04	
		YN99_YEAST						0.04
		YO075_YEAST						0.00
		FUN30_YEAST						
		YHJ1_YEAST		0.00				
		YL247_YEAST						
		YA044_YEAST	0.00			0.00	0.00	0.00
		YJY5_YEAST						
		YBQ6_YEAST				0.00		
3.31	3.63	OLA1_YEAST	0.08	0.54	0.19	0.96	0.00	1.84
		YG3Y_YEAST				0.26	0.18	
		YG4I_YEAST						
		YD133_YEAST						
		YOL19_YEAST		0.00		0.00		
		YP041_YEAST						
		YIG4_YEAST				0.00		
		FMP41_YEAST				0.00	0.00	
		YMRF1_YEAST						
		YN00_YEAST						
		YHC1_YEAST				0.18	0.38	0.20
		YIV6_YEAST						
		YJ66_YEAST				0.09	0.00	0.12
		YKH1_YEAST						
		YM71_YEAST				0.18	0.16	0.30

		YFH6_YEAST				0.00		
	1.94	YP091_YEAST		0.04	0.03	0.03		0.06
		YP115_YEAST						
		YNB0_YEAST				0.00	0.23	0.00
		YNT4_YEAST						
		IRC10_YEAST						
		JIP4_YEAST						
		MRP8_YEAST				0.18	0.47	
		RSN1_YEAST		0.00	0.00			
		YBI6_YEAST		0.00	0.00			
		YBJ5_YEAST						
		YBV8_YEAST						
		YB191_YEAST						
		YB75_YEAST						
		YB96_YEAST						
		YB9F_YEAST						
		YB9P_YEAST						
		YCQ6_YEAST						
		YD012_YEAST		0.00				
		YD144_YEAST			0.00	0.00	0.00	
		PAL1_YEAST		0.05		0.05		
		YD391_YEAST					0.11	
		YEA7_YEAST						
		YEF3_YEAST						
		YEW7_YEAST						
		YEN1_YEAST						
		YER0_YEAST						
		YGI2_YEAST						
		YG2V_YEAST						
		YG32_YEAST				0.00		
		YG37_YEAST				0.00		
		YG3A_YEAST						
		YG4E_YEAST					0.00	
		YG5L_YEAST						
		YG5X_YEAST		0.08				
		YHO0_YEAST						
		YHP7_YEAST		0.00		0.00		0.14
0.53		YHS7_YEAST	0.11	0.33	0.14	0.00	0.16	
		YHU6_YEAST						
		YH09_YEAST				0.00		
		YIJ1_YEAST	0.00	0.03				
		YIM7_YEAST						
		YIS3_YEAST		0.04	0.04			
0.00	0.00	YJ133_YEAST		0.00	0.00	0.00	0.00	0.00
0.80	0.00	YJR1_YEAST		0.00	0.00	0.00	0.06	0.00
		YJV7_YEAST				0.00		
		YJ16_YEAST						0.00

		YJ81_YEAST						
		YJ9J_YEAST					0.07	
		YKF4_YEAST	0.04	0.00				
		YKH0_YEAST						
		YKH7_YEAST		0.00		0.06		0.00
		YKJ8_YEAST						
		YKK5_YEAST		0.00				
		YKM8_YEAST					0.08	
		YKN0_YEAST						
		YKP1_YEAST						
		YKV5_YEAST				0.00		
		YKZ1_YEAST				0.06		
		YK03_YEAST						
		YK23_YEAST				0.00	0.00	
		YK50_YEAST		0.00	0.00	0.00		
		YL104_YEAST				0.23	0.00	
		YL149_YEAST						
		YL177_YEAST						
		YL179_YEAST						
		YL301_YEAST				0.66	0.67	0.41
		YL361_YEAST						
		YL392_YEAST						
		YL460_YEAST					0.00	
		YMC0_YEAST						
		YMF0_YEAST						
		YMH9_YEAST						
		YML9_YEAST			0.00	0.07		
		YMO3_YEAST						
0.18	0.18	YMS1_YEAST	0.00	0.00	0.03	0.04	0.03	0.04
		YMX6_YEAST	0.03	0.02		0.00		0.05
		YMY8_YEAST						
		YM11_YEAST						
		YM27_YEAST				0.00	0.00	
		YM32_YEAST						
		YM44_YEAST				0.00		
		YM54_YEAST					0.00	
		YM244_YEAST						
		YM8A_YEAST						
		YM8C_YEAST						
0.78		YM91_YEAST		0.00		0.08	0.08	
6.31	4.16	YM94_YEAST	0.00	0.08	0.08	0.10	0.35	0.34
		YM96_YEAST						
		YNC2_YEAST		0.00		0.00		
		YNK8_YEAST					0.11	
		YNN4_YEAST				0.08	0.14	0.06
		YNS1_YEAST						
		YNT3_YEAST						

		YNU0_YEAST						0.00
1.14	0.51	YNU8_YEAST	0.16	0.34	0.18	0.18	0.00	0.16
		YN53_YEAST				0.00	0.03	
		YO022_YEAST				0.08	0.21	
		YO083_YEAST						
		YO086_YEAST						
		YO051_YEAST				0.13	0.20	0.06
		YO112_YEAST						
	1.18	YO227_YEAST		0.04	0.00			0.04
		YO289_YEAST				0.00		
		YO304_YEAST						
		YO316_YEAST			0.00			
		YP034_YEAST						
		YP245_YEAST		0.00				
		YP074_YEAST						
		YG5B_YEAST				0.09	0.06	
		YP184_YEAST				0.04	0.00	
		TBS1_YEAST						
		YK44_YEAST	0.00			0.00		
		ESBP6_YEAST						
		YO087_YEAST						
		FMP40_YEAST						
		YKG9_YEAST						
		YG1D_YEAST						
		YJX8_YEAST						
	0.84	YL023_YEAST			0.00			0.09
		YL064_YEAST		0.00		0.08		
		YEY6_YEAST						
0.10	0.81	KRE33_YEAST	0.02	0.05	0.03	0.08	0.04	0.09
		YBY7_YEAST				0.00	0.15	0.15
		YCF7_YEAST						
		YP225_YEAST						
		YO287_YEAST						
		YCY0_YEAST						
		YBC8_YEAST		0.00				
		YGZA_YEAST						
		YCE7_YEAST						
		YBZ1_YEAST						
		YD161_YEAST				0.21		
		YP045_YEAST						
		YHG9_YEAST				0.05	0.05	
		YN8B_YEAST		0.06		0.00		
		YK01_YEAST						
0.58	0.38	YC16_YEAST	0.18	0.47	0.00	0.00	0.18	0.18
		UPP_YEAST				0.12	0.42	0.12
		DCUP_YEAST						
		HEM4_YEAST				0.09	0.19	

0.11	1.17	UGPA1_YEAST	0.11	0.08	0.23	0.64	0.44	2.52
		ATH1_YEAST	0.00	0.00				
3.06		AMPL_YEAST		0.00		0.13	0.18	
		VMA22_YEAST						
		VID30_YEAST					0.00	
		PEP3_YEAST						
1.06		PEP5_YEAST	0.00	0.02	0.02	0.03	0.02	
		IML1_YEAST					0.00	
		VAM7_YEAST						
		VAC8_YEAST		0.04	0.05	0.00		
0.90	1.88	VPS1_YEAST	0.00	0.34	0.16	0.49	0.29	1.07
		VPS13_YEAST						
		VPS20_YEAST						
		VPS21_YEAST						
		VPS26_YEAST						
		PEP11_YEAST				0.09	0.09	0.00
		VPS3_YEAST						
		VPS30_YEAST						
		VPS33_YEAST		0.00		0.00		
		VPS35_YEAST		0.00		0.00		0.03
		VPS41_YEAST						
		VPS5_YEAST						
		VPS54_YEAST						0.00
		VPS66_YEAST						
		DID2_YEAST				0.00	0.00	
		VTC2_YEAST						
0.00		SNF7_YEAST		0.00		0.00	0.00	0.00
		SNF8_YEAST						
0.49		VAL1_YEAST	0.00	0.04	0.08	0.00	0.04	
		SYV_YEAST				0.00	0.02	
		VRP1_YEAST		0.00				
		FAT1_YEAST						
0.37	0.90	SCS2_YEAST	0.11	0.00	0.11	0.00	0.11	0.37
0.14	0.65	SEC18_YEAST		0.09	0.09	0.04	0.10	0.42
0.40	0.21	VATA_YEAST	0.03	0.00	0.05	0.07	0.06	0.23
		VPH1_YEAST		0.00	0.03	0.06		
2.07	9.06	VATB_YEAST	0.49	0.59	0.39	0.34	1.44	1.15
		VATC_YEAST				0.00		
		VA0D_YEAST				0.09	0.09	0.42
		VATD_YEAST			0.00	0.10		
		VATE_YEAST						
		VATG_YEAST						
		YBK4_YEAST				0.00		
		YCW2_YEAST						
	0.71	YMZ2_YEAST			0.00			0.03
		YP247_YEAST						
		YFB0_YEAST						

		YRF11_YEAST		0.01				
		YRF13_YEAST			0.01			
		YBP2_YEAST						
3.43	1.07	GIS2_YEAST	0.41	0.41	0.41	0.00	0.51	1.75
		RME1_YEAST						
		RTS2_YEAST						
		SFP1_YEAST				0.00		
		STP3_YEAST		0.00				0.00
		YP022_YEAST						
0.00		ZUO1_YEAST		0.00	0.00		0.00	

Table S2. **GO terms ranking analysis of proteins detected/enriched during heat stress induction within the WT and KO strains.** GO terms analysis was conducted using the DAVID software. The comparison table indicates the ranking of each term within the two strains. The degree of change in the rank of the GO term in KO compared to the WT is listed under *Delta.*

Category
SP_PIR_KEYWORDS
SP_PIR_KEYWORDS
SP_PIR_KEYWORDS
GOTERM_BP_FAT
GOTERM_BP_FAT
GOTERM_BP_FAT
GOTERM_BP_FAT
GOTERM_CC_FAT
GOTERM_CC_FAT
GOTERM_BP_FAT
GOTERM_BP_FAT
GOTERM_BP_FAT
GOTERM_CC_FAT
GOTERM_CC_FAT
UP_SEQ_FEATURE
GOTERM_BP_FAT
SP_PIR_KEYWORDS
SP_PIR_KEYWORDS
GOTERM_CC_FAT
GOTERM_BP_FAT
GOTERM_BP_FAT
GOTERM_BP_FAT
GOTERM_CC_FAT
GOTERM_BP_FAT
GOTERM_BP_FAT
SP_PIR_KEYWORDS
UP_SEQ_FEATURE
GOTERM_CC_FAT
GOTERM_BP_FAT
GOTERM_CC_FAT
GOTERM_BP_FAT
GOTERM_CC_FAT
GOTERM_BP_FAT
GOTERM_BP_FAT
SP_PIR_KEYWORDS
GOTERM_BP_FAT
KEGG_PATHWAY
SP_PIR_KEYWORDS
UP_SEQ_FEATURE
GOTERM_BP_FAT
SP_PIR_KEYWORDS
GOTERM_BP_FAT
GOTERM_BP_FAT
GOTERM_BP_FAT
SP_PIR_KEYWORDS
GOTERM_BP_FAT
SP_PIR_KEYWORDS
GOTERM_BP_FAT

GOTERM_BP_FAT
GOTERM_BP_FAT
SP_PIR_KEYWORDS
GOTERM_CC_FAT
GOTERM_CC_FAT
GOTERM_BP_FAT
GOTERM_BP_FAT
GOTERM_BP_FAT
GOTERM_MF_FAT
SP_PIR_KEYWORDS
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Term
phosphoprotein
cytoplasm
oxidoreductase
GO-0046164_alcohol catabolic process
GO-0044275_cellular carbohydrate catabolic process
GO-0055114_oxidation reduction
GO-0046365_monosaccharide catabolic process
GO-0031980_mitochondrial lumen
GO-0005759_mitochondrial matrix
GO-0019320_hexose catabolic process
GO-0006007_glucose catabolic process
GO-0016052_carbohydrate catabolic process
GO-0070013_intracellular organelle lumen
GO-0043233_organelle lumen
transit peptide-Mitochondrion
GO-0006091_generation of precursor metabolites and energy
transit peptide
nad
GO-0031974_membrane-enclosed lumen
GO-0009266_response to temperature stimulus
GO-0006006_glucose metabolic process
GO-0006732_coenzyme metabolic process
GO-0005829_cytosol
GO-0005996_monosaccharide metabolic process
GO-0051186_cofactor metabolic process
glycolysis
binding site-Substrate
GO-0005739_mitochondrion
GO-0019318_hexose metabolic process
GO-0001950_plasma membrane enriched fraction
GO-0006096_glycolysis
GO-0030529_ribonucleoprotein complex
GO-0019362_pyridine nucleotide metabolic process
GO-0009408_response to heat
nucleotide-binding
GO-0034605_cellular response to heat
sce00010-Glycolysis / Gluconeogenesis
acetylation
nucleotide phosphate-binding region-NAD
GO-0046496_nicotinamide nucleotide metabolic process
lyase
GO-0007039_vacuolar protein catabolic process
GO-0006769_nicotinamide metabolic process
GO-0009820_alkaloid metabolic process
protein biosynthesis
GO-0044271_nitrogen compound biosynthetic process
molecular chaperone
GO-0042026_protein refolding

GO-0032268_regulation of cellular protein metabolic process
GO-0009628_response to abiotic stimulus
stress-induced protein
GO-0042645_mitochondrial nucleoid
GO-0009295_nucleoid
GO-0046394_carboxylic acid biosynthetic process
GO-0016053_organic acid biosynthetic process
GO-0006733_oxidoreduction coenzyme metabolic process
GO-0048037_cofactor binding
Aminoacyl-tRNA synthetase
GO-0043228_non-membrane-bounded organelle
GO-0043232_intracellular non-membrane-bounded organelle
GO-0044429_mitochondrial part
ribosome biogenesis
atp-binding
GO-0019748_secondary metabolic process
stress response
GO-0008652_cellular amino acid biosynthetic process
proteasome
GO-0009309_amine biosynthetic process
GO-0005730_nucleolus
GO-0006090_pyruvate metabolic process
rrna processing
GO-0030684_preribosome
ribonucleoprotein
GO-0006418_tRNA aminoacylation for protein translation
nadp
GO-0034660_ncRNA metabolic process
heat shock
GO-0000267_cell fraction
GO-0006417_regulation of translation
GO-0043603_cellular amide metabolic process
mitochondrion
binding site-NAD
GO-0000314_organellar small ribosomal subunit
GO-0005763_mitochondrial small ribosomal subunit
GO-0015980_energy derivation by oxidation of organic compounds
GO-0006457_protein folding
GO-0009310_amine catabolic process
GO-0042254_ribosome biogenesis
GO-0010608_posttranscriptional regulation of gene expression
homotetramer
GO-0043039_tRNA aminoacylation
GO-0043038_amino acid activation
GO-0031597_cytosolic proteasome complex
GO-0034515_proteasome storage granule
GO-0006575_cellular amino acid derivative metabolic process
ligase
GO-0005624_membrane fraction
GO-0005626_insoluble fraction

pyridoxal phosphate
tricarboxylic acid cycle
GO-0004812_aminoacyl-tRNA ligase activity
amino-acid biosynthesis
threonine protease
GO-0015935_small ribosomal subunit
GO-0016876_ligase activity, forming aminoacyl-tRNA and related compounds
GO-0016875_ligase activity, forming carbon-oxygen bonds
GO-0044257_cellular protein catabolic process
Aminotransferase
allosteric enzyme
GO-0032543_mitochondrial translation
GO-0006364_rRNA processing
GO-0016620_oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as accepto
homodimer
GO-0000502_proteasome complex
GO-0034637_cellular carbohydrate biosynthetic process
GO-0030163_protein catabolic process
GO-0005761_mitochondrial ribosome
GO-0000313_organellar ribosome
GO-0006739_NADP metabolic process
GO-0043648_dicarboxylic acid metabolic process
GO-0009063_cellular amino acid catabolic process
GO-0005839_proteasome core complex
GO-0044445_cytosolic part
Initiation factor
GO-0022613_ribonucleoprotein complex biogenesis
GO-0050662_coenzyme binding
sce00290-Valine, leucine and isoleucine biosynthesis
GO-0009064_glutamine family amino acid metabolic process
GO-0016072_rRNA metabolic process
GO-0016836_hydro-lyase activity
GO-0006084_acetyl-CoA metabolic process
GO-0009109_coenzyme catabolic process
hydro-lyase
IPR001353-Proteasome, subunit alpha/beta
GO-0046356_acetyl-CoA catabolic process
GO-0006099_tricarboxylic acid cycle
GO-0019319_hexose biosynthetic process
IPR016040-NAD(P)-binding domain
carbon-oxygen lyase
GO-0030686_90S preribosome
GO-0051187_cofactor catabolic process
metal ion-binding site-Zinc 1; catalytic
GO-0006098_pentose-phosphate shunt
GO-0006800_oxygen and reactive oxygen species metabolic process
GO-0004298_threonine-type endopeptidase activity
GO-0070003_threonine-type peptidase activity
site-Transition state stabilizer
GO-0009081_branched chain family amino acid metabolic process

GO-0000166_nucleotide binding
GO-0009165_nucleotide biosynthetic process
GO-0044452_nucleolar part
GO-0019773_proteasome core complex, alpha-subunit complex
purine biosynthesis
GO-0005840_ribosome
GO-0006112_energy reserve metabolic process
GO-0007005_mitochondrion organization
GO-0051082_unfolded protein binding
GO-0034404_nucleobase, nucleoside and nucleotide biosynthetic process
GO-0034654_nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process
GO-0046961_proton-transporting ATPase activity, rotational mechanism
IPR013154-Alcohol dehydrogenase GroES-like
GO-0019674_NAD metabolic process
GO-0033178_proton-transporting two-sector ATPase complex, catalytic domain
GO-0006119_oxidative phosphorylation
GO-0016054_organic acid catabolic process
GO-0046395_carboxylic acid catabolic process
sce00280-Valine, leucine and isoleucine degradation
GO-0034470_ncRNA processing
GO-0046364_monosaccharide biosynthetic process
GO-0044265_cellular macromolecule catabolic process
metalloprotein
GO-0006979_response to oxidative stress
sce03050-Proteasome
GO-0030687_preribosome, large subunit precursor
IPR000426-Proteasome, alpha-subunit, conserved site
IPR002085-Alcohol dehydrogenase superfamily, zinc-containing
GO-0008219_cell death
GO-0016265_death
GO-0009082_branched chain family amino acid biosynthetic process
GO-0016051_carbohydrate biosynthetic process
GO-0019842_vitamin binding
GO-0005732_small nucleolar ribonucleoprotein complex
sce00970-Aminoacyl-tRNA biosynthesis
GO-0006536_glutamate metabolic process
metal ion-binding site-Zinc 2
short sequence motif-"HIGH" region
GO-0006163_purine nucleotide metabolic process
proteinase
branched-chain amino acid biosynthesis
GO-0005991_trehalose metabolic process
IPR013785-Aldolase-type TIM barrel
GO-0046165_alcohol biosynthetic process
sce00250-Alanine, aspartate and glutamate metabolism
GO-0006576_biogenic amine metabolic process
sce00020-Citrate cycle (TCA cycle)
GO-0016887_ATPase activity
GO-0006094_gluconeogenesis
active site-Proton acceptor

rna-binding
GO-0070279_vitamin B6 binding
GO-0030170_pyridoxal phosphate binding
GO-0006164_purine nucleotide biosynthetic process
active site-Nucleophile
GO-0009057_macromolecule catabolic process
IPR016160-Aldehyde dehydrogenase, conserved site
GO-0004033_aldo-keto reductase activity
GO-0004029_aldehyde dehydrogenase (NAD) activity
GO-0031981_nuclear lumen
GO-0016137_glycoside metabolic process
GO-0019829_cation-transporting ATPase activity
GO-0003743_translation initiation factor activity
compositionally biased region-Lys-rich
GO-0032040_small-subunit processome
GO-0017076_purine nucleotide binding
GO-0042802_identical protein binding
sce00030-Pentose phosphate pathway
short sequence motif-"KMSKS" region
sce00500-Starch and sucrose metabolism
GO-0016209_antioxidant activity
sce00340-Histidine metabolism
Isomerase
GO-0006412_translation
purine nucleotide biosynthesis
GO-0006734_NADH metabolic process
GO-0006537_glutamate biosynthetic process
IPR002314-Aminoacyl-tRNA synthetase, class II (G, H, P and S), conserved region
IPR015590-Aldehyde dehydrogenase
GO-0009199_ribonucleoside triphosphate metabolic process
membrane-associated complex
sce00650-Butanoate metabolism
IPR014729-Rossmann-like alpha/beta/alpha sandwich fold
GO-0009259_ribonucleotide metabolic process
IPR013149-Alcohol dehydrogenase, zinc-binding
IPR001412-Aminoacyl-tRNA synthetase, class I, conserved site
IPR005937-26S proteasome subunit P45
isopeptide bond
sce00350-Tyrosine metabolism
hydrolase
mutagenesis site
GO-0005832_chaperonin-containing T-complex
binding site-Glyceraldehyde 3-phosphate
GO-0009141_nucleoside triphosphate metabolic process
metal-binding
GO-0004030_aldehyde dehydrogenase [NAD(P)+] activity
GO-0033279_ribosomal subunit
GO-0009150_purine ribonucleotide metabolic process
GO-0045333_cellular respiration
active site-For GATase activity

GO-0015992_proton transport
GO-0006818_hydrogen transport
GO-0009084_glutamine family amino acid biosynthetic process
GO-0009060_aerobic respiration
GO-0015078_hydrogen ion transmembrane transporter activity
GO-0001882_nucleoside binding
GO-0051287_NAD or NADH binding
SM00382-AAA
region of interest-Substrate binding
IPR018181-Heat shock protein 70, conserved site
IPR013126-Heat shock protein 70
IPR001023-Heat shock protein Hsp70
GO-0042219_cellular amino acid derivative catabolic process
GO-0019321_pentose metabolic process
GO-0009260_ribonucleotide biosynthetic process
GO-0009144_purine nucleoside triphosphate metabolic process
GO-0009205_purine ribonucleoside triphosphate metabolic process
Hydrogen ion transport
GO-0008483_transaminase activity
GO-0032555_purine ribonucleotide binding
GO-0032553_ribonucleotide binding
GO-0005992_trehalose biosynthetic process
GO-0006013_mannose metabolic process
GO-0046351_disaccharide biosynthetic process
GO-0016138_glycoside biosynthetic process
sce00071-Fatty acid metabolism
gluconeogenesis
GO-0030554_adenyl nucleotide binding
ATP
GO-0009201_ribonucleoside triphosphate biosynthetic process
GO-0006458_'de novo' protein folding
iron-sulfur
ubl conjugation
GO-0001883_purine nucleoside binding
nucleotide phosphate-binding region-NADP
sce00410-beta-Alanine metabolism
GO-0009152_purine ribonucleotide biosynthetic process
gtp-binding
sce00640-Propanoate metabolism
GO-0005977_glycogen metabolic process
GO-0015986_ATP synthesis coupled proton transport
GO-0015985_energy coupled proton transport, down electrochemical gradient
IPR003959-ATPase, AAA-type, core
IPR000793-ATPase, F1/V1/A1 complex, alpha/beta subunit, C-terminal
IPR020003-ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain, active site
IPR000194-ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain
IPR004100-ATPase, F1/V1/A1 complex, alpha/beta subunit, N-terminal
ribosomal protein
pyridine nucleotide biosynthesis
site-Lowers pKa of active site Tyr

GO-0004032_aldehyde reductase activity
PIRSF000097-aldo-keto reductase
GO-0043094_cellular metabolic compound salvage
tryptophan biosynthesis
pentose phosphate pathway
pentose shunt
intramolecular oxidoreductase
cf(1)
nucleotide phosphate-binding region-GTP
Redox-active center
GO-0000470_maturation of LSU-rRNA
GO-0000463_maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
GO-0004090_carbonyl reductase (NADPH) activity
metal ion-binding site-Magnesium
GO-0009142_nucleoside triphosphate biosynthetic process
metal ion-binding site-Zinc
GO-0022624_proteasome accessory complex
GO-0000932_cytoplasmic mRNA processing body
GO-0005838_proteasome regulatory particle
GO-0006541_glutamine metabolic process
GO-0015077_monovalent inorganic cation transmembrane transporter activity
sce00620-Pyruvate metabolism
GO-0000275_mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)
GO-0006568_tryptophan metabolic process
GO-0006586_indolalkylamine metabolic process
GO-0042430_indole and derivative metabolic process
GO-0042434_indole derivative metabolic process
GO-0005978_glycogen biosynthetic process
GO-0016469_proton-transporting two-sector ATPase complex
glutamine amidotransferase
blocked amino end
nucleus
active site-Proton donor
GO-0006399_tRNA metabolic process
sce00051-Fructose and mannose metabolism
IPR016162-Aldehyde dehydrogenase, N-terminal
IPR018170-Aldo/keto reductase, conserved site
IPR013027-FAD-dependent pyridine nucleotide-disulphide oxidoreductase
IPR002328-Alcohol dehydrogenase, zinc-containing, conserved site
GO-0009206_purine ribonucleoside triphosphate biosynthetic process
GO-0009145_purine nucleoside triphosphate biosynthetic process
IPR015421-Pyridoxal phosphate-dependent transferase, major region, subdomain 1
mitochondrial matrix
GO-0009072_aromatic amino acid family metabolic process
GO-0016769_transferase activity, transferring nitrogenous groups
Chaperone
GO-0000002_mitochondrial genome maintenance
cross-link-Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)
IPR006195-Aminoacyl-tRNA synthetase, class II, conserved region
GO-0006446_regulation of translational initiation

sce00260-Glycine, serine and threonine metabolism
iron
GO-0000162_tryptophan biosynthetic process
GO-0006549_isoleucine metabolic process
GO-0046219_indolalkylamine biosynthetic process
GO-0042435_indole derivative biosynthetic process
GO-0070469_respiratory chain
GO-0042625_ATPase activity, coupled to transmembrane movement of ions
GO-0008540_proteasome regulatory particle, base subcomplex
GO-0019363_pyridine nucleotide biosynthetic process
GO-0006356_regulation of transcription from RNA polymerase I promoter
GO-0032559_adenyl ribonucleotide binding
GO-0008135_translation factor activity, nucleic acid binding
IPR001312-Hexokinase
IPR002939-Chaperone DnaJ, C-terminal
IPR019807-Hexokinase, conserved site
GO-0006913_nucleocytoplasmic transport
GO-0051169_nuclear transport
GO-0045261_proton-transporting ATP synthase complex, catalytic core F(1)
GO-0005746_mitochondrial respiratory chain
IPR013328-Dehydrogenase, multihelical
GO-0004396_hexokinase activity
IPR003593-ATPase, AAA+ type, core
GO-0005524_ATP binding
GO-0030120_vesicle coat
GO-0046034_ATP metabolic process
transferase
protein degradation
alcohol metabolism
aromatic amino acid biosynthesis
GO-0033365_protein localization in organelle
GO-0046933_hydrogen ion transporting ATP synthase activity, rotational mechanism
Flavoprotein
monomer
GO-0006566_threonine metabolic process
GO-0006116_NADH oxidation
GO-0006413_translational initiation
dna replication
SM00651-Sm
sce00330-Arginine and proline metabolism
sce00270-Cysteine and methionine metabolism
trehalose biosynthesis
glycogen/starch biosynthesis
region of interest-Glyceraldehyde 3-phosphate binding
region of interest-Interaction surface for TPR repeats
site-Activates thiol group during catalysis
IPR001327-Pyridine nucleotide-disulphide oxidoreductase, NAD-binding region
GO-0034455_t-UTP complex
GO-0012506_vesicle membrane
GO-0030659_cytoplasmic vesicle membrane

GO-0030662_coated vesicle membrane
GO-0051188_cofactor biosynthetic process
IPR004154-Anticodon-binding
GO-0051536_iron-sulfur cluster binding
GO-0051540_metal cluster binding
GO-0042398_cellular amino acid derivative biosynthetic process
GO-0045239_tricarboxylic acid cycle enzyme complex
GO-0017102_methionyl glutamyl tRNA synthetase complex
translation regulation
oxo-acid-lyase
ATP biosynthesis
GO-0044042_glucan metabolic process
GO-0006073_cellular glucan metabolic process
GO-0000460_maturation of 5.8S rRNA
GO-0000466_maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
GO-0016744_transferase activity, transferring aldehyde or ketonic groups
GO-0042402_biogenic amine catabolic process
hexosyltransferase
glycogen biosynthesis
GO-0000462_maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
GO-0009108_coenzyme biosynthetic process
GO-0019200_carbohydrate kinase activity
GO-0009069_serine family amino acid metabolic process
GO-0008541_proteasome regulatory particle, lid subcomplex
sce00630-Glyoxylate and dicarboxylate metabolism
GO-0031298_replication fork protection complex
magnesium
GO-0046323_glucose import
GO-0043335_protein unfolding
sce00980-Metabolism of xenobiotics by cytochrome P450
IPR006649-Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core
IPR001395-Aldo/keto reductase
IPR001163-Like-Sm ribonucleoprotein, core
respiratory chain
dna-directed rna polymerase
GO-0006801_superoxide metabolic process
GO-0006083_acetate metabolic process
GO-0030663_COPI coated vesicle membrane
GO-0019774_proteasome core complex, beta-subunit complex
GO-0030126_COPI vesicle coat
IPR001189-Manganese/iron superoxide dismutase
IPR005476-Transketolase, C-terminal
IPR006424-Glyceraldehyde-3-phosphate dehydrogenase, type I
IPR000173-Glyceraldehyde 3-phosphate dehydrogenase
cytosol
GO-0006754_ATP biosynthetic process
GO-0042773_ATP synthesis coupled electron transport
GO-0045454_cell redox homeostasis
GO-0042775_mitochondrial ATP synthesis coupled electron transport
manganese

PIRSF000349-SODismutase
PIRSF000526-hexokinase
PIRSF000149-GAP_DH
PIRSF001274-F-type ATP synthase, alpha/beta subunits/V-type ATPase, subunit B
GO-0005657_replication fork
Carbohydrate transport and metabolism
sce00190-Oxidative phosphorylation
GO-0030490_maturation of SSU-rRNA
GO-0000302_response to reactive oxygen species
GO-0046417_chorismate metabolic process
GO-0009073_aromatic amino acid family biosynthetic process
IPR001926-Pyridoxal phosphate-dependent enzyme, beta subunit
IPR000994-Peptidase M24, structural domain
GO-0004365_glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity
GO-0008943_glyceraldehyde-3-phosphate dehydrogenase activity
Histidine biosynthesis
GO-0016860_intramolecular oxidoreductase activity
ammonia-lyase
binding site-NAD; via carbonyl oxygen
GO-0000096_sulfur amino acid metabolic process
potassium
atp synthesis
4fe-4s
GO-0033692_cellular polysaccharide biosynthetic process
GO-0000139_Golgi membrane
GO-0016861_intramolecular oxidoreductase activity, interconverting aldoses and ketoses
sce00380-Tryptophan metabolism
GO-0015672_monovalent inorganic cation transport
PIRSF000091-alcohol dehydrogenase
GO-0005946_alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)
GO-0030869_RENT complex
GO-0005625_soluble fraction
GO-0043614_multi-eIF complex
GO-0000221_vacuolar proton-transporting V-type ATPase, V1 domain
GO-0033180_proton-transporting V-type ATPase, V1 domain
GO-0005688_snRNP U6
GO-0006407_rRNA export from nucleus
GO-0051029_rRNA transport
Posttranslational modification, protein turnover, chaperones
GO-0005666_DNA-directed RNA polymerase III complex
GO-0005984_disaccharide metabolic process
GO-0004175_endopeptidase activity
nucleotide phosphate-binding region-ATP
GO-0006595_polyamine metabolic process
GO-0042401_biogenic amine biosynthetic process
domain-Glutamine amidotransferase type-1
binding site-NADP
phosphotransferase
electron transport
IPR006073-GTP1/OBG

GO-0032984_macromolecular complex disassembly
GO-0034623_cellular macromolecular complex disassembly
sce00910-Nitrogen metabolism
GO-0044455_mitochondrial membrane part
GO-0009066_aspartate family amino acid metabolic process
sce00400-Phenylalanine, tyrosine and tryptophan biosynthesis
GO-0000001_mitochondrion inheritance
GO-0048311_mitochondrion distribution
GO-0048475_coated membrane
GO-0043596_nuclear replication fork
GO-0030117_membrane coat
P-loop
GO-0019365_pyridine nucleotide salvage
GO-0046497_nicotinate nucleotide metabolic process
GO-0006567_threonine catabolic process
GO-0019413_acetate biosynthetic process
GO-0019568_arabinose catabolic process
GO-0042843_D-xylose catabolic process
GO-0006598_polyamine catabolic process
GO-0019566_arabinose metabolic process
GO-0019357_nicotinate nucleotide biosynthetic process
GO-0019358_nicotinate nucleotide salvage
GO-0006108_malate metabolic process
GO-0000461_endonucleolytic cleavage to generate mature 3'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU
GO-0000428_DNA-directed RNA polymerase complex
GO-0030880_RNA polymerase complex
GO-0006368_RNA elongation from RNA polymerase II promoter
GO-0044264_cellular polysaccharide metabolic process
GO-0019898_extrinsic to membrane
Fatty acid biosynthesis
compositionally biased region-Glu-rich
GO-0033176_proton-transporting V-type ATPase complex
GO-0016471_vacuolar proton-transporting V-type ATPase complex
GO-0010494_stress granule
peripheral membrane protein
cobalt
carbon-nitrogen lyase
GMP biosynthesis
repeat-CXXCXGXG motif
metal ion-binding site-Potassium; via carbonyl oxygen
zinc finger region-CR-type
GO-0045275_respiratory chain complex III
GO-0005750_mitochondrial respiratory chain complex III
GO-0016684_oxidoreductase activity, acting on peroxide as acceptor
GO-0060590_ATPase regulator activity
GO-0004601_peroxidase activity
GO-0003688_DNA replication origin binding
GO-0000447_endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricist
IPR013155-Valyl/Leucyl/Isoleucyl-tRNA synthetase, class I, anticodon-binding
IPR000649-Initiation factor 2B related

IPR015928-Aconitase/3-isopropylmalate dehydratase, swivel
IPR001830-Glycosyl transferase, family 20
IPR005475-Transketolase, central region
IPR015932-Aconitase/3-isopropylmalate dehydratase large subunit, alpha/beta/alpha, subdomain 2
IPR000573-Aconitase A/isopropylmalate dehydratase small subunit, swivel
IPR015931-Aconitase/3-isopropylmalate dehydratase large subunit, alpha/beta/alpha, subdomain 1/3
IPR001030-Aconitase/3-isopropylmalate dehydratase large subunit, alpha/beta/alpha
IPR018136-Aconitase family, 4Fe-4S cluster binding site
GO-0050661_NADP or NADPH binding
GO-0022904_respiratory electron transport chain
GO-0000183_chromatin silencing at rDNA
calmodulin-binding
metal ion-binding site-Iron-sulfur (4Fe-4S)
compositionally biased region-Gly-rich
nucleotide phosphate-binding region-FAD
GO-0034220_ion transmembrane transport
sce00052-Galactose metabolism
GO-0006997_nucleus organization
GO-0016615_malate dehydrogenase activity
GO-0004784_superoxide dismutase activity
GO-0016721_oxidoreductase activity, acting on superoxide radicals as acceptor
GO-0003825_alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity
GO-0004805_trehalose-phosphatase activity
GO-0005851_eukaryotic translation initiation factor 2B complex
GO-0031428_box C/D snoRNP complex
coenzyme A
purine nucleotide binding
carbon-carbon lyase
lipid synthesis
binding site-S-adenosyl-L-methionine
GO-0044433_cytoplasmic vesicle part
GO-0033554_cellular response to stress
glycosyltransferase
GO-0019843_rRNA binding
GO-0003899_DNA-directed RNA polymerase activity
GO-0034062_RNA polymerase activity
GO-0030660_Golgi-associated vesicle membrane
GO-0051640_organelle localization
GO-0005811_lipid particle
GO-0005198_structural molecule activity
GO-0030515_snoRNA binding
domain-RRM
GO-0022411_cellular component disassembly
GO-0009168_purine ribonucleoside monophosphate biosynthetic process

Rank in WT	Rank in KO	*Delta*
1	1	0
2	4	2
3	5	2
4	6	2
5	7	2
6	10	4
7	3	-4
8	14	6
9	15	6
10	8	-2
11	9	-2
12	11	-1
13	77	64
14	76	62
15	42	27
16	24	8
17	44	27
18	31	13
19	71	52
20	22	2
21	16	-5
22	27	5
23	2	-21
24	13	-11
25	17	-8
26	21	-5
27	12	-15
28	40	12
29	19	-10
30	23	-7
31	25	-6
32	79	47
33	37	4
34	43	9
35	121	86
36	45	9
37	64	27
38	36	-2
39	81	42
40	48	8
41	30	-11
42	20	-22
43	54	11
44	55	11
45	135	90
46	18	-28
47	75	28
48	66	18

49	165	116
50	32	-18
51	26	-25
52	59	7
53	60	7
54	53	-1
55	52	-3
56	58	2
57	38	-19
58	198	140
59	102	43
60	101	41
61	70	9
62	264	202
63	110	47
64	67	3
65	57	-8
66	47	-19
67	34	-33
68	49	-19
69	459	390
70	96	26
71		
72	194	122
73	213	140
74	273	199
75	100	25
76		
77	33	-44
78	99	21
79	132	53
80	73	-7
81	136	55
82	236	154
83	83	0
84	84	0
85	87	2
86	133	47
87	90	3
88		
89	140	51
90	193	103
91	325	234
92	326	234
93	28	-65
94	29	-65
95	92	-3
96	304	208
97	126	29
98	127	29

99	106	7
100	145	45
101	327	226
102	78	-24
103	35	-68
104	74	-30
105	334	229
106	335	229
107	56	-51
108	430	322
109	72	-37
110	152	42
111		
112	159	47
113	219	106
114	62	-52
115	94	-21
116	61	-55
117	109	-8
118	108	-10
119	65	-54
120	118	-2
121	147	26
122	41	-81
123	39	-84
124	386	262
125		
126	68	-58
127		
128	146	18
129		
130	93	-37
131	170	39
132	171	39
133	111	-22
134	46	-88
135	196	61
136	197	61
137	142	5
138	125	-13
139	149	10
140	498	358
141	180	39
142	341	199
143	69	-74
144	241	97
145	50	-95
146	51	-95
147	134	-13
148	189	41

149	314	165
150	128	-22
151		
152	103	-49
153	254	101
154	85	-69
155	184	29
156	318	162
157	221	64
158	151	-7
159	150	-9
160	308	148
161	349	188
162	422	260
163	480	317
164		
165	225	60
166	226	60
167	415	248
168		
169	123	-46
170	98	-72
171	277	106
172	80	-92
173	89	-84
174	310	136
175	124	-51
176	355	179
177	424	247
178	423	245
179	227	48
180	139	-41
181	166	-15
182		
183		
184	148	-36
185	442	257
186		
187	272	85
188	130	-58
189	262	73
190	86	-104
191	63	-128
192	141	-51
193	265	72
194	202	8
195	402	207
196	332	136
197	222	25
198	119	-79

199		
200	181	-19
201	182	-19
202	319	117
203	258	55
204	107	-97
205	214	9
206	186	-20
207	256	49
208		
209	95	-114
210	361	151
211		
212		
213		
214		
215	229	14
216	91	-125
217		
218	160	-58
219	129	-90
220	217	-3
221	104	-117
222	224	2
223	230	7
224		
225	208	-17
226		
227	237	10
228		
229	312	83
230	156	-74
231		
232	162	-70
233	433	200
234		
235		
236	248	12
237	223	-14
238	164	-74
239	419	180
240	362	122
241		
242		
243	131	-112
244	281	37
245	105	-140
246	282	36
247	228	-19
248	517	269

249	502	253
250	503	253
251	252	1
252	176	-76
253	377	124
254	463	209
255	183	-72
256	172	-84
257	220	-37
258	239	-19
259	238	-21
260	240	-20
261	157	-104
262	114	-148
263	158	-105
264		
265		
266		
267		
268		
269		
270	117	-153
271	169	-102
272	116	-156
273	115	-158
274	507	233
275	421	146
276	509	233
277	88	-189
278		
279	440	161
280	467	187
281	200	-81
282	516	234
283	276	-7
284	323	39
285	271	-14
286		
287	462	175
288	515	227
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291	471	180
292	393	101
293	398	105
294	388	94
295	390	95
296	138	-158
297	317	20
298	185	-113

299	192	-107
300	299	-1
301	82	-219
302	383	81
303	206	-97
304	205	-99
305	204	-101
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307		
308	235	-73
309	379	70
310	378	68
311	209	-102
312	259	-53
313		
314	97	-217
315	231	-84
316	479	163
317	232	-85
318	454	136
319	455	136
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321		
322	293	-29
323	298	-25
324	297	-27
325	292	-33
326	291	-35
327		
328		
329	311	-18
330		
331	260	-71
332		
333	195	-138
334	215	-119
335	216	-119
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338		
339		
340	307	-33
341		
342	173	-169
343		
344	473	129
345		
346	285	-61
347	434	87
348		

349	283	-66
350	512	162
351	450	99
352	445	93
353	451	98
354	449	95
355	456	101
356		
357		
358	287	-71
359		
360		
361		
362	242	-120
363	461	98
364	243	-121
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366		
367		
368		
369	376	7
370	255	-115
371	365	-6
372		
373	143	-230
374		
375	179	-196
376	247	-129
377		
378	245	-133
379		
380		
381	144	-237
382	476	94
383	250	-133
384		
385		
386	431	45
387		
388	425	37
389	244	-145
390	279	-111
391	278	-113
392		
393	280	-113
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395		
396		
397	153	-244
398	155	-243

399	154	-245
400	249	-151
401		
402		
403		
404	453	49
405	286	-119
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409		
410		
411		
412	437	25
413	436	23
414	163	-251
415	270	-145
416	345	-71
417	510	93
418		
419	351	-68
420	266	-154
421	284	-137
422		
423		
424	499	75
425	300	-125
426	320	-106
427	322	-105
428		
429		
430	414	-16
431		
432	354	-78
433	470	37
434	305	-129
435		
436	289	-147
437	112	-325
438	290	-148
439		
440		
441		
442		
443	161	-282
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445		
446	342	-104
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448	400	-48

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450	337	-113
451		
452		
453		
454	357	-97
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456		
457	416	-41
458	296	-162
459	295	-164
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461		
462		
463		
464		
465	275	-190
466		
467		
468	375	-93
469	472	3
470		
471		
472		
473	435	-38
474	330	-144
475	474	-1
476		
477		
478	168	-310
479		
480		
481		
482		
483		
484		
485		
486		
487	344	-143
488	418	-70
489	201	-288
490	203	-287
491	427	-64
492	333	-159
493	500	7
494		
495		
496	257	-239
497	452	-45
498		

499	487	-12
500	488	-12
501		
502		
503	360	-143
504	353	-151
505		
506		
507	188	-319
508	464	-44
509	187	-322
510		
511	370	-141
512	373	-139
513		
514		
515	369	-146
516	372	-144
517	366	-151
518	367	-151
519	368	-151
520	371	-149
521		
522		
523		
524		
525	513	-12
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528		
529		
530		
531		
532		
533	381	-152
534		
535	382	-153
536	380	-156
537		
538	384	-154
539		
540	347	-193
541	346	-195
542	329	-213
543	484	-59
544	328	-216
545		
546		
547		
548		

549	392	-157
550	199	-351
551	399	-152
552	389	-163
553	394	-159
554	391	-163
555	397	-158
556	396	-160
557	233	-324
558		
559		
560		
561		
562		
563		
564		
565	359	-206
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567		
568	413	-155
569	412	-157
570	211	-359
571	210	-361
572		
573		
574		
575		
576	486	-90
577		
578		
579	207	-372
580	352	-228
581	313	-268
582		
583		
584		
585	338	-247
586		
587		
588		
589		
590		
591		
592	167	-425

Table S3. Analyzing the fold increase of the various proteins associated with the four GO term categories selected in Table 1. The summary spreadsheet contains a non-over lapping list of proteins under the categories listed in Table 1 that were either expressed only upon heat stress induction or had increased expression upon heat stress induction. The emPAI scores were used to calculate the fold change in protein levels upon heat stress induction.

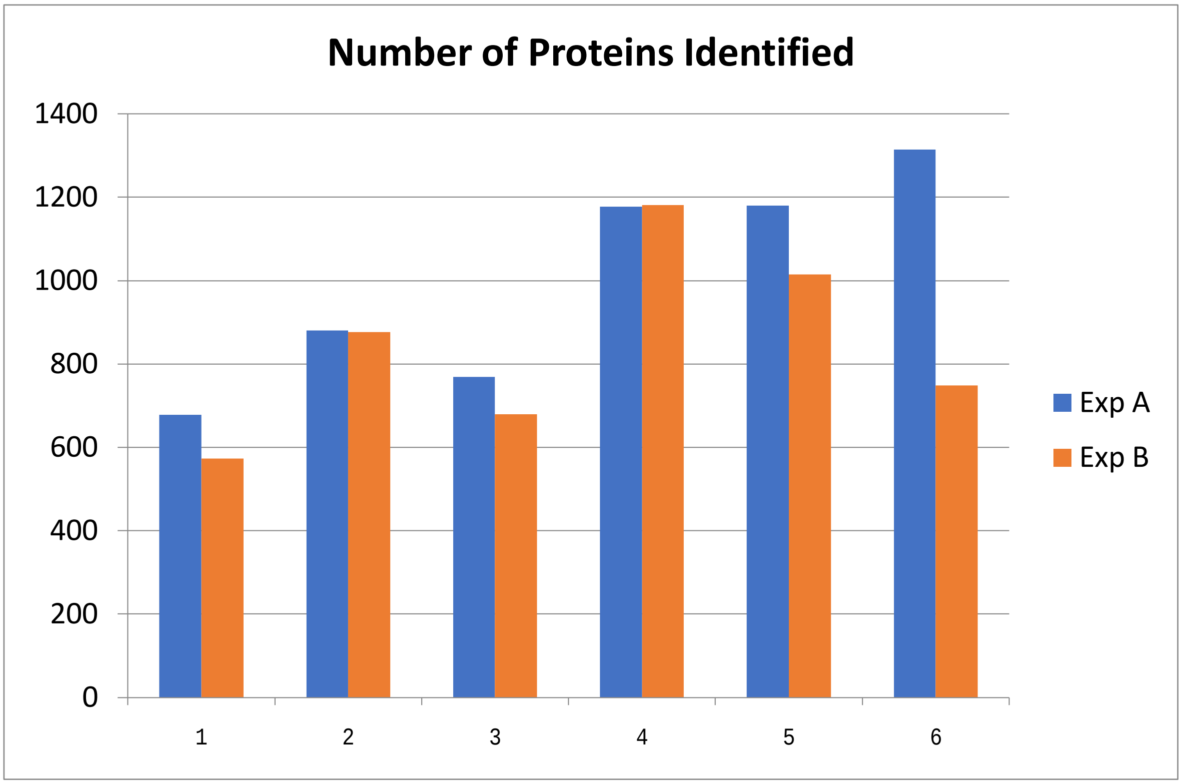
Clusters associated with specific GO Terms

		Fold-Increase Upon Heat Shock				
		Wildtype		Knockout		
Gene Name	SwissProt	A	B	A	B	Cluster
UTP4	UTP4_YEAST	2.8	HS Only	HS Only	1.0	Wildtype Enriched, 90S Ribosome associated
RRP12	RRP12_YEAST	HS Only	2.2	1.6	1.0	
UTP7	UTP7_YEAST	4.2	1.8	1.0	0.2	
UTP8	UTP8_YEAST	0.6	4.8	0.4	1.0	
RPP0	RLA0_YEAST	3.5	1.0	1.2	0.6	
DIM1	DIM1_YEAST	HS Only	HS Only	HS Only	1.0	
UTP9	UTP9_YEAST	6.0	HS Only	0.6	GR Only	
RRP9	RRP9_YEAST	2.2	HS Only	2.2	1.0	
CMS1	CMS1_YEAST	1.6	3.3	1.0	1.0	
SOF1	DCA13_YEAST	2.2	HS Only	0.5	1.0	
IMP3	IMP3_YEAST	2.1	2.1	0.5	0.5	
HAS1	HAS1_YEAST	1.4	2.7	0.8	0.8	
ERB1	ERB1_YEAS7	4.0	3.0	1.0	0.3	
NOP58	NOP58_YEAS7	2.6	2.2	1.4	1.2	
NOP56	NOP56_YEAST	2.3	2.1	1.1	1.2	
ECM16	DHR1_YEAST	0.5	5.0	1.0	GR Only	
NAN1	UTP17_YEAST	1.0	5.8	0.5	0.4	
AIM10	SYPM_YEAST	HS Only	HS Only			Wildtype Enriched, tRNA activation-associated
YDR341C	SYRC_YEAST	HS Only	HS Only	HS Only		
ILS1	SYIC_YEAST	HS Only	HS Only	HS Only		
HTS1	SYH_YEAST	HS Only	HS Only	HS Only		
WRS1	SYWC_YEAST	3.3	HS Only	HS Only	GR Only	
CDC60	SYLC_YEAST	HS Only	HS Only	1.0	HS Only	
DPS1	SYDC_YEAST	HS Only	HS Only	1.0	HS Only	
MES1	SYMC_YEAST	5.8	2.0	3.3	2.0	
THS1	SYTC_YEAST	HS Only	7.0	HS Only	4.5	
YHR020W	YHI0_YEAST	2.0	6.3	0.8	1.0	
GUS1	SYEC_YEAST	2.3	HS Only	1.0	GR Only	
ALA1	SYAC_YEAST	HS Only	HS Only			
ARC1	G4P1_YEAST	HS Only	HS Only	1.0		
NOC3	NOC3_YEAST	HS Only	2.0	2.0	HS Only	e-enriched, ribosome biogenesis associated
ESF1	ESF1_YEAST	HS Only	HS Only	1.0	1.0	
NSA2	NSA2_YEAS7	HS Only	HS Only	GR Only	GR Only	
SPB4	SPB4_YEAS7	HS Only	HS Only	HS Only	GR Only	
NOP6	NOP6_YEAST	HS Only	HS Only	1.0	2.3	
NOP2	NOP2_YEAST	4.4	HS Only	2.8	2.2	
NOP12	NOP12_YEAST	4.3	3.5	1.8	0.6	
GAR1	GAR1_YEAST	3.6	1.0	2.2	1.6	
NOG1	NOG1_YEAST	3.5	3.2	1.7	1.4	
PXR1	PXR1_YEAS7	3.3	2.3	1.4	GR Only	
NIP7	NIP7_YEAST	2.2	3.6	1.0	1.0	
NOP15	NOP15_YEAST	2.2	HS Only	2.2	1.0	
KRI1	KRI1_YEAST	2.2	HS Only	1.0	GR Only	
RPF1	RPF1_YEAST	2.2	HS Only	1.0	0.5	

BRX1	BRX1_YEAST	2.1	3.3	2.1	1.6	Wdiltyp
SAS10	SAS10_YEAST	2.0		0.3	2.0	
NOP10	NOP10_YEAST	2.0	9.3	1.0	0.5	
RCL1	RCL1_YEAST	GR Only			3.2	Knockout-enriched, 90S associated
UTP21	UTP21_YEAST		1.0	2.3	HS Only	
ENP2	NOL10_YEAST	GR Only		HS Only	HS Only	
RPS14A	RS14A_YEAST	0.5	HS Only	HS Only	HS Only	
UTP13	UTP13_YEAST	GR Only	1.0	3.0	GR Only	
SLX9	SLX9_YEAST			HS Only	HS Only	
DED81	SYNC_YEAST		HS Only	HS Only	HS Only	KO, tRNA
MSD1	SYDM_YEAST		HS Only	HS Only	HS Only	
RIX7	RIX7_YEAST	HS Only		HS Only	HS Only	Knockout-enriched, ribosome biogenesis associated
SNU13	SNU13_YEAST	1.7	1.4	1.5	2.7	
MRT4	MRT4_YEAST	HS Only	1.9	3.9	5.1	
URB1	URB1_YEAST	1.0	1.0	2.1	GR Only	
NOP8	NOP8_YEAST	1.0	HS Only	2.2		
DBP6	DBP6_YEAS7	1.0	HS Only	GR Only	GR Only	
SES1	SYSC_YEAST	HS Only	HS Only	1.0	3.0	Heat Shock Responsive in both genotypes
EMG1	EMG1_YEAST	3.4	HS Only	3.0	3.4	
TYS1	SYYC_YEAST	HS Only	HS Only	3.4	HS Only	
FRS1	SYFB_YEAST	HS Only	4.6	5.8	11.8	
SCL1	PSA6_YEAST	6.5	HS Only	12.8	15.4	
CKB1	CSK2B_YEAST	HS Only	HS Only	HS Only	HS Only	
CKB2	CSK2C_YEAST	HS Only	HS Only	HS Only	HS Only	
GRS1	SYG_YEAST	HS Only	HS Only	HS Only	HS Only	
LOC1	LOC1_YEAS7	HS Only	HS Only	HS Only	HS Only	
NOP53	NOP53_YEAST	HS Only	HS Only	HS Only	HS Only	
SPB1	SPB1_YEAST	HS Only	HS Only	HS Only	HS Only	
VAS1	SYV_YEAST	HS Only	HS Only	HS Only	HS Only	
RIO2	RIO2_YEAST	HS Only	HS Only	HS Only	HS Only	

Table S4. **An overall summary of the protein yield resulting from the 2D LC-MS/MS experiments.** The graph indicates the yield of protein identification for the two replicates. The table lists the number of peptides as well as protein identified along with the false discovery rate for each run. The normal condition in denoted by “log growth or GR” and the stress condition is denoted by “heat shock or HS”.

Table S4. Summary of Proteomics Experiments



Data for Graph

		Replicate A			Replicate B		
ulture Conditio	Genotype	Peptides	Exp A	FDR	Peptides	Exp B	FDR
Log Growth	Wildtype	4155	678	3.32%	4024	573	2.19%
	YCA-1 Knockout	5832	880	3.41%	5918	876	2.75%
	YCA-1 Mutant	5899	769	3.07%	5188	680	2.66%
Heat Shock	Wildtype	7688	1178	2.41%	7633	1181	2.40%
	YCA-1 Knockout	7765	1180	2.49%	6390	1015	1.80%
	YCA-1 Mutant	9613	1315	2.62%	3691	748	3.17%

ACC1	ACT1	ADE5,7	ADH1	AHA1
ARC1	ARO1	ARP2	ARP3	ATP2
CCT3	CCT8	CDC10	CDC19	CDC48
CHA1	CHC1	CHS1	CLU1	COR1
DBP2	DED1	DHH1	DNF1	DNF2
ECM29	ECM33	ENO1	ENO2	ERG6
ETT1	EXG1	FAA4	FAS1	FAS2
FBA1	FKS1	FLC2	GAS1	GCD6
GCN1	GFA1	GLN1	GPH1	GSF2
GUS1	HSC82	HSP42	HSP60	IDH2
IKI3	ILV1	ILV2	KAP123	KRE6
LAP4	LEM3	LSB1	LSB3	LYS12
MCM4	MDJ1	MES1	MIR1	MKT1
NCP1	NOG2	NOP1	NOP56	NPA3
NPL3	NRP1	NTH2	NUC1	PDR12
PFK1	PFK2	PIL1	PIN3	PMT2
PSA1	REP1	RET2	RNQ1	RPA190
RPC40	RPL1A	RPL3	RPL4A	RPL4B
RPN5	RPP0	RPS0	RPS14A	RPS1B
RPS3	RPS5	RPT5	RRP3	RSP5
RVB1	SAH1	SAM2	SCS2	SEC27
SEC61	SEH1	SGT2	SIS1	SPF1
SPT5	SRP1	SSA1	SSA2	SSB1
SSB2	SSC1	SSO1	SUB35	SUP45
TDH1	TEF1	THS1	TIF1	TOM40
TUB1	TUB2	TUB3	UBA4	UBI4
URA2	URA7	VAC8	VMA1	VMA2
VPS1	VPS13	VTC4	WWM1	YAP1802
YBL081W	YDJ1	YEF3	YNL208W	YPK1

Table S5. List of proteins interacting with Yca1 identified by LC-MS analysis of FL-RFP pulldown. FL-RFP fusion protein was expressed in Δ*yca1* cells under normal growth conditions and used to isolate interacting proteins with anti-RFP antibody. The isolated interacting proteins were separated via SDS-PAGE and resolved via silver nitrate staining. Proteins were identified via LC-MS/MS analysis and are listed above. *n*=3.

Site	Peptide Sequence	Modification	Localization	Ascore
K48	LIFAGkQLEDGR	K6 Gly Gly	100%	1,000.00
K63	TLSDYNIQkESTLHLVLR	K9 GlyGly	100%	1,000.00

Table S6. Ubiquitin linkages identified by LC-MS. Modifications within the ubiquitin protein were identified by LC-MS using the Scaffold PTM software. The modification site along with the peptide sequence and modification observed are depicted above. The Ascore reflects the positional accuracy of the modification site.

ACC1	ETT1	KAP123	RPC40	SAM2	*YCA1*
ARC1	FAA4	MES1	RPT5	SUP45	YEF1
DBP2	GCN1	NOG2	RSP5	THS1	YPK1
DED1	GUS1	NPL3	RVB1	URA7	

Table S7. Aggregation prone proteins present within the Yca1 interactome. An independent study identified 177 proteins that were prone to rapid aggregation (within 8 minutes at 46°C) were identified via LC-MS (Wallace, Kear-Scott et al. 2015). Listed above are the proteins that were present in the Yca1 interactome, including Yca1 (italicized) and were classified as aggregation prone in the other study.

Appendix II

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The non-death role of metacaspase proteases

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The activation of caspase proteases and the targeting of protein substrates act as key steps in the engagement and conduct of apoptosis/programmed cell death. However, the discovery of caspase involvement in diverse non-apoptotic cellular functions strongly suggests that these proteins may have evolved from a core behavior unrelated to the induction of cell death. The presence of similar proteases, termed metacaspases, in single cell organisms supports the contention that such proteins may have co-evolved or derived from a critical non-death function. Indeed, the benefit(s) for single cell life forms to retain proteins solely dedicated to self destruction would be countered by a strong selection pressure to curb or eliminate such processes. Examination of metacaspase biology provides evidence that these ancient protease forerunners of the caspase family also retain versatility in function, i.e., death and non-death cell functions. Here, we provide a critical review that highlights the non-death roles of metacaspases that have been described thus far, and the impact that these observations have for our understanding of the evolution and cellular utility of this protease family.

Keywords: metacaspase, caspase, non-death, cell cycle, proteostasis

INTRODUCTION

The conserved family of clan CD proteases, caspases, has been extensively characterized in programmed cell death or apoptosis, a function that is vital for homeostasis of complex organisms. Despite the well established death centric role, there is increasing evidence for caspase involvement in non-apoptotic scenarios, such as terminal differentiation of numerous cell types, non-death cellular remodeling events and immune system adaptation. In addition to the study of caspase function in multi-cellular life forms, the discovery of functional caspase orthologs in lower eukaryotes, such as fungi and protozoa (termed metacaspases) suggests these proteins emerged early in the evolutionary record (Uren et al., 2000; Aravind and Koonin, 2002).

Interestingly, recent investigations of metacaspase function have revealed these enzymes play a role in various non-apoptotic or "non-death" processes, in a manner analogous to the metazoan caspase family. Here, we critically review the literature and the latest studies which examine the physiologic function of metacaspase proteases. We conclude that the versatility displayed by the caspase protease family may simply reflect primordial death and non-death functions that initially evolved from para- and metacaspase activity, a functional diversity that is clearly present in unicellular organisms such as yeast and trypanosomatids.

METACASPASES IN CELL CYCLE REGULATION

One of the earliest reports indicative of a non-death role for metacaspases was derived from observations in the protozoan *Trypanosoma brucei*. Here, the expression of several metacaspases (MCA2/3/5) was shown to be critical for the viability of the bloodstream form of the parasite. RNAi induced knockdown of the expression of these metacaspase genes was accompanied by severe growth retardation and cell cycle defects of the circulating *Trypanosoma* (Helms et al., 2006). Furthermore, the Δ*mca2/3*Δ*mca5* mutants showed no significant difference in cell death kinetics in response to prostaglandin D_2 treatment, observations which support a cellular role for *Trypanosoma* metacaspase beyond the apoptosis cascade.

A subsequent study in the related kinetoplast protozoan, *Leishmania major*, further supported the role of metacaspases in cell cycle dynamics. The *L. major* metacaspase (LmjMCA), which is syntenic to MCA5 in *T. brucei*, was observed to be a critical component that regulated stage progression during cellular division (Ambit et al., 2008). For example, during logarithmic growth, LmjMCA expression increased when compared to stationary phase cultures. Moreover, the association of LmjMCA with mitotic spindles during cellular division provided convincing evidence that this metacaspase impacted cell cycle progression. Accordingly, the overexpression of LmjMCA resulted in severe growth retardation with concurrent defects in kinetoplast segregation, multiple mitotic nuclei, and changes in ploidy with a reduced number of cells undergoing cytokinesis. Attempts to create an LmjMCA null strain also resulted in striking cell cycle defects, leading to lethality. Together, these observations suggest that LmjMCA plays a critical role in the management of cell cycle progression.

The mechanism by which a protozoan metacaspase exerts cell cycle control is not entirely clear, although a number of studies suggest that the subcellular localization of the enzyme as well as the level of expression may dictate this non-death activity. First, the RAB11 marker for recycling endosomes was observed to co-localize with a large proportion of the metacaspases in a distinctive compartment between the nucleus and the kinetoplast (Helms et al., 2006). However, the recycling process of VSG was observed to be independent of the metacaspases.

RAB11 positive endosomes are known to be involved in kinetoplast division leading to cytokinesis in the procyclic form of *T. brucei* (Jeffries et al., 2001; Kohl et al., 2003). Thus, the role of these metacaspases in cytokinesis of the bloodstream form of *T. brucei* may argue a non-death role in cell cycle progression, yet specific experiments to support this contention have yet to be undertaken. More recently, overexpression of the *Trypanosoma cruzi TcMCA3* has been linked to a non-death biologic activity, resulting in a reduced growth rate and a transient G1/S block. Additionally, overexpression of TcMCA5 lacking the Ct region (pro, gln, and tyr rich region) led to increase in hypodiploid cells, which implicates the Ct region in dictating metacaspase function (Laverrière et al., 2012). Of note, MCA5 is syntenic in the three protozoa species (Mottram et al., 2003); however, the ability of the Ct region to mediate metacaspase function has yet to be explored in *L. major* and *T. brucei*. Together, these observations in related protozoa species argue that metacaspases regulate cell cycle progression, a function that appears to be independent of promoting cell death.

The metacaspase involvement in cell cycle control appears to be a well conserved phenomenon that extends across phyla. In *Saccharomyces cerevisiae*, deleting the single metacaspase Yca1 (Δ*yca1*) or altering the proteolytic activity of the enzyme leads to altered DNA content and growth rate, which is marked by a slowed G1/S transition (Lee et al., 2008). A similar trend has also been reported for *T. cruzi* (Laverrière et al., 2012). In addition, yca1 null cells failed to respond to a nocodazole-induced mitotic G2/M checkpoint in conditions that favored cell growth. Taken together, these observations implicate Yca1 in regulation of cell cycle checkpoints. Similarly, the metacaspase of the related yeast species, *Schizosaccharomyces pombe* also impacts cell cycle dynamics. In this instance, overexpression of the fission yeast metacaspase, Pca1, led to accelerated growth, a feature which was much improved upon cadmium induced oxidative stress (Lim et al., 2007). The precise mechanism by which a metacaspase protease regulates cell cycle progression remains unknown yet is of considerable interest.

METACASPASE REGULATION OF PROTEOSTASIS AND PROTEIN AGGREGATE FORMATION

The ability of the pombe metacaspase to promote cell cycle advance during oxidative stress strongly suggests that this clade of enzymes may have a cytoprotective role, a feature that appears contrary to the well-described death centric behavior described to date. Consequently, in a subsequent study in *S. cerevisiae* we identified the regulation of protein aggregates as a function by which Yca1 may confer improved fitness and survival (Lee et al., 2010). A genome wide proteomic analysis showed that Δ*yca1* cells are enriched for the Hsp70 family of chaperones (Ssa1, Ssa2, and Ssa4) as well as Hsp104 remodeling chaperone that is involved in the disaggregation of insoluble protein aggregates (Parsell et al., 1994). Furthermore, the normally cytosolic YCA1-GFP was observed to co-localize with Hsp104-RFP, a marker for protein aggregates, under heat stress independent of its catalytic activity. Consequently, filter-trap analyses showed that the loss of Yca1 or its catalytic activity was synonymous with increased levels of insoluble protein aggregates (Lee et al., 2010). Truncated forms of Yca1 lacking the polyQ region were observed to shift from the insoluble protein fraction to a more equitable distribution, with the truncated Yca1 contained in both the soluble and insoluble protein fractions. These observations would suggest that the polyQ region is responsible (in part) for the targeting of Yca1 to aggregated material/proteins and that the stability and/or dissipation of protein aggregates are controlled by the yeast metacaspase Yca1. This unexpected feature of Yca1 appears to be independent of invoking cell death and is associated with maintaining proper cell cycle progression.

As noted with cell cycle regulation and metacaspase activity, the apparent role of a metacaspase(s) in regulating protein levels may also be a conserved molecular function for this otherwise death centric protein. In support of this contention, a study in the filamentous fungus, *Aspergillus fumigatus* revealed that loss of metacaspase expression led to a blunted response to endoplasmic stress (ER) induction (Richie et al., 2007). Specifically, the induction of ER stress in cells lacking functional metacaspase using 2-deoxy-D-glucose (2-DG), tunicamycin (TM), and dithiothreitol (DTT) displayed retardation in growth. Moreover, the increased sensitivity to the glucose analog, 2-DG induced stress in Δ*casA*/Δ*casB* cells was particularly highlighted in the study. 2-DG is known to induce the unfolded protein response (UPR) which delays protein synthesis in order to allow for either the successful re-folding or degradation of misfolded proteins to ensure ER homeostasis (Wu and Kaufman, 2006). In addition to regulating protein homeostasis, these authors also observed that apoptosis induction proceeded independent of metacaspase activity. For example, there was no significant change in the number of PI-positive protoplasts, an observation that is strikingly similar to the observations of metacaspase independent cell death that have been reported in *S. cerevisiae* (Madeo et al., 2009). Although not definitive, the protein homeostatic behavior attributed to metacaspases in yeast and fungi species in the above mentioned studies imply an ancient non-death regulatory role for these enzymes.

Given the observations above it is tempting to speculate that all caspase/metacaspase enzymes have evolved a proteostasis function. Nevertheless, a separate study in *A. nidulans* suggests that unlike in *A. fumigatus*, where loss of both metacaspases had an additive impact on stress outcomes, the metacaspases in *A. nidulans* may actually retain inhibitory or antagonistic functions related to maintaining protein stability (Colabardini et al., 2010; Tsiatsiani et al., 2011). Here, ER stress was induced by treating cells with farnesol, which is also known to induce the UPR, as well as DTT and 2-DG. Spotting assays with the different treatments showed that the loss of *cas*B had a much more significant effect on growth in comparison to the Δ*cas*A cells. Overexpression of pkcA in Δ*cas*A cells restored the sensitivity to farnesol-induced apoptosis. These observations led the authors to speculate that in *A. nidulans* metacaspases may function antagonistically with *cas*A promoting death while *cas*B has a protective role during ER stress (Colabardini et al., 2010).

FUNCTIONAL OVERLAP BETWEEN CASPASES AND METACASPASES

The cellular behavior of metacaspases described thus far provides substantial evidence that these proteases are physiologically active and retain critical function(s) independent of apoptosis.

We have previously argued that death and differentiation may be of a common origin and that different stimuli/substrates may dictate the outcome (Fernando and Megeney, 2007). The physiological functions of metacaspases discussed thus far which are mirrored by their metazoan counterparts lend further support to the hypothesis (**Figure 1**). For example, the ability of metacaspases to regulate cell cycle events have also been observed for their metazoan counterparts; human hepatoma cells that lack caspase 3 activity have also been shown to bypass the G2/M mitotic checkpoint in response to nocodazole treatment (Hsu et al., 2006) and thus implicating an evolutionarily conserved function for caspase and metacaspases between different phylogeny (Tsiatsiani et al., 2011). To date, it remains unclear whether metacaspases have the ability to alter cell fate in a manner similar to metazoan caspases. With reference to mammalian caspase enzymes, upregulation of caspase 3 activity is a critical step in promoting cell differentiation in virtually all progenitor cell types examined from skeletal muscle, to neurons, hematopoietic cell lineages and ES cells (Fernando et al., 2002, 2005; Fujita et al., 2008; Janzen et al., 2008). Moreover, the role of caspase 3 in determining cellular differentiation is conserved across the phyla, from *Drosophila* to humans (Abdul-Ghani and Megeney, 2008).

The importance of caspase 8 activity for trophoblast fusion during human placental development (Black et al., 2004) and caspase 9 as an initiator of lens fiber epithelial development (Weber and Menko, 2005) suggests that both initiator and executioner caspase enzymes have the ability to function in non-death scenarios. The metacaspases involved in non-death functions described here thus far belong to or are known to resemble the type I category, which is thought to be similar to the initiator or pro-caspases in metazoans; both sets possess a regulatory region in the N-terminal. As for type II metacaspases, which are predominantly present in plants (Tsiatsiani et al., 2011), they have yet to be reported in processes other than cell death. Given these observations it is tempting to speculate that the non-death function of initiator caspases may have evolved from the non-death targeting activity of type I metacaspase enzymes.

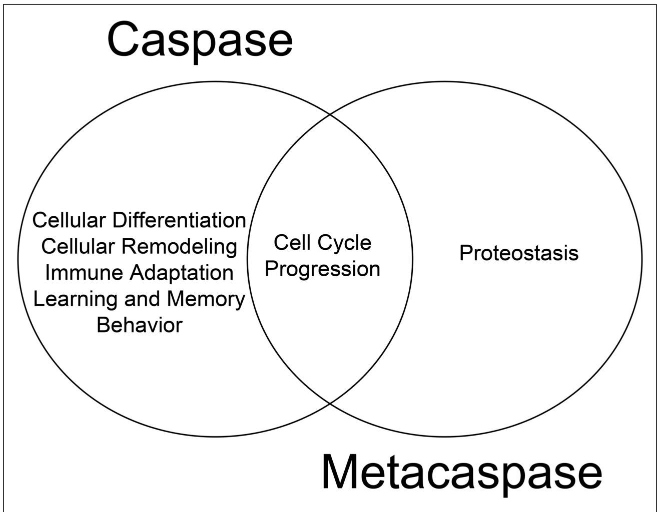

FIGURE 1 | Functional overlap of caspase and metacaspase function. Regulation of cell cycle progression is a conserved function for both proteases, suggesting a common evolutionary origin. Additional non-death functions of metacaspases such as the role of Yca1 in proteostasis has yet to be confirmed as a feature of caspase biology.

The role of metacaspases in maintaining protein homeostasis is a more recent discovery that is unique to *S. cerevisiae* and has yet to be explored extensively in other organisms. Nonetheless, the novel findings generated from the yeast studies provide support for the postulation that Yca1 regulation of protein aggregates may be a mechanism by which the cell increases fitness and adaptation to stress (Lee et al., 2008, 2010). The beneficial role of Yca1 in proteostasis is largely in contrast to the negative role ascribed to mammalian caspases in the same context. Here, caspase proteases have garnered considerable interest for as causative agents in various neurodegenerative/neuromuscular disease conditions such as Alzheimer's disease, Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS), and inclusion body myopathies. In these instances, caspase activation is believed to contribute to the development of a proteotoxic environment by cleaving various proteins that in turn promote aggregate formation, leading to cell stress and eventual cell death (Rothstein, 2009; Rohn, 2010; Graham et al., 2011).

In contrast to the well-accepted contention that activated caspases are synonymous with deleterious activity in neurons, a number of studies suggest that caspase activity may be required for neural cell adaptation and may counteract proteotoxicity. First, caspase activation has been shown to mediate long-term potentiation, learning, dendrite, and axon remodeling, all of which are independent of cell death (Huesmann and Clayton, 2006; Fernando and Megeney, 2007; D'Amelio et al., 2010; Li et al., 2010). More recently, caspase 3 has been reported to cleave TDP-43 in mouse primary cortical neurons, a response which attenuates TDP-43-induced apoptosis (Suzuki et al., 2011). Abnormal aggregated forms of hyperphosphorylated TDP-43 are the major components of ubiquitinated inclusion bodies (IBs) that characterize ALS and frontotemporal lobar degeneration with ubiquitinated inclusions (FTLD-U; Neumann et al., 2006). The study of Suzuki et al. (2011) demonstrated that ER stress or staurosporine treatment led to caspase cleavage of TDP-43 and generation of C-terminal fragments (CTFs). The death inducing ability of the resulting CTF aggregates were lower than the wildtype TDP-43, and of particular note a caspase cleavage resistant mutant of TDP-43 showed a magnified death response compared to the wildtype protein; an observation that emphasizes a cytoprotective response of the caspase cleavage event (Suzuki et al., 2011). Contrary to the study by Suzuki et al. (2011), other groups have shown that CTFs of TDP-43 can itself be toxic and induce cell death (Johnson et al., 2008; Zhang et al., 2009). However, the cell death in these latter studies may be simply a reflection of a caspase activation pattern that is unrestrained and is coincident with the TDP-43 modifications, rather than disease causing *per se*. Indeed, a reasonable supposition may be that the caspase activation that accompanies protein aggregation in neurodegenerative disease conditions is an adaptive response to rid the cell of toxic materials rather than a disease propagating alteration (**Figure 2**). The corollary to this model would suggest that caspase mediated cell

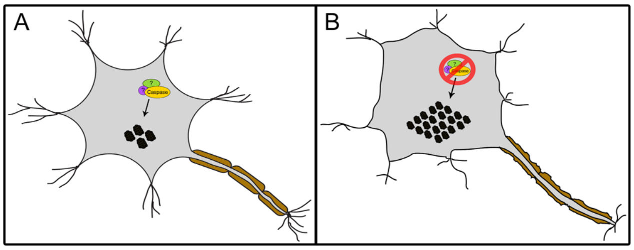

FIGURE 2 | A proposed model of a caspase-dependent mechanism involved in maintaining proteostasis. The interaction of caspases, possibly with yet unidentified additional cofactors, facilitates the regulation of protein aggregates (black circles) within mammalian cells such as neurons **(A)**. The loss of this mechanism leads to increase in aggregate levels resulting in stress **(B)**.

death ensues from excess activation of an otherwise beneficial response.

Interestingly, a recent structural comparison between the *T. brucei* metacaspase, MCA2 and caspase 7 suggests that despite overall structural similarity, metacaspases and caspases differ in their internal design (McLuskey et al., 2012). In addition, both proteases contain specific residues that facilitate substrate binding to the S1 pocket. Albeit these residues are not conserved between the proteases, the authors suggest that proteases within this family may share a common mechanism for substrate recognition. However, the Y31 residue involved in substrate binding and recognition is only conserved in *T. brucei* metacaspases (McLuskey et al., 2012). Thus, future structural analyses of other metacaspases are required to determine whether all metacaspases contain an amino acid residue equivalent to the Y31 residue within their N-terminal region. Of note, caspase 7 lacks an equivalent N-terminal region that is present in MCA2 and thus a comparison to initiator or pro-caspases such as caspases 8 or 10 may be favorable. Nonetheless, the structural similarities exhibited in this study reinforce the functional overlap between metacaspases and caspases in both death and non-death scenarios and further support the argument that both classes of proteases are evolutionarily conserved. Overall, the current evidence presented here suggests that metacaspase proteins act beyond their well described role in apoptosis. The non-death activity of metacaspase proteases reflect an ancient and conserved function that appears to extend to metazoan caspases, and may well represent the evolutionary origin of the death and non-death roles for these same proteins. Future studies to address proteostasis activity in the metazoan caspase family will be a critical step to evaluate and support such a hypothesis.

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REFERENCES

Abdul-Ghani, M., and Megeney, L. A. (2008). Rehabilitation of a contract killer: caspase-3 directs stem cell differentiation. *Cell Stem Cell* 2, 515–516.

Ambit, A., Fasel, N., Coombs, G. H., and Mottram, J. C. (2008). An essential role for the *Leishmania major* metacaspase in cell cycle progression. *Cell Death Differ.* 15, 113–122.

Aravind, L., and Koonin, E. V. (2002). Classification of caspase-hemoglobinase fold: detection of new families and implications for the origin of eukaryotic separins. *Proteins* 46, 355–367.

Black, S., Kadyrov, M., Kaufmann, P., Ugele, B., Emans, N., and Huppertz, B. (2004). Syncytial fusion of human trophoblast depends on caspase 8. *Cell Death Differ.* 11, 90–98.

Colabardini, A. C., De Castro, P. A., De Gouvea, P. F., Savoldi, M., Malavazi, I., Goldman, M. M. S., and Goldman, G. H. (2010). Involvement of the *Aspergillus nidulans* protein kinase C with farnesol tolerance is related to the unfolded protein response. *Mol. Microbiol.* 78, 1259–1279.

D'Amelio, M., Cavallucci, V., and Cecconi, F. (2010). Neuronal caspase-3 signaling: not only cell death. *Cell Death Differ.* 17, 1104–1114.

Fernando, P., Brunette, S., and Megeney, L. A. (2005). Neural stem cell differentiation is dependent upon endogenous caspase-3 activity. *FASEB J.* 19, 1671–1673.

Fernando, P., Kelly, J. F., Balazsi, K., Slack, R. S., and Megeney, L. A. (2002). Caspase 3 activity is required for skeletal muscle differentiation. *Proc. Natl. Acad. Sci. U.S.A.* 99, 11025–11030.

Fernando, P., and Megeney, L. A. (2007). Is caspase-dependent apoptosis only cell differentiation taken to the extreme? *FASEB J.* 21, 8–17.

Fujita, J., Crane, A. M., Souza, M. K., Dejosez, M., Kyba, M., Flavell, R. A., Thomson, J. A., and Zwaka, T. P. (2008). Caspase activity mediates the differentiation of embryonic stem cells. *Cell Stem Cell* 2, 595–601.

Graham, R. K., Ehrnhoefer, D. E., and Hayden, M. R. (2011). Caspase-6 and neurodegeneration. *Trends Neurosci.* 34, 646–656.

Helms, M. J., Ambit, A., Appleton, P., Tetley, L., Coombs, G. H., and Mottram, J. C. (2006). Bloodstream form of *Trypanosoma brucei* depend upon multiple metacaspases associated with RAB11-positive endosomes. *J. Cell Sci.* 119, 1105–1117.

Huesmann, G. R., and Clayton, D. F. (2006). Dynamic role of postsynaptic caspase-3 and BIRC4 in zebra finch song-response habituation. *Neuron* 52, 1061–1072.

Hsu, S. L., Yu, C. T., Yin, S. C., Tang, M. J., Tien, A. C., Wu, Y. M., and Huang, C.-Y. (2006). Caspase 3, periodically expressed and activated at G2/M transition, is required for nocodazole-induced mitotic checkpoint. *Apoptosis* 11, 765–771.

Janzen, V., Fleming, H. E., Riedt, T., Karlsson, G., Riese, M. J., Celso, C. L., Reynolds, G., Milne, C. D., Paige, C. J., Karlsson, S., Woo, M., and Scadden, D. T. (2008). Hematopoietic stem cell responsiveness to exogenous signals is limited by caspase-3. *Cell Stem Cell* 2, 584–594.

Jeffries, T. R., Morgan, G. W., and Field, M. C. (2001). A developmentally regulated Rab11 homologue in *Trypanosoma brucei* is involved in recycling processes. *J. Cell Sci.* 114, 2617–2626.

Johnson, B. S., McCaffery, J. M., Lindquist, S., and Gitler, A. D. (2008). A yeast TDP-43 proteinopathy model: exploring the molecular determinants of TDP-43 aggregation and cellular toxicity. *Proc. Natl. Acad. Sci. U.S.A.* 105, 6439–6444.

Kohl, L., Robinson, D., and Bastin, P. (2003). Novel roles for the flagellum in cell morphogenesis and cytokinesis of trypanosomes. *EMBO J.* 22, 5336–5346.

Laverrière, M., Cazzulo, J. J., and Alvarez, V. E. (2012). Antagonic activities of *Trypanosoma cruzi* metacaspases affect the balance between cell proliferation, death and differentiation. *Cell Death Differ.* 19, 1358–1369.

Lee, R. E. C., Brunette, S., Puente, L. G., and Megeney, L. A. (2010). Metacaspase Yca1 is required for clearance of insoluble protein aggregates. *Proc. Natl. Acad. Sci. U.S.A.* 107, 13348–13353.

Lee, R. E. C., Puente, L. G., Kaern, M., and Megeney, L. A. (2008). A non-death role of the yeast metacaspase: Yca1p alters cell cycle dynamics. *PLoS ONE* 3, e2956. doi: 10.1371/journal.pone.0002956

Li, Z., Jo, J., Jia, J. M., Lo, S. C., Whitcomb, D. J., Jiao, S., Cho, K., and Sheng, M. (2010). Caspase-3 activation via mitochondria is required for long-term depression and AMPA receptor internalization. *Cell* 141, 859–871.

Lim, H.-W., Kim, S.-J., Park, E.-H., and Lim, C.-J. (2007). Overexpression of a metacaspase gene stimulates cell growth and stress response in *Schizosaccharomyces cerevisiae*. *Can. J. Microbiol.* 53,1016–1023.

Madeo, F., Carmona-Gutierrez, D., Ring, J., Buttner, S., Eisenberg, T., and Kroemer, G. (2009). Caspase-dependent and caspase-independent cell death pathways in yeast. *Biochem. Biophys. Res. Commun.* 382, 227–231.

McLuskey, K., Rudolf, J., Proto, W. R., Isaacs, N. W., Coombs, G. H., Moss, C. X., and Mottram, J. C. (2012). Crystal structure of a *Trypanosoma brucei* metacaspase. *Proc. Natl. Acad. Sci. U.S.A.* 109, 7469–7474.

Mottram, J. C., Helms, M. J., Coombs, G. H., and Sajid, M. (2003). Clan CD cysteine peptidases of parasitic protozoa. *Trends Parasitol.* 19, 182–187.

Neumann, M., Sampathu, D. M., Kwong, L. K., Truax, A. C., Micsenyi, M. C., Chou, T. T., Bruce, J., Schuck, T., Grossman, M., Clark, C. M., McCluskey, L. F., Miller, B. L., Masliah, E., MacKenzie, I. R., Feldman, H., Feiden, W., Kretzschmar, H. A., Trojanowski, J. Q., and Lee, V. M-Y. (2006). Ubiquitinated TDP-43 in frontotemporal lobar degeneration and amyotrophic lateral sclerosis. *Science* 314, 130–133.

Parsell, D. A., Kowal, A. S., Singer, M. A., and Lindquist, S. (1994). Protein disaggregation mediated by heat-shock protein Hsp104. *Nature* 372, 475–478.

Richie, D. L., Miley, M. D., Bhabhra, R., Robson, R. D., Rhodes, J. C., and Askew, D. S. (2007). The *Aspergillus fumigatus* metacaspases CasA and CasB facilitate growth under conditions of endoplasmic reticulum stress. *Mol. Microbiol.* 63, 591–604.

Rohn, T. T. (2010). The role of caspases in Alzheimer's disease; potential novel therapeutic opportunities. *Apoptosis* 15, 1403–1409.

Rothstein, J. D. (2009). Current hypotheses for the underlying biology of amyotrophic lateral sclerosis. *Ann. Neurol.* 65(Suppl. 1), S3–S9.

Suzuki, H., Lee, K., and Matsuoka, M. (2011). TDP-43-induced death is associated with altered regulation of BIM and Bcl-xL and attenuated by caspase-mediated TDP-43 cleavage. *J. Biol. Chem.* 286, 13171–13183.

Tsiatsiani, L., Van Breusegem, F., Gallois, P., Zavialov, A., Lam, E., and Bozhkov, P. V. (2011). Metacaspases. *Cell Death Differ.* 18, 1279–1288.

Uren, A. G., O'Rourke, K., Aravind, L., Teresa Pisabarro, M., Seshagiri, S., Koonin, E. V., and Dixit, V. M. (2000). Identification of paracaspases and metacaspases: two ancient families of caspase-like proteins, one of which plays a key role in MALT lymphoma. *Mol. Cell* 6, 961–967.

Weber, G. F., and Menko, A. S. (2005). The canonical intrinsic mitochondrial death pathway has a non-apoptotic role in signaling lens cell differentiation. *J. Biol. Chem.* 280, 22135–22145.

Wu, J., and Kaufman, R. J. (2006). From acute ER stress to physiological roles of the unfolded protein response. *Cell Death Differ.* 13, 374–384.

Zhang, Y. J., Xu, Y. F., Cook, C., Gendron, T. F., Roettges, P., Link, C. D., Lin, W. L., Tong, J., Castanedes-Casey, M., Ash, P., Gass, J., Rangachari, V., Buratti, E., Baralle, F., Golde, T. E., Dickson, D. W., and Petrucelli, L. (2009). Aberrant cleavage of TDP-43 enhances aggregation and cellular toxicity. *Proc. Natl. Acad. Sci. U.S.A.* 106, 7607–7612.

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Appendix III

Manuscript:

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The role of Yca1 in proteostasis. Yca1 regulates the composition of the insoluble proteome☆

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Proteostasis, the process of balancing protein production with protein degradation is vital to normal cell function. Defects within the mechanisms that control proteostasis lead to increased content of a specialized insoluble protein fraction that forms dense aggregates within the cell. We have previously implicated the *Saccharomyces cerevisiae* metacaspase Yca1 as an active participant in maintaining proteostasis, whereby Yca1 acts to limit aggregate content. Here, we further characterized the proteostasis role of Yca1 by conducting proteomic analysis of the insoluble protein fraction in wildtype and Yca1 knockout cells, under normal and heat stressed conditions. Our findings suggest that the composition of insoluble protein fraction is non-specific and comprises a wide array of protein species rather than a limited repertoire of aggregate susceptible proteins or peptides. Interestingly, the loss of Yca1 led to a significant decrease of proteins that control ribosome biogenesis and protein synthesis within the insoluble fraction, indicating that the cell may invoke a compensatory mechanism to limit protein production during stress, a feature dependent on Yca1 activity. Finally, we noted that protein degradation factors such as Cdc48 co-localize with Yca1 to the insoluble fraction, supporting the hypothesis that Yca1 may act primarily to dissolve or reduce accumulated aggregates.
This article is part of a Special Issue entitled: From protein structures to clinical applications.

1. Introduction

The regulation of protein content and solubility is an indispensible feature which ensures the fidelity of key fundamental processes within the cell. Within this context the endoplasmic reticulum (ER) provides the first oversight step to ensure appropriate protein behavior, a unique environment which is optimized for post-translational modifications and proper folding of newly synthesized peptides. Disturbances within the cell such as flaws during protein biogenesis, environmental stresses and age related decline disrupt the fidelity provided by the quality control mechanisms, allowing for misfolded and/or damaged proteins to aggregate [1]. Accordingly, this accumulation of protein aggregates has been associated with the progression and/or initiation of various neurodegenerative diseases such as Alzheimer's, Huntington's, Parkinson's, amyotrophic lateral sclerosis (ALS) as well as various inclusion body myopathies [2,3].

Currently, it is well agreed upon that the extent of β-sheet organization determines the structure of aggregates, which can either be amorphous or amyloid in nature [4,5]. Indeed, examinations of the morphology of protein aggregates suggest that these structures are in fact ordered and arise from specific interactions between misfolded protein intermediates [6]. Specifically, stretches of hydrophobic residues that are exposed in conformers, may act as the seed to promote peptide/protein

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aggregation [7,8]. However, aggregation prone protein species can also prompt numerous other protein species to aggregate or confine them within the aggregate structures, suggesting that aggregation is a proteome wide phenomenon [9–11]. In addition to aggregate composition, there is considerable debate regarding the cellular role of aggregates. The standard hypothesis suggests that aggregate buildup is detrimental and a significant contributor to cellular dysfunction. In support of this supposition, disease causing proteins (in a wide variety of neurodegenerative diseases) are generally identified within aggregate material [12–14]. However, the alternative model suggests that the cell sequesters non-functional proteins as a defense mechanism, limiting exposure of the cell to an otherwise toxic structure [15].

The study of protein aggregation control has benefited from the use of tractable model systems. In *Saccharomyces cerevisiae*, aggregates are known to be sequestered and deposited in various regions and can either undergo re-solubilization by the Hsp40/Hsp70 bi-chaperone system and the AAA+ activity of Hsp104 or are targeted for degradation by one of two ways; proteosomal degradation or via autophagy [16–18]. Furthermore, during conditions of stress such as heat shock treatment, the bi-chaperone system has been shown to be more important for “thermotolerance” and re-solubilization rather than targeting the aggregated proteins for degradation [1,19]. Recent evidence suggests that proteases, such as the metacaspase Yca1, also play a key role in non-death processes such as regulation of cell cycle progression and maintaining proteostasis [20,21]. Specifically, Yca1 has been shown to condense into distinct discernible foci which coincided with Hsp104 foci formation. Furthermore, Yca1 strongly associated with components of the bi-chaperone system, namely Ssa1/2 (Hsp70) and Ydj1, as well as the small heat shock protein Hsp42 and the AAA+ ATPase, Cdc48 [21]. Strikingly, the loss of Yca1 expression or loss of Yca1 catalytic activity resulted in an increase in insoluble protein content. Taken together these observations suggest that Yca1 protease activity is an indispensible component of the aggregate control machinery.

Here, we utilized the study of Yca1 function to further delineate the mechanisms that control aggregate formation and dissolution. In wildtype yeast, we noted that the insoluble proteome was comprised of a large number of protein species rather than a limited protein cohort. The loss of Yca1 led to a significant decrease in ribosomal proteins and translational control factors within the insoluble fraction, suggesting that control over general protein production in response to aggregate accumulation is disrupted with the removal of Yca1. In addition, we noted that recruitment of the AAA+ ATPase Cdc48 to the insoluble protein fraction was strongly dependent on Yca1 expression, whereas other recruitment of other components of the chaperone system remained unaffected within the insoluble protein fraction. We interpret this observation to suggest that Yca1 protease activity is targeted to dismantle protein aggregates rather than limit aggregate formation per se.

2. Materials and methods

2.1. *Yeast strains and growth conditions*

The wildtype BY4741 and Δ*yca1* strains of *S. cerevisiae* (Open Biosystems) were grown in acidified YPD media (1% yeast extract, 2% peptone and 2% glucose, pH 3.5). 5 ml starter cultures of YPD were inoculated with a single colony and grown overnight. Larger YPD cultures were then inoculated from the starter cultures and grown to mid-logarithmic phase (OD_{600} 0.5–0.6) at 30 °C with orbital rotation. Cells were then collected via centrifugation at 2800 rpm for 5 min, washed with water and re-collected then stored at −80 °C for later processing. For heat shock treatment, mid-logarithmic cultures were further incubated at 42 °C for 1 h before collection.

2.2. *Protein extraction*

Frozen cell pellets were suspended in modified RIPA buffer (50 mM Tris–HCl, 1 mM EDTA, 1% glycerol, 1% NP-40, pH 7.4) containing protease inhibitors (Calciobiochem, Darmstadt, Germany) and added to tubes containing 0.7 g of glass beads (Sigma-Aldrich, Ontario, Canada). Cells were lysed using the Disruptor Genie (Scientific Industries, New York, USA) at 4 °C with alternating 1 min cycles of breaking and 1 min on ice for a total of 12 min. The cell lysate was further cleared by centrifugation at 2000 rpm for 1 min followed by 3000 rpm for another minute. The final protein lysate was aliquoted and stored at −80 °C.

2.3. *Sample preparation*

The total protein extracts were fractioned into soluble and insoluble via centrifugation as described in [22]. Equal amounts of total protein extract were subjected to centrifugation at 15,000 g for 15 min. For the 2D LC–MS analysis the supernatant (soluble fraction) was discarded and the resulting protein pellet (insoluble fraction) was further washed in modified RIPA buffer and re-collected via centrifugation. The modified RIPA buffer was discarded and the final pellet containing the insoluble protein fraction was solubilized in buffer consisting of 8 M urea, 2% dithiothreitol and 50 mM Tris–HCl pH 8.

2.4. *SDS-PAGE and silver staining*

The total protein extract was fractioned into soluble and insoluble as described above. The insoluble protein pellet was dissolved in modified RIPA buffer via vortex and loaded onto a 10% acrylamide gel containing SDS (0.1% w/v) with equal volume of sample buffer. The electrophoretic separation of the insoluble protein fraction was conducted at 100 V for 10–14 h. The corresponding soluble fraction was also separated similarly on separate gels. After separation, the proteins were either stained using the silver stain method described in [23] or transferred onto a membrane for western hybridization [21].

2.5. *Western hybridization*

Proteins fractioned via SDS-PAGE were transferred to 0.45 μM PVDF membrane (Millipore) on a TRANS-BLOT SD apparatus (Bio-Rad). Membranes were blocked with TBST containing 5% skim milk for minimum of 1 h after which they were supplemented with primary antibody and further incubated at 4 º C overnight. Bands were detected using primary antibodies specific for Cdc48 (Thomas Sommer, Max Delbruck Institute, Germany) as well as for Ydj1 and Ssa2 (Abcam) and β-tubulin. Densitometry analysis of the resulting bands was conducted using ImageJ software.

2.6. Protein digest

Proteins were reduced by addition of dithiothreitol and alkylated by the addition of iodoacetamide before dilution of the sample in 100 mM ammonium bicarbonate to reduce the concentration of urea to < 2 M. Proteins were digested using trypsin (Promega). The resulting peptides were purified by ZipTip (Milllipore), concentrated by Vacufuge (Eppendorf), and resuspended in 0.1% trifluoroacetic acid.

2.7. 2D-LC–MS/MS

Mass spectral analysis was performed at the OHRI Proteomics Core Facility (Ottawa, Canada). Peptides were analyzed by 2D-LC–MS/MS on an LTQ Orbitrap XL hybrid mass spectrometer with nanospray source (Thermo Scientific, USA) and an UltiMate 3000 RSLC nano HPLC (Dionex). Peptides were loaded onto a POROS 10S (Dionex) and eluted using ammonium acetate salt steps (0 mM, 10 mM, 20 mM, 50 mM, 100 mM, 500 mM) onto a PepMap C18 trap column (Dionex) for 5 min at 15 μl per minute, then eluted over a 60 min gradient of 3%–45% acetonitrile with 0.1% formic acid at 0.3 μl per minute onto a 10-cm analytical column (New Objective Picofrit self-packed with Agilent Zorbax C18), and nanosprayed into the mass spectrometer. MS scans were acquired in the Orbitrap module and MS^2 scans were acquired in the ion trap module using data-dependent acquisition of the top 5 ions from each MS scan. Total data acquisition time = 9 h. Between samples, the system was washed three times with 1 M ammonium acetate salt injection on the SCX column and a 60 min acetonitrile gradient over the C18 columns.

2.8. Protein identification using MASCOT

MASCOT 2.3.01 software (Matrix Science) was used to infer peptide and protein identities from the mass spectra. The observed MS/MS spectra were matched against *S. cerevisiae* (6973 sequences) from the SwissProt database (version 57.15) and also against 248 sequences from a Contaminants database (downloaded from maxquant.org, June 9th 2011). Mass tolerance parameters were MS tolerance of ±5 ppm and MS/MS tolerance of 0.6 Da. Enzyme specificity was set to 'Trypsin/P'. Oxidation of methionine, carbamidomethylation of cysteine, protein N-terminal acetylation, deamidation, and/or conversion of Glu or Gln to Pyro-Glu were allowed as variable modifications. The emPAI scores reported by Mascot were used as estimates of protein abundance. Mascot's Decoy Search function was used to calculate False Discovery Rate (FDR).

2.9. Bioinformatics

Data was summarized and basic comparisons performed using the Excel spreadsheet program (Microsoft). GO terms annotation was performed using the Functional Annotation Chart tool of the web service DAVID (*Nature Protocols 2009; 4(1)*:44 & *Genome Biology 2003; 4(5)*:P3). Relative enrichment of GO terms was determined using the web service FunSpec (http://funspec.med.utoronto.ca/).

3. Results

3.1. Composition of the insoluble protein fraction

Here, we used a proteomic approach to examine the composition of the insoluble protein fraction as a surrogate to model/understand protein aggregate formation in yeast. The metacaspase Yca1 has been implicated in regulating levels of protein aggregates and hence we further validated this hypothesis by comparing the composition of the insoluble protein fraction of the wildtype BY4741 (WT) to the Δ*yca1* (KO) strain under normal and heat stressed conditions by using a two dimensional liquid chromatography–tandem mass spectrometry (2D LC–MS) approach which also provides the relative protein abundance. In this study we altered our approach for obtaining the insoluble fraction than reported previously in [20]. Initial experimentation of the insoluble fraction after conducting the NP-40 detergent washes resulted in low yield with regards to protein identification in comparison to what was observed from a silver stained acrylamide gel of the same fraction (Fig. 1). We postulated that the presence of NP-40 as well as glycerol in the

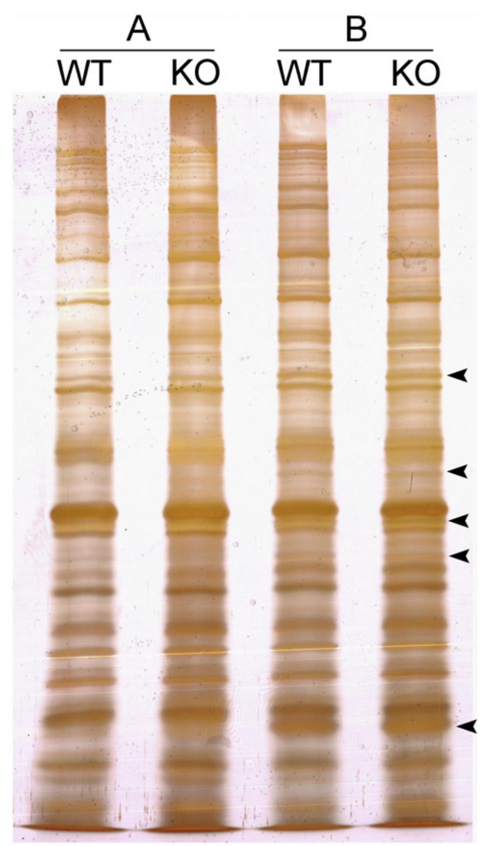

Fig. 1 – Insoluble protein composition differs with induction of heat stress. Silver stained gel depicting the protein profile within the wildtype and knockout strains during normal growth (A) and with heat stress treatment (B). Arrows indicate the differences in the electrophoretic profile during heat stress in comparison to normal growth.

suspension buffer may be interfering with the 2D LC–MS and hence opted to use an alternate buffer that was known to be compatible with this form of online MS analysis (see Materials and methods). Importantly, similar results using this NP-40 buffer for insoluble protein isolation have been reported by other groups for LC–MS analysis [24]. Therefore, we reverted to the original method as described in [22] where the insoluble fraction was simply obtained by high speed centrifugation. Here, we included an additional wash step with the same buffer used for lysis and suspension and eliminated the NP-40 rich detergent washes to minimize interference during the LC–MS analysis. Furthermore, this method yielded the insoluble fraction in its entirety without any exclusion that may have resulted from repeated detergent washes and have not been accounted for previously.

Within the total 2120 proteins that were observed by the MASCOT search engine, a proportion of these proteins were exclusive to either condition. In the first data set we detected 678 proteins in normal growth conditions and 1178 proteins in heat stress conditions for the wildtpe BY4741 strain. For the Yca1 knockout strain we detected 880 proteins in normal growth conditions and 1180 proteins during heat stress. In the second data set we detected 573 proteins in normal growth conditions and 876 proteins during heat stress for the BY4741 strain and 1181 proteins in normal conditions and 1015 proteins during heat stress for the knockout mutant (Table S1). This increase in proteins levels is similar to what we have previously observed [21]. Furthermore, functional clustering using the DAVID software resulted in the identification of 592 categories for proteins within the insoluble fraction for the wildtype while the Yca1 knockout showed 518 categories (Table S2). Additionally, we also included the insoluble protein fraction of the catalytically inactive mutant of Yca1, C297A, in our 2D LC–MS analysis and the corresponding data is also included in Table S1. However, we chose to primarily focus on the data generated from the wildtype and knockout strains for this study.

3.2. *Enrichment analysis of proteins interacting with Yca1*

Prior observations by our group suggest that Yca1 can interact with Cdc48 and proteins of the Hsp40 and Hsp70 family [21]. Furthermore, these Yca1-interacting proteins are also active members of protein re-solubilization/degradation machinery, acting to limit the occurrence of misfolded proteins [1]. However, what remains unknown is whether these proteins control aggregate deposition by remaining within the soluble or insoluble fraction. For example, one may predict a number of scenarios whereby the aggregate control machinery resides within the soluble fraction of the proteome to limit aggregate deposition. Alternatively, such Yca1 interacting proteins may reside largely within the insoluble fraction to dissolve aggregate composition. To address these alternate functional scenarios, we examined the relative abundance of these proteins during normal conditions and assessed enrichment following the induction of heat stress. As shown in Fig. 2A, the induction of heat stress led to a dramatic 9 fold increase in levels of Cdc48 in the wildtype while the loss of Yca1 only showed a modest 3 fold increase. Surprisingly, we did not observe any significant increase in the levels of Ydj1, Ssa1 and Ssa2, which are active components of the re-solubilization machinery as well as for Ded1. We further verified the LC–MS data by western hybridization (Fig. 2B) and assessed the change in levels of Cdc48, Ydj1 and Ssa2 following heat stress by densitometry (Fig. 2C). We observed that Cdc48 levels were reduced in the insoluble fraction of the knockout strain compared to the wildtype while Ydj1 and Ssa2 levels were similar in both strains, which are in agreement with the data generated from LC–MS. We also examined the changes in the level of these proteins upon heat stress within the soluble fraction. In both the wildtype and Yca1 knockout strains, Ydj1 and Ssa2 levels were observed to be similar between the soluble and insoluble fractions. Interestingly, in the Yca1 knockout strain, the reduced level of Cdc48 observed in the insoluble fraction was accompanied by an increased localization of Cdc48 within the soluble fraction in comparison to the wildtype. Thus, Cdc48 enrichment within the insoluble fraction is dependent on the presence of Yca1.

3.3. *Loss of Yca1 influences ribosomal protein function in the insoluble fraction during stress*

We have previously observed that the electrophoretic profile of the insoluble protein fraction is variable and not specific to a single or a few protein species [21]. To further validate this observation we used the DAVID software to retrieve the Gene Ontology (GO) terms associated with the proteins that were observed to be enriched as a result of heat shock in both Yca1 backgrounds. We noted that the GO term ranking for processes relating to protein synthesis/translational machinery showed a large decrease in the knockout strain (Table 1). Thus, we furthered our analysis on four of the affected GO terms; "GO:0030686~90S preribosome", "GO:0043039~tRNA aminoacylation", "GO:0043038~amino acid activation" and "SP-PIR Ribosome biogenesis". We generated a non-overlapping list of 73 proteins associated with these GO terms that are affected by the induction of heat stress (Table S3). To identify proteins that showed a fold increase in the wildtype, suggesting a requirement for Yca1, we chose to highlight three proteins of significant interest ERB1, NOP12 and YHR020W (Fig. 3). ERB1 is a constituent of the 66S pre-ribosomal complex required for the maturation of the 5.8S and 25S rRNAs [25]. NOP12 is a nucleolar protein involved in the large subunit biogenesis and 25 s rRNA maturation [26]. YHR020W is an uncharacterized essential protein in yeast which shares similarity with proline-tRNA ligase and is postulated to interact with ribosomes [27,28]. All three proteins were considerably enriched during heat stress in the wildtype amounting to larger than threefold, whereas within the knockout strains their levels either remained the same or were reduced.

3.4. *Prion protein levels are unaffected in Δyca1 cells*

Interestingly in yeast, aggregates of prionogenic proteins, such as [PSI$^+$], are known to be cytoplasmically inherited by daughter cells which ensure the transfer of epigenetic traits [29]. To assess for a role of Yca1 in regulating levels of such misfolded proteins we searched our protein list for known prions that may be present in the insoluble protein fraction. Our data generated from the 2D LC–MS analysis included the [NU+] prion protein form of NEW1 and the prion form of RNQ1

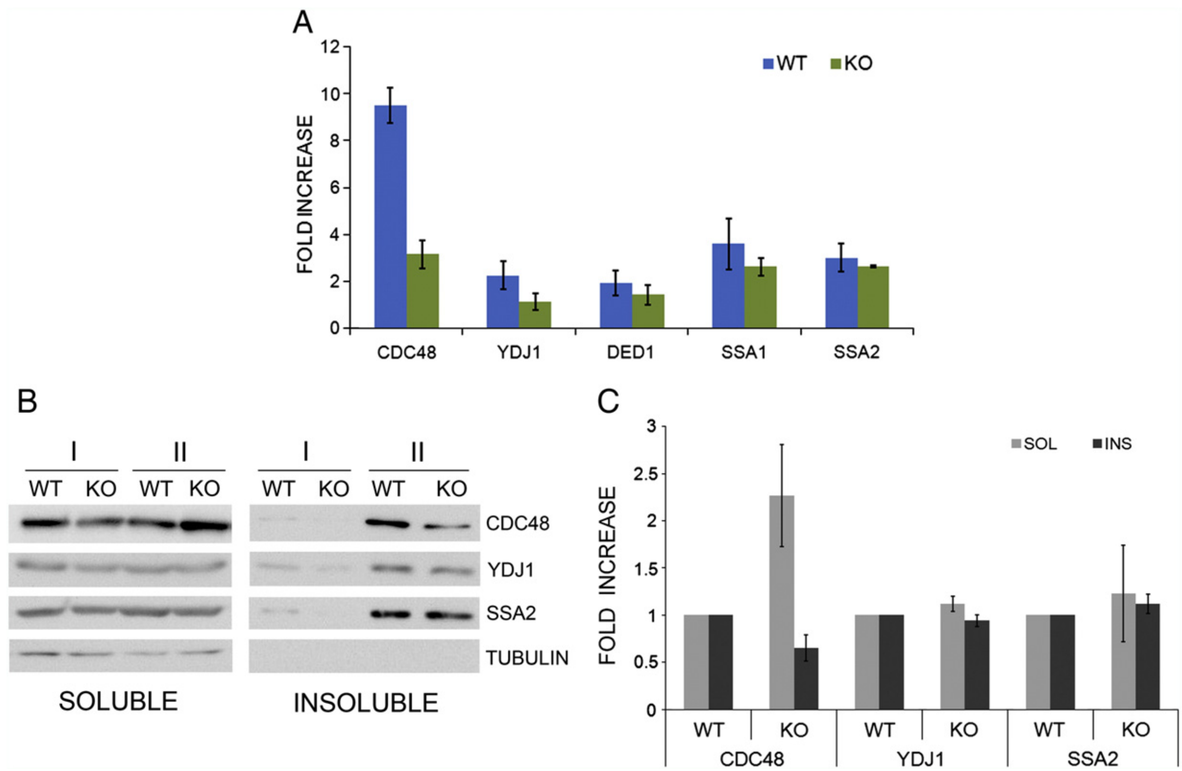

Fig. 2 – Cdc48 recruitment to the insoluble protein fraction is Yca1-dependent. (A) A graphical representation of the average fold increase observed for each of the Yca1-interacting protein upon the induction of heat stress in the two strains obtained from the 2D LC–MS analysis (n = 2; ± SEM). (B) Western blot showing the levels of Cdc48, Ydj1 and Ssa2 within the soluble and insoluble fractions during normal (I) and heat stress (II) and the respective enrichment determined by densitometry analysis, normalized to the wildtype (C, n = 3; ± SEM; SOL — soluble, INS — insoluble). β-tubulin levels in the respective soluble fraction served as a loading control.

protein [PIN+]. We analyzed the relative abundance using emPAI scores of [NU+] which is depicted in Fig. 4. Under normal growth circumstances, [NU+] levels were more abundant in the knockout strain. Consequently, the induction of heat stress led to a reduction in [NU+] levels.

4. Discussion

In this study we identified the constituents of the insoluble protein fraction in wildtype and Yca1 null backgrounds during normal growth and heat stress. Surprisingly, the 2D LC–MS analysis led to the identification of over 2000 proteins within the insoluble fraction. Although these proteins are not exclusive components protein aggregates, this dataset suggests that the physical prelude to aggregate formation i.e. deposition to an insoluble protein compartment, is far more complex than has been previously suggested. A cohort of these proteins within our dataset could result from being confined within larger structures in the cell that resist solubilization but do not represent true insoluble protein species, a feature that has been reported previously [11]. Nonetheless, our approach implicates a wide array of proteins that may be targeted for aggregation, under normal conditions and stress. As such the dataset generated from this study will serve as a useful tool for subsequent investigations in this field.

Table 1 – GO term ranking for ribosomal and protein synthesis related processes in wildtype and Yca1 knockout strains under heat stress.

Category	Term	Rank in WT	Rank in KO
GOTERM_CC_FAT	GO-0030686_90S preribosome	140	498
GOTERM_BP_FAT	GO-0043039_tRNA aminoacylation	91	325
GOTERM_BP_FAT	GO-0043038_amino acid activation	92	326
SP_PIR_KEYWORDS	Ribosome biogenesis	62	264

To further validate the role of Yca1 in regulating cellular aggregate levels, we assessed the expression of Yca1-interacting that had been previously and independently confirmed as components of protein aggregate remodeling platforms. The reduced levels of Cdc48 in the insoluble fraction and the concomitant retention within the soluble fraction of the Yca1 null strain during stressed conditions suggests a dependency on Yca1 to relocate Cdc48 to the insoluble protein fraction. Cdc48 is an AAA+ ATPase and has been well characterized in its role in ERAD factories as well as in the formation and clearing protein aggregates [30,31]. Therefore, it may be reasonable to conjecture that the presence of Cdc48 in the insoluble fraction may be to perform a similar role, i.e. re-solubilization or targeting aggregates for degradation. Interestingly, the other chaperone proteins known to interact with Yca1 did not display a similar

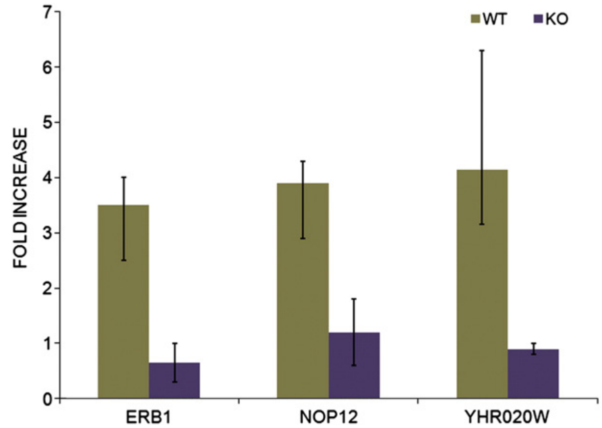

Fig. 3 – Heat stress induces enrichment of proteins of the translational machinery. A diagrammatic depiction of the fold increase in ribosomal processes related proteins during heat stress induction in the wildtype and knockout strains (n = 2; ± SEM).

co-localization to the insoluble fraction. This observation may indicate that the Yca1 and Hsp40/70 interactions are transient and do not persist within the insoluble compartment.

Additionally, the reduction in [NU+] levels suggest that during stress conditions in Yca1 null cells as well as wildtype cells may reflect a disparity between prion biology and proteostasis. Furthermore, of the numerous prions known in yeast [32], we were only able to detect two in our analyses, which does not present us with sufficient data to further investigate our speculation.

Our observation regarding alterations in ribosomal function as a result of heat stress induction was unexpected. Our analyses suggest that the ribosomal proteins listed in Table S2 are indeed affected by the stressed condition leading to their localization within the insoluble protein fraction and a proportion of these proteins may depend on Yca1 for this to occur. Previous reports in yeast suggest that cells favor re-solubilization over degradation of aggregates [1,19] Thus, it is tempting to speculate that Yca1 function may also have implications on ribosome biogenesis and protein synthesis.

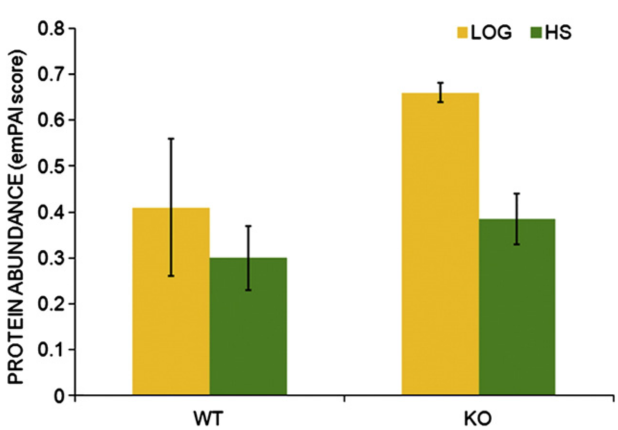

Fig. 4 – [NU+] prion protein level is Yca1 independent. The relative abundance of the [NU+] protein as represented by the emPAI score in each strain is depicted above for the two conditions (n = 2; ± SEM).

5. Conclusions

To further characterize the role of Yca1 in proteostasis we conducted a 2D LC–MS analysis of the insoluble protein fraction in wildtype and Yca1 knockout cells. The resulting analysis determined that the composition of the insoluble protein fraction was non-specific and comprised a wide array of proteins. Furthermore, Cdc48 levels within this fraction are dependent on the presence of Yca1. Despite previous reports our observations do not support the hypothesis that Yca1 has a role in prion biology. However, our results suggest that loss of Yca1 affects ribosomal protein function.

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.jprot.2013.01.014.

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REFERENCES

[1] Tyedmers J, Mogk A, Bukau B. Cellular strategies for controlling protein aggregation. Nat Rev Mol Cell Biol 2010;11:777–88.

[2] Douglas PM, Cyr DM. Interplay between protein homeostasis networks in protein aggregation and proteotoxicity. Biopolymers 2009;93:229–36.

[3] Shrestha A, Megeney LA. The non-death role of metacaspase proteases. Front Oncol 2012;2, http://dx.doi.org/10.3389/fonc2012.00078.

[4] Dobson CM. Protein folding and misfolding. Nature 2003;426: 884–90.

[5] Kopito RR. Aggresomes, inclusion bodies and protein aggregation. Trends Cell Biol 2000;10:524–30.

[6] Speed MA, Wang DIC, King J. Specific aggregation of partially folded polypeptide chains: the molecular basis of inclusion body composition. Nat Biotechnol 1996;14:1283–7.

[7] Rajan RS, Illing ME, Bence NF, Kopito RR. Specificity in intracellular protein aggregation and inclusion body formation. Proc Natl Acad Sci U S A 2001;98:13060–5.

[8] Gidalevitz T, Ben-Zvi A, Ho KH, Brignull HR, Morimoto RI. Progressive disruption of cellular protein folding in models of polyglutamine diseases. Science 2006;311:1471–4.

[9] Ben-Zvi AP, Goloubinoff P. Proteinaceous infectious behavior in non-pathogenic proteins is controlled by molecular chaperones. J Biol Chem 2002;277:49422–7.

[10] Chai Y, Shao J, Miller VM, Williams A, Paulson HL. Live-cell imaging reveals divergent intracellular dynamics of polyglutamine disease proteins and supports a sequestration model of pathogenesis. Proc Natl Acad Sci U S A 2002;99: 9310–5.

[11] Bates GP. One misfolded protein allows others to sneak by. Science 2006;311:1385–6.

[12] Mackenzie IRA, Rademakers R, Neumann M. TDP-43 and FUS in amyotrophic lateral sclerosis and frontotemporal dementia. Neurology 2010;9:995–1007.

[13] Neumann M, Sampathu DM, Kwong LK, Truax AC, Micsenyi MC, Chou TT, et al. Ubiquitinated TDP-43 in frontotemporal lobar degeneration and amyotrophic lateral sclerosis. Science 2006;314:130–3.
[14] Ross CA, Poirier MA. Protein aggregation and neurodegenerative disease. Nat Med 2004;10:S10–7.
[15] Lansbury PT, Lashuel HA. A century old debate on protein aggregation and neurodegeneration enters the clinic. Nature 2006;443:774–9.
[16] Glover JR, Lindquist S. Hsp104, Hsp70, and Hsp40: a novel chaperone system that rescues previously aggregated proteins. Cell 1998;94:73–82.
[17] Kaganovich D, Kopito R, Frydman J. Misfolded proteins partition between two distinct quality control compartments. Nature 2008;454:1088–95.
[18] Parsell DA, Kowal AS, Singer MA, Lindquist S. Protein disaggregation mediated by heat-shock protein Hsp104. Nature 1994;372:475–8.
[19] Sanchez Y, Lindquist SL. Hsp104 required for induced thermotolerance. Science 1990;248:1112–5.
[20] Lee REC, Puente LG, Kaern M, Megeney LA. A non-death role of the yeast metacaspase:Yca1p alters cell cycle dynamics. PLoS One 2008;3:e2956, http://dx.doi.org/10.1371/journal.pone.000.2956.
[21] Lee REC, Brunette S, Puente LG, Megeney LA. Metacaspase Yca1 is required for clearance of insoluble protein aggregates. Proc Natl Acad Sci U S A 2010;107:13348–53.
[22] Cashikar AG, Duendald M, Lindquist SL. A chaperone pathway in protein disaggregation. Hsp26 alters the nature of protein aggregates to facilitate reactivation by Hsp104. J Biol Chem 2005;280:23869–75.
[23] Shevchenko A, Wilm M, Vorm O, Mann M. Mass spectrometric sequencing of proteins silver-stained polyacrylamide gels. Anal Chem 1996;68:850–8.
[24] Yeung YG, Nieves E, Angeletti R, Stanley ER. Removal of detergents from protein digests for mass spectrometry analysis. Anal Biochem 2008;382:135–7.
[25] Pestov DG, Stockelman MG, Strezoska Z, Lau LF. ERB1, the yeast homolog of mammalian Bop1, is an essential gene required for maturation of the 25S and 5.8S ribosomal RNAs. Nucleic Acids Res 2001;29:3621–30.
[26] Wu K, Wu P, Aris JP. Nucleolar protein Nop12p participates in synthesis of 25S rRNA in *Saccharomyces cerevisiae*. Nucleic Acids Res 2001;29:2938–49.
[27] Tatusov RL, Galperin MY, Natale DA, Koonin EV. The COG database: a tool for genome-scale analysis of protein functions and evolution. Nucleic Acids Res 2000;28:33–6.
[28] Fleischer TC, Weaver CM, McAfee KJ, Jennings JL, Link AJ. Systematic identification and functional screens of uncharacterized proteins associated with eukaryotic ribosomal complexes. Genes Dev 2006;20:1294–307.
[29] Serio TR, Lindquist SL. Protein-only inheritance in yeast: something to [PSI+]-ched about. Trends Cell Biol 2000;10: 98–105.
[30] Jentsch S, Rumpf S. Cdc48 (p97): a 'molecular gearbox' in the ubiquitin pathway? Trends Biochem Sci 2006;32:6–11.
[31] Kobayashi T, Manno A, Kakizuka K. Involvement of valosin-containing protein (VCP)/p97 in the formation and clearance of abnormal protein aggregates. Genes Cells 2007;12:889–901.
[32] Halfmann R, Alberti S, Lindquist S. Prions, protein homeostasis, and phenotypic diversity. Trends Cell Biol 2010;20:125–33.

Appendix IV

Manuscript:

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Chapter 14

Monitoring the Proteostasis Function of the *Saccharomyces cerevisiae* Metacaspase Yca1

Amit Shrestha, Robin E.C. Lee, and Lynn A. Megeney

Abstract

The functional versatility of metacaspase proteases has been established by reports of their involvement in non-apoptotic cellular processes, in addition to their canonical role in apoptosis/programmed cell death. While the budding yeast metacaspase Yca1 has been well characterized for its role in cell death regulation, more recent examinations suggest that the protease may be involved in key processes that increase survival and fitness. More specifically, examinations suggest that Yca1 is central to maintaining cellular proteostasis as it interacts with major components involved in protein biosynthesis and functions to limit aggregate deposition. Here, we describe the methods utilized to analyze the role Yca1 in proteostasis.

Key words Aggregates, Filtration, Heat stress, Immunoprecipitation, Metacaspase, Proteostasis, Protocols, Vacuole morphology

1 Introduction

Caspase enzymes, and related proteases, are broadly conserved across the phyla of extant organisms. Structural investigations have revealed that proteases within the clan CD family C14 share similar quaternary architecture and an invariant cysteine–histidine catalytic dyad [1, 2]. In fungi, plants, and protozoa, such proteases are termed metacaspases [3]. Metacaspases can be further subdivided based on the presence or absence of a proline-rich N-terminal prodomain, referred to as "type I" and "type II" classes respectively. When compared across organisms, the number and type of metacaspases expressed is highly variable [4]. To date, only a single type I metacaspase has been identified in *Saccharomyces cerevisiae* [5]. This protease, termed Yca1 (also referred to as Mca1), harbors a unique poly Q/N motif in its prodomain, upstream of its caspase-like domain. The functional importance of this motif remains largely unknown; however, it is suggested from metazoan initiator caspases that the motifs within the prodomains of type I metacaspases

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facilitate protein–protein interactions and contribute to the regulation of proteolytic activity [6, 7].

Metacaspase function in *S. cerevisiae* has been extensively explored within a death-centric perspective, owing to the preexisting view of caspase proteases as de facto mediators of programmed cell death. Under such circumstances, various studies have shown Yca1 involvement as an essential feature that progresses the apoptotic phenotype induced by various insults [4, 8]. However, observations of cell-death events independent of Yca1, such as the inability of the proapoptotic hBax protein to engage Yca1 and accelerate toxicity in yeast [9], argue against a death-only function for Yca1. Importantly, the evolutionary retention of death-specific machinery in single celled organisms, such as *S. cerevisiae*, supports the premise that this protease may have evolved or coevolved non-death functions [10].

Investigation of metacaspase biology in *S. cerevisiae* has since elucidated "non-death" functions for Yca1, which may be shared by other counterparts in trypanosoma and other yeast species [11]. Initially, a loss of function model demonstrated that Yca1 coordinated processes that affect cell cycle timing and cellular fitness; *Δyca1* cells displayed a delay in the G1/S transition and disruption of microtubule assembly, via nocodazole exposure, did not halt progression of *Δyca1* cells through the G2/M checkpoint [7]. Subsequently, attempts to identify a molecular role for Yca1 under these pro-survival parameters suggested that the protease functions to ensure fidelity of protein turnover. Immunoprecipitation [12] using the tandem affinity purification (TAP) method led to identification of Cdc48, Hsp40, and Hsp70 as high-affinity interaction partners with Yca1 [13]. These Yca1-interacting proteins are central contributors to cellular proteostasis; Cdc48 is involved in ER-associated degradation and its level within the insoluble proteome depends on the presence of Yca1 [14]; and Hsp40/70 together with Hsp100 constitute the "bi-chaperone" system that actively re-solubilize misfolded proteins under stress conditions [15, 16]. Furthermore, fluorescent microscopy studies showed that Yca1 and Hsp104, a protein involved in aggregate dissolution that serves as a marker for aggregated material, can co-localize in cells collected from heat-stressed and aged cultures [13].

Additional comparisons between wild-type and *Δyca1* cells implicated *Δyca1* cells with a protein turnover phenotype. Sedimentation of cellular protein [17–19] to separate the insoluble protein fraction followed by membrane filtration showed that *Δyca1* cells accumulate a greater amount of insoluble material [13]. In addition, analysis of vacuolar morphology via fluorescence microscopy and lipophilic styryl dyes [20] demonstrated that the loss of Yca1 resulted in increased vacuole formation, possibly the consequence of an increased protein aggregate load. Together, these findings support the hypothesis that Yca1 increases cellular fitness as a bona fide player in cellular proteostasis.

The discovery of a well-entrenched non-death function of Yca1 has established metacaspases as versatile biological entities. As such, the ability of Yca1 to cycle between death and non-death activities demands stringent forms of analysis to accurately differentiate the mechanisms that contribute to divergent cell fates. For example, screening for known hallmark features of death such as the integrity of the nucleus via DNA stains [13], may aid in delineating processes that contribute to cell fate, yet these measures do not distinguish the physiological roles of Yca1. This chapter consists of the detailed protocols, which are instrumental in defining and assessing the non-death, proteostasis function of the budding yeast metacaspase Yca1.

2 Materials

2.1 Yeast Growth Conditions

1. YPD medium: 1 % (w/v) yeast extract, 2 % (w/v) Bacto Peptone, 2 % (v/v) dextrose, pH 3.5 (*see* **Note 1**).
2. Orbital incubator (a range of 25–42 °C).

2.2 Protein Extraction

1. Buffer A: 50 mM Tris–HCl, 1 mM EDTA, 150 mM NaCl, 1 % (v/v) glycerol, 1 % (v/v) NP-40, pH 7.4. Store at 4 °C.
2. Buffer B: 50 mM Tris–HCl, 1 mM EDTA, 1 % (v/v) glycerol, 0.1 % (v/v) NP-40, pH 7.4. Store at 4 °C.
3. Protease inhibitors (Calbiochem Cocktail Set IV or similar).
4. Acid washed glass beads, 0.4–0.6 mm in diameter (Sigma).
5. 27 G × ½ (0.4 mm × 13 mm) needles (Becton Dickinson).
6. 15 mL tubes (Sarstedt).

2.3 Sedimentation Assay

1. Buffer B: 50 mM Tris–HCl, 1 mM EDTA, 1 % (v/v) glycerol, 0.1 % (v/v) NP-40, pH 7.4. Store at 4 °C.
2. Protease inhibitors (Calbiochem Cocktail Set IV or similar).
3. Wash buffer: 98 % (v/v) buffer B, 2 % (v/v) NP40.

2.4 Filter Trap Assay

1. Bio-Dot SF microfiltration apparatus (Bio-Rad Labs).
2. Bio-Dot SF Filter paper (Bio-Rad Labs).
3. 0.45 μm PVDF membrane (e.g., Immobilon).
4. Buffer B: 50 mM Tris–HCl, 1 mM EDTA, 1 % (v/v) glycerol, 0.1 % (v/v) NP-40, pH 7.4. Store at 4 °C.
5. Protease inhibitors (Calbiochem Cocktail Set IV or similar).
6. Wetting buffer: 80 % (v/v) buffer B, 20 % (v/v) methanol.
7. Coomassie Blue solution: 0.1 % (w/v) Coomassie Blue R-250, 45 % (v/v) methanol, 10 % (v/v) acetic acid, 45 % (v/v) water.
8. Destain solution: 45 % (v/v) methanol, 10 % (v/v) acetic acid, 45 % (v/v) water.

9. Vacuum source.
10. Scotch Tape.

2.5 Vacuole Staining

1. YPD medium: 1 % (w/v) yeast extract, 2 % (w/v) Bacto Peptone, 2 % (v/v) dextrose, pH 3.5.
2. FM lipophilic styryl dye (e.g., Molecular Probes).
3. Phosphate buffered saline (PBS), pH 7.4.
4. Aluminum foil.
5. 37 % (v/v) Formaldehyde.
6. Coverslips: 24 × 50 mm (Fisher Scientific).
7. Poly-L-Lysine coated glass slides (Sigma).

2.6 Immunoprecipitation

1. Dynabeads (Dynal Biotech).
2. Magnetic stand (Dynal Biotech).
3. Buffer C: 20 mM HEPES, 0.1 % (v/v) Tween 20, 2 mM $MgCl_2$, 300 mM NaCl, pH 7.4. Store at 4 °C.
4. Protease Inhibitors (Calbiochem Cocktail Set IV or similar).
5. Buffer D:50 mM Tris–HCl, 2 % (w/v) SDS, 0.1 % (w/v) bromophenol blue, 10 % (v/v) glycerol, 150 mM NaCl, pH 6.8.
6. 0.1 M sodium phosphate buffer: 19 mM monosodium phosphate, 81 mM disodium phosphate, pH 7.4.
7. Ammonium sulfate buffer: 3 M ammonium sulfate, 19 mM monosodium phosphate, 81 mM disodium phosphate, pH 7.4.
8. Phosphate buffered saline (PBS), pH 7.4.
9. 0.1 M Citric acid, pH 3.1.
10. Dimethylformamide (DMF).
11. Triton-X 100.
12. Antibody: nonspecific Rabbit IgG (Chemicon, *see* **Note 2**).

2.7 DNA Staining

1. 70 % (v/v) Ethanol.
2. 50 mM Sodium citrate.
3. 0.2 mg/mL RNase A.
4. Phosphate buffered saline (PBS), pH 7.4.
5. SYTOX Green (Molecular Probes).

3 Methods

3.1 Normal and Heat Stress Growth Conditions

1. Inoculate a 3 mL aliquot of medium with a single yeast colony. This will be the starter culture.
2. Grow for 12–16 h at 30 °C, 225 rpm until OD_{660} is at least between 0.8 and 1.0.

3. Transfer between 5 and 10 μL of culture to fresh 50 mL of media.
4. Incubate freshly inoculated 50 mL culture at 30 °C, 225 rpm. Incubation time depends on doubling time of yeast strain used.
5. At OD_{660} 0.6–0.8, collect cells via centrifugation at 4,600 × *g* for 5 min at room temperature (*see* **Note 3**).
6. Discard supernatant and resuspend the cells in sterile autoclaved water.
7. Centrifuge at 4,600 × *g* for 5 min at room temperature to collect the cells.
8. Discard supernatant and store cell pellet at −80 °C. Cells may be stored up to 3 months at −80 °C.
9. For heat stress and recovery, prepare four additional flasks with 50 mL media and inoculate as stated in **steps 3** and **4**. Use the same starter culture for all samples.
10. At OD_{660} 0.6–0.8, transfer culture to 42 °C and incubate for 1 h, 225 rpm.
11. Collect heat-stressed cells as described in **steps 5–8** (*see* **Note 4**).
12. For recovery, after 42 °C treatment, transfer cultures to 30 °C and incubate further at 225 rpm.
13. Collect cells as described in **steps 5–8** every 30 min.

3.2 Protein Extraction

1. Thaw frozen cells on ice.
2. Add 300 μL of ice-cold buffer A or buffer B supplemented with 0.5 % (v/v) protease inhibitors (*see* **Note 5**).
3. Transfer cell suspension to a chilled microcentrifuge containing 0.7 g of acid-washed glass beads.
4. Lyse cells by placing the microcentrifuge tube containing the cell suspension onto the disruptor vortex for 1 min at 4 °C.
5. After vortex, let suspension stand at 4 °C for 1 min.
6. Repeat **steps 4** and **5** for five more cycles.
7. After lysis, use needle to pierce the bottom of the microcentrifuge tube.
8. Remove needle and place into chilled 15 cm culture tube on ice (*see* **Note 6**).
9. Elute mixture from microcentrifuge tube via centrifugation at 260 × *g* for 1 min at 4 °C.
10. Transfer entire extract from culture tube to fresh microcentrifuge tube on ice.
11. Clear cell debris via centrifugation at 350 × *g* for 1 min at 4 °C.
12. Transfer supernatant to a new microcentrifuge tube on ice.

13. Clear additional cell debris via centrifugation at 800 × *g* for 1 min at 4 °C.
14. Transfer supernatant to chilled new microcentrifuge tube. This is the total cellular protein extract. The extract may be split into aliquots and stored in −80 °C.

3.3 Sedimentation Assay

1. Quantify total protein extract and take equal amount of protein from all samples.
2. Normalize volume with buffer B containing 0.5 % (v/v) protease inhibitors.
3. Sediment protein by centrifugation at 15,000 × *g* for 15 min at 4 °C.
4. Transfer supernatant to separate microcentrifuge tube. This fraction contains soluble proteins. Store on ice for the remainder of the procedure. The remaining pellet fraction contains insoluble proteins.
5. Add 400 μL of wash buffer to the tube containing the protein pellet.
6. Vortex at setting 3 for 10 s.
7. Centrifuge at 15,000 × *g* for 15 min to collect the protein pellet.
8. Discard supernatant and repeat **steps 5**–**7**.
9. Add original amount of buffer B containing 0.5 % (v/v) protease inhibitors to the protein pellet.
10. Vortex sample at 4 °C to completely dissolve the pellet.
11. The resulting fractions may be analyzed via SDS-PAGE or Filter Trap Assay.

3.4 Filter Trap Assay

1. Prepare protein fractions as described under Subheading 3.3 starting with 2,000 μg of total protein lysate. Adjust volume to set concentration to 5 μg/μL.
2. Serially dilute both of the fractions for each experimental sample: Start with 75 μL of the sample plus 125 μL buffer B containing 0.5 % (v/v) protease inhibitors. Mix well by gentle vortex (setting 3) for 10 s. Label this mixture as D1.
3. For dilution 2 (D2), take 100 μL of D1 and add that to 100 μL of buffer B containing 0.5 % (v/v) protease inhibitors. Mix by gentle vortex for 10 s.
4. For dilution 3 (D3), take 100 μL of D2 and add that to 100 μL of buffer B containing 0.5 % (v/v) protease inhibitors. Mix by gentle vortex for 10 s.
5. For dilution 4 (D4), take 100 μL of D3 and add that to 100 μL of buffer B containing 0.5 % (v/v) protease inhibitors. Mix by gentle vortex for 10 s. Discard 100 μL.

6. Normalize volume of all samples and place on ice. A minimum volume of 200 μL is recommended.
7. Assemble Bio-Dot SF apparatus as described in the product manual.
8. Soak 3× Bio-Dot SF filter paper in wetting buffer for 10 min.
9. Cut a 9 × 12 cm sized piece of 45 μm PVDF membrane and place in 100 % (v/v) methanol for 2 min.
10. After activation, discard methanol and rinse membrane with water. Transfer the membrane to wetting buffer.
11. Place the filter papers above the support plate followed by the activated membrane on top of the filter paper.
12. Place the sample template on top of the membrane and tighten the screws on the sample template.
13. Attach the apparatus to the vacuum source. Set the valve in the apparatus to atmosphere setting. Ensure that the vacuum is not turned on.
14. To equilibrate the wells, add 100 μL of buffer B to all wells and turn on vacuum for 30 s to filter the buffer through. Ensure that the membrane does not dry out during filtration (*see* **Note 7**).
15. Turn off vacuum and discard any leftover liquid in the wells.
16. Load the samples on the wells starting with the most dilute for each set (in the order of D4, D3, D2, and then D1). Fill all unused wells with buffer (same volume as sample) and seal them off using Scotch Tape.
17. Let sample stand in the wells for 10 min at room temperature to allow for protein binding to the membrane.
18. After incubation, filter the sample through by turning on the vacuum source (*see* **Note 8**).
19. Seal off wells with Scotch Tape as soon as the sample has filtered through to prevent drying (*see* **Note 9**).
20. Add 200 μL of buffer B containing 0.5 % (v/v) protease inhibitors to each sample well and let stand for 2 min at room temperature.
21. Repeat the filtration process as described in **steps 18** and **19**.
22. After filtration, leave the vacuum on and unscrew the sample template.
23. Turn off the vacuum, remove the membrane and let it air-dry completely.
24. Activate the membrane in methanol as described in **steps 9** and **10**.
25. Place the membrane into Coomassie Blue R-250 solution and stain for 15 min on a rocking platform.

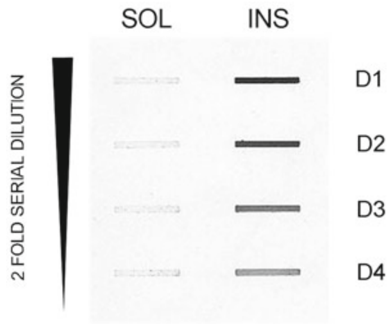

Fig. 1 Filter trap analyses of insoluble protein aggregates. Twofold serial dilutions of the soluble (SOL) and insoluble (INS) protein fractions were filtered through a 0.45 μM PVDF membrane and stained with Coomassie Blue solution. The labels on the *right* indicate the different dilutions (D1–D4)

26. After staining, remove the membrane and place into the destain solution (*see* **Note 10**).
27. Wash the membrane on rocking platform for 10 min, changing solution every 5 min.
28. After destaining, wash the membrane with water and dry completely.
29. Analyze the resulting bands via densitometry (Fig. 1). (We use the ImageJ software for densitometry analyses.)

3.5 Immuno-precipitation

1. Add 2 mL of DMF to 60 mg of dry M-270 epoxy Dynabeads.
2. Vortex the beads for 2 min and keep at 4 °C. The beads may be stored indefinitely at 4 °C.
3. Vortex the stock of beads for 1–2 min and transfer 200 μL of beads into a microcentrifuge tube (*see* **Note 11**).
4. Place tube on magnetic stand to separate beads from DMF for 1 min and discard the supernatant.
5. Wash the beads with 1 mL of sodium phosphate buffer: gently resuspend the beads in the buffer by rotation and then place tube on magnet for 1 min.
6. Discard supernatant and repeat **step 5** for additional two times.
7. Immediately, add 230 μL of sodium phosphate buffer to the dry beads.
8. Add 10 μL of antibody (10 mg/mL stock concentration) to the mixture and vortex for 15 s.
9. Add 120 μL of ammonium sulfate buffer to the mixture.
10. Incubate the mixture at 37 °C for 16–24 h on a nutator.
11. Following incubation, wash the beads four times with 1 mL of PBS as described in **step 5**.

12. Discard supernatant and resuspend the beads in 1 mL of PBS containing 1 % (v/v) Triton-X 100 and wash for 10 min on nutator.
13. Discard supernatant and wash the beads twice with 1 mL PBS for a 1 min.
14. Discard supernatant and perform four washes, 10 min each with 1 mL of 0.1 M citric acid.
15. Discard supernatant and repeat **step 13**.
16. Resuspend the antibody-conjugated beads in 400 μL of PBS.
17. Store beads at 4 °C. The antibody-conjugated beads should be used within 14 days of preparation.
18. Grow cells to OD_{660} between 0.6–0.8 and collect as described in Subheading 3.1.
19. Resuspend the cells in 300 μL of buffer C containing 0.5 % (v/v) protease inhibitors.
20. Lyse the cells and elute as described in Subheading 3.2, **steps 4–10**.
21. Centrifuge lysate at 20,000 × g for 15 min at 4 °C.
22. Collect supernatant and transfer to a fresh microcentrifuge tube.
23. Determine protein concentration.
24. Aliquot 15 mg of protein lysate.
25. Add 50 μL of conjugated magnetic beads to lysate.
26. Mix sample via rotation at 4 °C for 3 h.
27. Place sample on magnetic stand and wash the beads with 1 mL of cold buffer C for a total of five times.
28. After final wash, discard the residual liquid.
29. Resuspend the beads in 40 μL of buffer D.
30. Elute co-purified protein by heating the mixture at 65 °C for 10 min.
31. Place tube on the magnet to separate the beads.
32. Transfer supernatant to a new microcentrifuge tube.
33. Add 2-β-mercaptoethanol to a final concentration of 100 mM.
34. Boil sample at 100 °C for 5 min and analyze via SDS-PAGE and silver staining.

3.6 Vacuolar Staining

1. Grow cells in 5 mL of YPD medium to an OD_{660} between 0.4 and 0.5.
2. Collect the cells by centrifugation at 4,600 × g for 5 min at room temperature.
3. Discard supernatant and resuspend the cells in 2 mL of YPD.

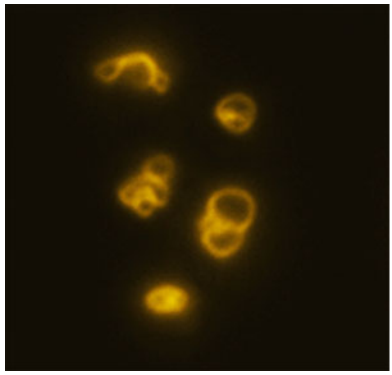

Fig. 2 Vacuolar morphology in yeast. *S. cerevisiae* BY4741 cells were stained with the lipophilic styryl dye, FM 4–64 for 1 h. Images of stained cells were captured using AxioVision 4.8 software on a Zeiss Axio Observer Z1 microscope (63× magnification). The above representation is a magnification of the area of interest depicting variable morphology and number of vacuoles

4. Dissolve the FM dye to a stock concentration of 100 μM in 1× PBS, pH 7.4. Protect from light and place on ice.
5. Add 20 μl of the stock to each sample (final concentration of FM dye is 1 μM).
6. Cover tubes with aluminum foil to protect dye from light.
7. Label vacuoles by further incubating cells with dye at 30 °C, 225 rpm for 1 h (*see* **Note 12**).
8. After incubation with dye, immediately place the cells on ice.
9. Add 270 μL of 37 % (v/v) formaldehyde solution to the sample and further incubate on ice for 15 min.
10. Transfer mixture to microcentrifuge tube and collect the cells by centrifugation 5,600 × *g* for 2 min.
11. Discard supernatant and resuspend the cells in 500 μL of 1× PBS.
12. Collect the cells via centrifugation as in **step 10**.
13. Resuspend the cells in 200 μL of 1× PBS. The cells may be stored at 4 °C for 24 h.
14. Spot 15–20 μL of fixed cells on microscope slide.
15. Place coverslip. Protect sample from light.
16. View and take pictures of the cells on the microscope (Fig. 2).

3.7 DNA Staining

1. Grow cells in 5 mL of YPD media to an OD_{660} between 0.4 and 0.5.
2. Transfer 1 mL of the culture to a microcentrifuge and collect cells via centrifugation at 1,400 × *g* for 5 min.
3. Resuspend the cells in 1 mL of cold 70 % (v/v) ethanol.

4. Incubate at 4 °C for 12 h (*see* **Note 13**).
5. Discard supernatant and resuspend the cells in 1 mL of 50 mM sodium citrate.
6. Collect the cells via centrifugation at 1,400 × *g* for 5 min at 4 °C.
7. Resuspend the cells in 500 μL of 50 mM sodium citrate containing 0.2 mg/mL RNase A.
8. Incubate cells at 37 °C for 20–24 h.
9. Add SYTOX Green dye to a final concentration of 3.7 μM.
10. Incubate at room temperature for 1 h in the dark.
11. Collect the cells via centrifugation in microcentrifuge at 5,600 × *g* for 2 min.
12. Discard supernatant and resuspend the cells in 400 μL of 1× PBS.
13. Collect the cells and resuspend in 400 μL of 1× PBS.
14. The cells may be viewed under the microscope or sorted via flow cytometry.

4 Notes

1. We buffer our YPD medium to a pH 3.5 using HCl. This medium is used throughout all experimentation. To prepare 500 mL of acidic YPD medium, dissolve 5 g of yeast extract and 10 g of Bacto Peptone in 425 mL of water. Add HCl to the medium until the pH reaches 3.5. The solution will have a "grainy" appearance. Make up the volume to 450 mL and autoclave. Make 20 % (w/v) dextrose solution and filter-sterilize. Add 50 mL of the dextrose solution to the autoclaved solution (2 % final concentration) to make the final acidic YPD medium.
2. The constant or crystallizable Fc region of Rabbit IgG binds with high affinity to the "protein A" component of the TAP tag. This antibody can be replaced with other antibodies that bind protein A, another epitope within the TAP tag or a different protein of interest.
3. When collecting cells or starting any treatment, ensure that the OD_{660} is similar across all samples ($OD_{660} \pm 0.05$).
4. To ensure credibility of heat-stressed samples, limit the time taken to collect the sample to 10 min. Cells may be collected at a higher centrifugal force (6,000–8,000 × *g*) for less amount of time (2–3 min) for this time point.
5. Buffer B is more hypotonic with a lower NP-40 concentration and is ideal for preparation and analysis of soluble and insoluble

protein fractions. For conducting normal immunoblots, prepare extracts using buffer A.

6. For efficient elution, ensure that the needle completely pierces the microcentrifuge tube. The out pour of the liquid when removing the needle is indicative of whether or not the tube has been sufficiently pierced. If elution is not complete, repeat the centrifugation in **step 9** for 15–20 s.
7. During the equilibration step, the 30 s filtration time may be excessive depending on the vacuum strength. This time may be adjusted accordingly. More importantly, monitor the filtration to ensure that the wells do not dry out completely. Partial or complete drying out of the membrane will affect binding of proteins to the membrane. Once the buffer in a majority of the wells has filtered through, turn off the vacuum and remove any excess liquid from the remaining wells. This step will also be indicative of the uniformity of the vacuum.
8. During filtration, ensure that there is no buildup of fluid within the tubing and around the flow valve to prevent backflow which may ruin the experiment if not corrected quickly. This can be prevented by increasing the vacuum strength by blocking the atmosphere line in the flow valve. We highly recommend getting acquainted with the apparatus before proceeding with the experiment. We usually see buildup around the flow valve after assembling the apparatus due to excess retention of buffer in the filter paper. In such instances, open the valve to drain the buffer before loading the samples.
9. Sealing off the wells helps maintain uniform vacuum across the apparatus and prevents drying. We find that sometimes the filtration can be length depending on the amount of protein used. In such instances keep adding buffer (few drops from a P1000 pipet) to the sample wells that have filtered through to prevent drying of the well until all samples have filtered through. This should be done in addition to the wash step.
10. To avoid nonuniform destaining of the membrane, do not pour the destain solution directly onto the membrane. Always place membrane onto the solution. Monitor the bands on the membrane to make sure that the higher dilutions (D3, D4) do not destain completely. The incubation time in the destain solution can be adjusted accordingly.
11. Keep all of the samples and buffers which are to be utilized on ice throughout the procedure.
12. Incubating the cells with the FM stain for a longer duration of time (1.5–2 h) may yield in better staining of the vacuoles. However, this may be accompanied by increased background staining. The concentration of the stain in culture may be increased but we do recommend a minimum 1 h incubation

period with the stain. In order to avoid high background staining, additional washes may be performed as described in **steps 11** and **12**. For staining vacuoles through the stress-recovery time course described in Subheading 3.1, incubate the cells with the stain for a minimum of 1 h before the 42 °C for 1 h treatment.

13. Ethanol-fixed cells can be stored for 36–48 h at 4 °C or for longer period (5 days) at −20 °C.

References

1. Aravind L, Koonin EV (2002) Classification of the caspase–hemoglobinase fold: detection of new families and implications for the origin of the eukaryotic separins. Proteins 46: 355–367
2. Wong AH, Yan C, Shi Y (2012) Crystal structure of the yeast metacaspase Yca1. J Biol Chem 287:29251–29259
3. Uren AG, O'Rourke K, Aravind L et al (2000) Identification of paracaspases and metacaspases: two ancient families of caspase-like proteins one of which plays a key role in MALT lymphoma. Mol Cell 6:961–967
4. Tsiatsiani L, Van Breusegem F, Gallois P et al (2011) Metacaspases. Cell Death Differ 18: 1279–1288
5. Madeo F, Herker E, Maldener C et al (2002) A caspase-related protease regulates apoptosis in yeast. Mol Cell 9:911–917
6. Carmona-Gutierrez D, Fröhlich KU, Kroemer G et al (2010) Metacaspases are caspases. Doubt no more. Cell Death Differ 17:377
7. Lee REC, Puente LG, Kaern M et al (2008) A non-death role of the yeast metacaspase: Yca1p alters cell cycle dynamics. PLoS ONE 3:e2956
8. Madeo F, Carmona-Gutierrez D, Ring J et al (2009) Caspase-dependent and caspase-independent cell death pathways in yeast. Biochem Biophys Res Commun 382:227–231
9. Guscetti F, Nath N, Denko N (2005) Functional characterization of human pro-apoptotic molecules in yeast S. cerevisiae. FASEB J 19:464–466
10. Fernando P, Megeney LA (2007) Is caspase-dependent apoptosis only cell differentiation taken to the extreme? FASEB J 21:8–17
11. Shrestha A, Megeney LA (2012) The non-death role of metacaspase proteases. Front Oncol 2:78
12. Mitchell L, Lambert JP, Gerdes M et al (2008) Functional dissection of the NuA4 histone acetyltransferase reveals its role as a genetic hub and that Eaf1 is essential for complex integrity. Mol Cell Biol 28:2244–2256
13. Lee REC, Brunette S, Puente LG et al (2010) Metacaspase Yca1 is required for clearance of insoluble protein aggregates. Proc Natl Acad Sci U S A 107:13348–13353
14. Shrestha A, Brunette S, Puente LG et al (2013) The role of Yca1 in proteostasis. Yca1 regulates the composition of the insoluble proteome. J Proteomics 81:24–30
15. Parsell DA, Kowal AS, Singer MA et al (1994) Protein disaggregation mediated by heat-shock protein Hsp104. Nature 372:475–478
16. Glover JR, Lindquist S (1998) Hsp104, Hsp70, and Hsp40: a novel chaperone system that rescues previously aggregated proteins. Cell 94:73–82
17. Cashikar AG, Duendald M, Lindquist SL (2005) A chaperone pathway in protein disaggregation. Hsp26 alters the nature of protein aggregates to facilitate reactivation by Hsp104. J Biol Chem 280:23869–23875
18. Haslbeck M, Miess A, Stromer T et al (2005) Disassembling protein aggregates in the yeast cytosol. The cooperation of Hsp26 with Ssa1 and Hsp104. J Biol Chem 280:23861–23868
19. Rand JD, Grant CM (2006) The thioredoxin system protects ribosomes against stress induced aggregation. Mol Biol Cell 17:387–401
20. Journo D, Winter G, Abeliovich H (2008) Monitoring autophagy in yeast using FM4-64 fluorescence. Methods Enzymol 451:79–88

Appendix V

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Yeast proteinopathy models: a robust tool for deciphering the basis of neurodegeneration

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ABSTRACT **Protein quality control or proteostasis is an essential determinant of basic cell health and aging. Eukaryotic cells have evolved a number of proteostatic mechanisms to ensure that proteins retain functional conformation, or are rapidly degraded when proteins misfold or self-aggregate. Disruption of proteostasis is now widely recognized as a key feature of aging related illness, specifically neurodegenerative disease. For example, Alzheimer's disease, Huntington's disease, Parkinson's disease and Amyotrophic Lateral Sclerosis (ALS) each target and afflict distinct neuronal cell subtypes, yet this diverse array of human pathologies share the defining feature of aberrant protein aggregation within the affected cell population. Here, we review the use of budding yeast as a robust proxy to study the intersection between proteostasis and neurodegenerative disease. The humanized yeast model has proven to be an amenable platform to identify both, conserved proteostatic mechanisms across eukaryotic phyla and novel disease specific molecular dysfunction. Moreover, we discuss the intriguing concept that yeast specific proteins may be utilized as bona fide therapeutic agents, to correct proteostasis errors across various forms of neurodegeneration.**

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Abbreviations:
α-syn - α-synuclein,
AD - Alzheimer's disease,
ALS - amyotrophic lateral sclerosis,
HD - Huntington's disease,
Htt - huntingtin protein,
Pab1 - Poly (A) binding protein,
Pbp1 - Pab1 - binding protein,
PD - Parkinson's disease,
TDP-43 - TAR DNA-binding protein of 43 kDa.

INTRODUCTION

The regulation of cellular protein levels is an indispensable feature that ensures fidelity of fundamental processes within all cell types. Although nascent peptide strands contain the requisite information to fold proteins into functional structures and confer biological activity, the dynamic nature of protein folding as well as the crowded cell environment pose significant barriers in maintaining protein homeostasis or proteostasis [1]. Consequently, cells have evolved sophisticated protein quality control networks to ensure correct folding of nascent peptides, refolding of misfolded proteins or when required directed proteolysis via a number of conserved mechanisms [2].

Loss of proteostatic control has emerged as a common cellular pathology in seemingly disparate forms of neurodegenerative disease [3]. Disruption to protein folding by various factors such as, mutations, errors in transcription/translation, environmental stress and age related decline can lead to the overwhelming of these quality control systems in susceptible neuron populations, resulting in the aggregation of misfolded proteins and their organization into larger aggregate structures [4]. For example, various peptides (nascent and modified) can instinctively form detergent resistant cross-β amyloidogenic structures which are inherently associated with the pathology observed in various neurodegenerative disorders [5]. These proteins include α-synuclein, the primary constituent in aggregate structures called Lewy bodies observed in Parkinson's disease (PD) as well as other diseases termed synucleopathies. The more prevalent neurodegenerative disorder, Alzheimer's disease (AD) is characterized by the presence of similar extracellular plaque structures containing accumulated β-amyloid peptide as well as intracellular buildup of a hyperphosphorylated microtubule associated protein referred to as tau. Similarly, intracellular cytotoxic aggregation of the huntingtin protein (Htt) is a hallmark feature of Huntington's disease (HD) [5]. More recently, highly ubiquitylated cytoplasmic inclusions of the TAR DNA-binding protein of 43 kDa (TDP-43) have been identified in neurons of Amyotrophic Lateral Sclerosis (ALS) affected patients [6]. The amyloid structures formed by these various protein species have also been implicated in compromising the expression of proteostasis machinery. For instance, in mouse models of HD, increased polyQ aggregation resulted in a steady decline in the expression of the chaperones Hsp70 and the Hsp40 [7].

A consensus has arisen supporting the concept that protein misfolding/aggregation and the progression of neurodegenerative disease are inherently linked. This model also suggests that ongoing aberrant protein misfolding and decline in proteostatic machinery function may accelerate the pathogenic cascade [3]. The prevailing dogma argues that the proteostasis errors are a cell autonomous pathology, yet misfolded protein species of α-synuclein, β-amyloid and tau have been shown to be capable of cell to cell transmission similar to that of prions. These seed templates lead to the misfolding of the specific protein species, yet also initiate aggregate seeding of other proteins species, magnifying the proteostasis imbalance [8]. Given these observations, there is an urgent unmet medical need to advance basic understanding of protein quality control systems and why perturbations in this core cellular activity propagates neurodegenerative disease.

In recent years, the field of neurodegeneration has derived significant benefit from the use of baker's yeast, *Saccharomyces cerevisiae,* to elucidate the molecular basis of various pathologies. [9-11]. As the core proteostasis machinery is remarkably well conserved across eukaryotes, yeast has emerged as a tractable organism to model proteostasis alterations in neural disease [1, 4, 10, 12]. Here, we discuss the insights derived from the use of humanized yeast models and whether the yeast proteome itself may offer novel therapeutic avenues to treat and reverse otherwise implacable aggregation mediated disease.

YEAST MODELS OF NEURODEGENERATION

The mislocalized accumulation of the pre-synaptic protein α-synuclein (α-syn) as a result of mutations or gene multiplications is a hallmark feature that defines PD and other disorders collectively termed synucleinopathies [13]. α-syn was one of the first neurodegeneration related proteins to be characterized in the yeast model, which has greatly enhanced our understanding of the toxicity associated with PD. Indeed, the pathogenic prion-like spreading feature of α-syn oligomers and fibrils has generated considerable interest from both basic scientists who study aggregation control as well as those interested in disease pathogenesis [13, 14]. The very first study conducted by Outeiro and Lindquist [15] in yeast characterized α-syn toxicity as an outcome of its redistribution within the cell, which led to the formation of cytotoxic inclusions. This study demonstrated that toxicity was directly correlated with the level of α-syn expression, yet also established dysfunction in various cellular processes, namely, lipid droplet accumulation, impairment in the proteostasis machinery and defects in vesicle trafficking [15]. Following this landmark report, numerous other studies utilizing yeast modeling of α-syn have added to the knowledge base, implicating defects in various cellular processes [10], as well as identifying normal cellular constituents that contribute to cytotoxicity, such as the correlation between mitochondria and reactive oxygen species formation that occurs in α-syn mediated cell death [16].

These studies highlight the great complexity in dealing with PD and neurodegenerative disorders in general, yet have confirmed the utility of the yeast system in addressing complex human disease pathology. Yeast models have also been instrumental in identifying other molecular determinants that modify α-syn cytotoxicity. In particular, the functional identification of the GTPase Rab1, as a suppressor of α-syn toxicity, stemmed from initial studies in yeast [17]. The observation that α-syn accumulation leads to ER-Golgi trafficking defects, which is present in PD and many other neurodegenerative disorders, led to the subsequent utilization of yeast overexpression libraries to screen for modifiers of α-syn toxicity. The yeast protein Ypt1; a Rab family related GTPase, was observed to directly interact with α-syn inclusions and suppress α-syn toxicity. The protective function of Ypt1 was also observed to be phylogenetically conserved, as its mammalian homolog Rab1 was able to rescue the loss of dopaminergic neuron loss in PD models in both *Drosophila* and *C. elegans* [17]. Subsequently, other members of the Rab family of GTPases have been also shown to suppress α-syn toxicity. For example, the highly expressed presynaptic protein RAB3A and the post-Golgi vesicle associated protein, RAB8A have been demonstrated to ameliorate vesicle trafficking defects associated with α-syn expression. The heavy reliance of dopaminergic neurons on vesicular trafficking is also suggested to be the reason that this subset of neurons is affected the most in PD [18]. More recently, α-syn expression has been shown to imbalance Rab homeostasis that results in Golgi fragmentation observed in PD. Golgi fragmentation was demonstrated to correlate with the expression levels of Rab 1, 2 and 8. Overexpression of Rab 1 and 8 and the ablation of Rab2 expression rescued the fragmentation phenotype [19].

In addition to Rab GTPases, studies using similar approaches continue to identify novel protein mediators of α-syn related cytotoxicity in PD, including endonuclease G (endoG) and the sorting protein VPS35 [20]. The cytotoxic mislocalization of the mitochondrial nuclease endoG in the nucleus of dopaminergic neurons in PD patients inspired its characterization in yeast PD models. In yeast, it was observed that expression of α-syn leads to DNA damage, which is mediated by endoG. This observation was further verified in fly models which showed that suppressing endoG increased the survival of α-syn expressing flies, implicating endoG as a critical mediator of α-syn toxicity and a potential target for therapeutic development [20]. VPS35 has also been shown to ameliorate neurodegeneration and antagonize α-syn inclusion formation. This is of particularly interest as mutations in VPS35 are linked to PD [21]. Increased gene expression of the translation initiation factor EIF4G1 has also been linked to protein misfolding as well as cases of familial PD [22]. Overexpression of the yeast homolog of EIF4G1, TIF4631, was toxic to cells lacking the *vps35* gene suggesting that VPS35 is protective against toxicity relating to EIF4G1 upregulation. Likewise, the PD-associated D620N mutation in VPS35 also had a similar effect. This genetic interaction between VPS35 and EIF4G1 was further confirmed in neurons of both *C. elegans* and transgenic mouse models [23]. Furthermore, loss of either VPS35 or TIF4631 expression in yeast reduces the survival rate against α-syn toxicity. Finally, staining of NeuN in the hippocampus suggested that VPS35 upregulation is protective against α-syn associated neurodegeneration [23]. As such, these studies highlight the ease and accuracy of the yeast model system to define the molecular pathogenesis of human PD.

Understanding the cellular etiology of ALS, a fatal and intractable neurodegenerative disorder, has also benefitted greatly by use of yeast model systems [9, 10]. A superb example of one such ALS related protein is TDP-43 (TAR DNA binding protein 43). TDP-43 was originally described as a regulator of RNA metabolism in the nucleus and has also been shown to have a cytoplasmic role in anterograde transport of trafficking mRNAs in neurons. Nevertheless, TDP-43 has been found to be a common cytoplasmic inclusion protein in ALS affected individuals [9, 24]. In addition, TDP-43 inclusions have been linked to many other neurodegenerative disorders such as Inclusion Body Myopathy with Paget disease of the bone and frontotemporal dementia (IBMPFD) as well as AD, PD and HD [25].

The first yeast TDP-43 proteinopathy model by Johnson *et. al.* [26] characterized TDP-43 to be nucleus specific and that overexpression of the protein led to its mislocalization into the cytoplasm where it formed aggregates, reducing overall cell survival. Interestingly, TDP-43 inclusions were observed to differ from those of the expanded polyglutamine Htt protein associated with HD, as TDP-43 aggregates were able to solubilize and were not resistant to detergent denaturation. This study used a deletion mutant approach to dissect the structural requirements within the protein to identify region(s) that were responsible for aggregation propensity and cytotoxicity and deduced that the C terminus of the protein was responsible for driving aggregation [26]. Further characterization of TDP-43 in yeast identified TDP-43 as having the innate ability to aggregate as pure TDP-43 readily formed inclusions, which were structurally identical to aggregates in degenerating neurons of patients with ALS and frontotemporal lobar degeneration with ubiquitin- and TDP-43-positive inclusions (FTLD-U). Use of the yeast model revealed that several reported pathogenic mutations linked to ALS mapped to the C-terminus of TDP-43, which accelerated TDP-43 aggregation and decreased survival [27]. These initial discoveries of TDP-43 disease biology have now been validated in various experimental models [9, 28].

The success of modifier gene discovery in α-syn yeast models of PD has also propelled the use of similar genome wide screens to elucidate TDP-43 induced toxicity, i.e. yeast overexpression screens have led to the identification of a pool of 40 genes that modify TDP-43 toxicity. This pool of factors contained the Poly (A) binding protein (Pab1) - binding protein, Pbp1 as a specific enhancer of TDP-43 toxicity; overexpression of Pbp1 increased TDP-43 toxicity whereas as Δ*pbp1* cells showed increased cell survival upon TDP-43 overexpression [29]. Interestingly, Pbp1 is an ortholog of the human ataxin-2 gene (*atxn2*), which has been implicated in spinocerebellar ataxia type 2 (SCA2) that is caused by glutamine expansion within the polyQ tract. This interaction between TDP-43 and Pbp1/Atx2 was further validated in *Drosophila* and humans. Moreover, the physical interaction between TDP-43 and Atx2 was shown to be dependent on RNA binding, as mutations within the RRMs as well as RNase treatment, dissolve the interaction between Atx2 and TDP-43 [29]. Atx2, which is normally granular or diffused within the cytoplasm, was observed to be aggregated in the spinal cord neurons of ALS patients, prompting the speculation that the TDP-43-Atx2 may have a causative link in ALS. Consequently, analysis of polyglutamine length of Atx2 in ALS patients led to the conclusion that the presence of an intermediate length glutamine expansion (27-33Q) was associated with an increased risk of ALS, a conclusion that was matched by the early age of onset in affected individuals [29].

Building on this early work, recent studies have implicated the Pab1 protein itself (an Atx2 interactor and component of cytoplasmic stress granules where mislocalized TDP-43 accumulates), as having a role in TDP-43 mediated toxicity. Using the fly model, investigators have shown that an Atx2 mutant lacking the PAM1 motif (through which it binds Pab1), cannot interact with TDP-43 and confer toxicity in the retina. Similarly, human PABPC1 was observed to be mislocalized in ALS patients [30]. This study also led to the identification of the yeast ORF *YGR054W,* whose human homolog is EIF2A, as having physical and genetic interactions with multiple TDP-43 modifying genes. Further investigation correlated TDP-43 expression with the level of EIF2A phosphorylation and that blocking EIF2A phosphorylation by knocking down the PERK homolog PEK, was able to rescue TDP-43 toxicity in *Drosophila*. Collectively, these studies raise the tantalizing premise that TDP-43 toxicity may be moderated, by modulating the base level of EIF2A phosphorylation [30].

TDP-43 toxicity appears to also segregate with modifications in DNA structure. Here, Armakola *et. al.* [31] used yeast deletion screens to identify the RNA lariat debranching enzyme, Dbr1, as a conditioner of TDP-43 toxicity. Dbr1 is a phylogenetically conserved phosphodiesterase that is required for RNA degradation; and *dbr1* deletion mitigated the toxic effects of wildtype TDP-43 and the mutant TDP-43 Q331K expression. This suppression of TDP-43 toxicity was also validated in the human M17 neuroblastoma cell line and primary neurons using a siRNA-based knockdown approach, suggesting that inhibiting the enzymatic activity of Dbr1 is sufficient to reduce TDP-43 toxicity [31]. Using a Dbr1 mutant panel, the authors reported that limiting Dbr1 enzymatic activity led to RNA lariat accumulation, directly correlated with TDP-43 toxicity. Fluorescence imaging in yeast showed that TDP-43 foci co-localized with intronic lariats of the *Act1* gene in the cytoplasm and the suppression of TDP-43 toxicity in Δ*dbr1* results from interactions of TDP-43 with the accumulated intronic lariats. The postulate derived from these experiments implied that TDP-43 associated toxicity in ALS and FTLD-U arose from a loss of essential TDP-43 RNA interactions [31, 32]. The identification of TDP-43 as a RNA binding protein inspired efforts to test other RNA binding proteins as ALS relevant targets, among which FUS/TLS, TAF15, EWSR1, HNRNPA1 and HNRNPA2B1 have received considerable attention. Functional analyses of these proteins in yeast and other models have shown that, together with TDP-43, these proteins constitute an assemblage of factors with innate aggregation propensity, a characteristic which is accelerated in disease-linked forms [32-34]. Furthermore, studies using a similar deletion approach recently identified that mutations within the microtubule associated protein, profilin 1 (PFN1), which disrupts its novel function in stress granule dynamics can ablate its ability to mediate ALS pathology [35]. Such studies suggest the yeast model remains a focal point to dissect the functional role of these candidate genes as well as identify additional candidates in ALS and other related pathologies [9].

The prior discussion has focused on the role of yeast models as a test bed to explore disease mechanisms in α-syn linked PD and TDP-43 linked ALS, yet yeast has served as an ideal platform to study the cell biology of various aggregation prone proteins that characterize neurodegeneration. Of note, is the recent elucidation that manipulation of the ubiquitin protease system (UPS) in yeast (by enhancing the expression level of Cdc48 and Vms1) can curtail UBB^{+1} induced mitochondrial stress, which is a hallmark feature of AD pathology [36], This study exemplifies the matchless speed and ease of application afforded by use of the yeast model to address outstanding issues in neurodegenerative disease [10].

YEAST PROTEIN DELIVERY AS A MEANS TO COMBAT NEURODEGENERATION

Much effort has focused on defining genetic susceptibility in neurodegenerative disease, yet this line of investigation has failed to provide new or effective clinical interventions. Indeed, the capacity to actively reverse aggregation and control protein misfolding will be an essential attribute when considering therapeutic solutions for proteinopathies. Provocative evidence now suggests that yeast specific proteins have the capacity to degrade aggregate prone human disease proteins. Although speculative at this point in time, the data does support the conjecture that yeast proteins may be eventually employed to combat human neurodegeneration. In this regard, the yeast specific Hsp104 chaperone disaggregase has shown considerable promise [37].

Hsp104 is an AAA+ chaperone of the heat shock protein family which is known for its ability to completely remodel denatured aggregates, conferring “thermotolerance” in yeast. Structurally, Hsp104 is hexameric pore-like structure consisting of an N-terminal domain, a middle domain (MD) flanked by two AAA (AAA-1/2) domains and a C-terminal domain. ATP hydrolysis at the two AAA domains is required for substrate translocation through the pore. The unique M-domain, which is absent in other AAA+ proteins, is suggested to be the molecular switch which mediates the ATPase activity of Hsp104 and co-ordinates interaction with other chaperones of the Hsp70 and Hsp40 families [38, 39]. Dissolution of misfolded peptides by Hsp104 is dictated by ATP hydrolysis at the two AAA domains, resulting in a “peristaltic” translocation of the substrate through the pore leading to the release of the native peptide for proper refolding at the C terminus by other chaperones. Hsp104 is also essential for the propagation of prions, which are structurally amyloid in nature and considered to be beneficial for yeast to adapt and survive in varying environments [39].

Metazoans lack the presence of a clear Hsp104 ortholog, yet despite its absence Hsp104 can be stably expressed and can rescue protein aggregation and prevent neurodegeneration [30]. For example, Hsp104 overexpression within a rat model for PD was able to prevent dopaminergic neuron loss. This rescue was attributed to the ability of Hsp104 to disassemble toxic oligomers of α-syn *in vitro* as well as prevent α-syn inclusion formation *in vivo* [40]. Hsp104 has been shown to have a wide clientele of disease associated substrates, including both wildtype and mutant protein forms, which can be dissembled and resolubilized within the cell. However, dissolution of prion substrates, such as Sup35 in yeast, was more challenging for Hsp104 than other misfolded substrates, suggesting a need for a better understanding of the Hsp104 mechanism and activity [37, 41]. Subsequent studies have focused on defining variants of Hsp104 that may impart enhanced disaggregase activity, and efforts to date have identified variants that modify proteinopathy associated with gain of function mutations for α-syn, TDP-43 (Figure 1) and other TDP-43 related RNA binding proteins such as FUS. Further examination *in vitro* revealed that the enhanced disaggregase activity was dictated by amino acid identity within the middle domain of Hsp104, and key mutations in this region increased chaperone collaboration leading to disaggregation of a wide range of substrates [37, 42, 43]. Therefore, deployment of Hsp104 variants may offer a novel means to mitigate aggregation based disorders. What remains more speculative is whether Hsp104 can be engineered to attack very precise or structurally unique aggregates [37].

The unexpected role of Hsp104 in mitigating human aggregate-sensitive disease proteins raises the prospect that additional unforeseen regulatory mechanisms may exist to manage this critical aspect of cell biology. As such, a novel proteostasis role has been identified for the clan C/D family of proteases, which include metacaspases and caspases. While this protease clan is typically associated with induction of programmed cell death, through broad range protein destruction, a growing body of evidence suggests that discrete activation of these proteases is essential for numerous complex cell behaviors, independent of inducing cell death [44, 45]. Evidence supporting this claim originates from the observation that the loss of yeast metacaspase, Yca1 (also known as Mca1) results in an increased retention of insoluble aggregated material and decreased cell fitness [46, 47]. This provocative study also confirmed Yca1 formed stable interactions with known chaperone proteins such as Hsp40/70 and Cdc48/VCP [46]. Subsequent studies have affirmed the involvement of Yca1 in protein quality control, demonstrating that Yca1 regulates the composition of the insoluble proteome, by moderating the level of proteins that manage translation and ribosome biogenesis during stress [48].

Most recently, Hill *et al.* [49] identified Yca1 as a critical component in the control of age related protein aggregation. Using synthetic genetic array (SGA) methodology, these investigators conducted an unbiased genome wide screen to identify regulatory factors that limit dispersal of protein aggregates during replicative cell aging, i.e. retention of aggregates in the mother cell during division. This study established that Yca1 shuttled between quality control compartments and limited protein aggregation in the daughter cell [49]. Given the strong association of Yca1 with the chaperone machinery, combinatorial delivery of this metacaspase along with Hsp104 may offer a unique mechanism to restrain aggregate toxicity in affected human neurons.

Admittedly, the delivery of yeast proteins as a therapeutic intervention to treat human neurodegeneration is an entirely speculative proposition. However, the emerging data for Hsp104 indicates that measured delivery of this protein in preclinical animal models of PD and Huntington's disease has no observable off target toxicity [40, 50, 51]. Similar concerns should be noted for metacaspase use as this protease has yet to be expressed and tested in any mammalian system.

The discovery in yeast, that a metacaspase subdues toxic aggregate formation, raises an interesting prospect, i.e. that mammalian/human caspase proteins may have retained similar beneficial proteostatic function(s). Early studies characterizing cellular pathology in neurodegenerative disease have noted that affected and dying neurons display robust elevation in effector caspase activity (caspase 3 and 6), with subcellular distribution to protein inclusions [52, 53]. The prevailing assumption is that this caspase activity profile is causative in the generation of disease linked inclusions, in keeping with the known pro-apoptotic role for caspase enzymes. Not surprisingly, these observations have led to the hypothesis that targeted inhibition of caspase activity may provide a viable therapeutic intervention to limit cell death and dysfunction across a broad spectrum of aggregate associated neural disease [54]. Despite the widespread appeal that caspase activity acts as a harbinger of neural degeneration, the concept defies a wealth of opposing data, demonstrating that caspase function is vital for neurogenesis/neural cell differentiation, synaptic remodeling and higher brain function(s) [55, 56]. Indeed, preliminary investigations have reported that targeted cleavage of TDP-43 by caspase 3 results in reduced TDP-43 aggregation [Figure 1]. This study also demonstrated that cleavage-resistant forms of TDP-43 were more toxic than the resulting cleavage products, suggesting that caspase mediated degradation is critical for reducing TDP-43 toxicity and perhaps limiting the advent of ALS [57]. As

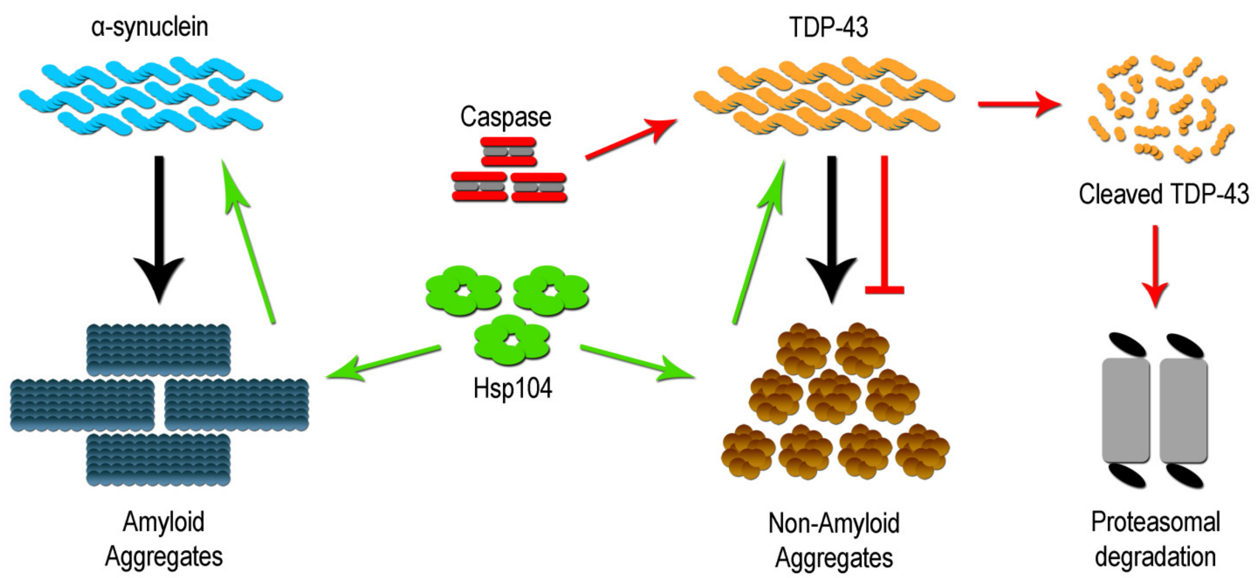

FIGURE 1: Therapeutic strategies to limit protein aggregation based disorders. Many neurodegeneration disorders are characterized by increased protein aggregation of diseased associated proteins like α-synuclein and TDP-43. The yeast specific disaggregase Hsp104 and its variants (green) have been shown to be an effective in limiting inclusion formation and accumulation. Hsp104 acts on the inclusion to dissolve and restore them to the properly folded soluble form (TDP-43) as well as eliminate toxic soluble oligomeric forms (α-synuclein) of the protein. Additionally, caspase/metacaspase family of proteases (red) have also been shown to limit inclusion formation by directly cleaving the disease associated protein (TDP-43), which is subsequently degraded by the proteasome.

such, the elevation of effector caspase activation in diseased cells may simply reflect an adaptive response whereby caspases engage to limit deposition or expansion of toxic aggregates. If one makes the reasonable assumption that caspase enzymes have retained the yeast metacaspase function through evolution, then a probable model would predict that caspases similarly integrate with chaperones and folding/refolding machinery to restrain aggregate deposition and growth.

CONCLUSION

In conclusion, we have demonstrated that deployment of the yeast model has provided exceptional advances in the study of neurodegenerative disorders including PD and ALS. Similar concerted efforts using yeast proteinopathy models have advanced understanding of disease related proteins such as tau, Aβ and prions. Likewise, the concept that yeast specific proteins, such as Hsp104 and/or Yca1, may be engineered to combat toxic human aggregates opens the door to entirely novel avenues of therapeutic intervention. The use of yeast proteins as therapeutic agents needs to be approached with considerable caution, yet the early studies in relevant animal models support the basic premise. Clearly, the ease and flexibility of the yeast model will ensure continued use of this eukaryotic cell as a preferred means to interrogate and define the molecular pathology of neurodegeneration.

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CONFLICT OF INTEREST

The author declares no conflict of interest.

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REFERENCES

1. Hartl FU, Bracher A, Hayer-Hartl M (**2011**). Molecular chaperones in protein folding and proteostasis. **Nature** 475(7356): 324-332.

2. Winkler J, Tyedmers J, Bukau B, Mogk A (**2012**). Chaperone networks in protein disaggregation and prion propagation. **Journal of structural biology** 179(2): 152-160.

3. Morimoto RI (**2008**). Proteotoxic stress and inducible chaperone networks in neurodegenerative disease and aging. **Genes & development** 22(11): 1427-1438.

4. Tyedmers J, Mogk A, Bukau B (**2010**). Cellular strategies for controlling protein aggregation. **Nature reviews Molecular cell biology** 11(11): 777-788.

5. Ross CA, Poirier MA (**2004**). Protein aggregation and neurodegenerative disease. **Nature medicine** 10 Suppl:S10-17.

6. Neumann M, Sampathu DM, Kwong LK, Truax AC, Micsenyi MC, Chou TT, Bruce J, Schuck T, Grossman M, Clark CM, McCluskey LF, Miller BL, Masliah E, Mackenzie IR, Feldman H, Feiden W, Kretzschmar HA, Trojanowski JQ, Lee VM (**2006**). Ubiquitinated TDP-43 in frontotemporal lobar degeneration and amyotrophic lateral sclerosis. **Science** 314(5796): 130-133.

7. Hay DG, Sathasivam K, Tobaben S, Stahl B, Marber M, Mestril R, Mahal A, Smith DL, Woodman B, Bates GP (**2004**). Progressive decrease in chaperone protein levels in a mouse model of Huntington's disease and induction of stress proteins as a therapeutic approach. **Human molecular genetics** 13(13): 1389-1405.

8. Polymenidou M, Cleveland DW (**2012**). Prion-like spread of protein aggregates in neurodegeneration. **The Journal of experimental medicine** 209(5): 889-893.

9. Figley MD, Gitler AD (**2013**). Yeast genetic screen reveals novel therapeutic strategy for ALS. **Rare diseases** 1:e24420.

10. Tenreiro S, Munder MC, Alberti S, Outeiro TF (**2013**). Harnessing the power of yeast to unravel the molecular basis of neurodegeneration. **Journal of neurochemistry** 127(4): 438-452.

11. Braun RJ, Buttner S, Ring J, Kroemer G, Madeo F (**2010**). Nervous yeast: modeling neurotoxic cell death. **Trends in biochemical sciences** 35(3): 135-144.

12. Braun RJ (**2015**). Ubiquitin-dependent proteolysis in yeast cells expressing neurotoxic proteins. **Frontiers in molecular neuroscience** 8:8.

13. Lashuel HA, Overk CR, Oueslati A, Masliah E (**2013**). The many faces of alpha-synuclein: from structure and toxicity to therapeutic target. **Nature reviews Neuroscience** 14(1): 38-48.

14. Alberti S, Halfmann R, King O, Kapila A, Lindquist S (**2009**). A systematic survey identifies prions and illuminates sequence features of prionogenic proteins. **Cell** 137(1): 146-158.

15. Outeiro TF, Lindquist S (**2003**). Yeast cells provide insight into alpha-synuclein biology and pathobiology. **Science** 302(5651): 1772-1775.

16. Buttner S, Bitto A, Ring J, Augsten M, Zabrocki P, Eisenberg T, Jungwirth H, Hutter S, Carmona-Gutierrez D, Kroemer G, Winderickx J, Madeo F (**2008**). Functional mitochondria are required for alpha-synuclein toxicity in aging yeast. **The Journal of biological chemistry** 283(12): 7554-7560.

17. Cooper AA, Gitler AD, Cashikar A, Haynes CM, Hill KJ, Bhullar B, Liu K, Xu K, Strathearn KE, Liu F, Cao S, Caldwell KA, Caldwell GA, Marsischky G, Kolodner RD, Labaer J, Rochet JC, Bonini NM, Lindquist S (**2006**). Alpha-synuclein blocks ER-Golgi traffic and Rab1 rescues neuron loss in Parkinson's models. **Science** 313(5785): 324-328.

18. Gitler AD, Bevis BJ, Shorter J, Strathearn KE, Hamamichi S, Su LJ, Caldwell KA, Caldwell GA, Rochet JC, McCaffery JM, Barlowe C, Lindquist S (**2008**). The Parkinson's disease protein alpha-synuclein disrupts cellular Rab homeostasis. **Proceedings of the National Academy of Sciences of the United States of America** 105(1): 145-150.

19. Rendon WO, Martinez-Alonso E, Tomas M, Martinez-Martinez N, Martinez-Menarguez JA (**2013**). Golgi fragmentation is Rab and SNARE dependent in cellular models of Parkinson's disease. **Histochemistry and cell biology** 139(5): 671-684.

20. Buttner S, Habernig L, Broeskamp F, Ruli D, Vogtle FN, Vlachos M, Macchi F, Kuttner V, Carmona-Gutierrez D, Eisenberg T, Ring J, Markaki M, Taskin AA, Benke S, Ruckenstuhl C, Braun R, Van den Haute C, Bammens T, van der Perren A, Frohlich KU, Winderickx J, Kroemer G, Baekelandt V, Tavernarakis N, Kovacs GG, Dengjel J, Meisinger C, Sigrist SJ, Madeo F (**2013**). Endonuclease G mediates alpha-synuclein cytotoxicity during Parkinson's disease. **The EMBO journal** 32(23): 3041-3054.

21. Vilarino-Guell C, Wider C, Ross OA, Dachsel JC, Kachergus JM, Lincoln SJ, Soto-Ortolaza AI, Cobb SA, Wilhoite GJ, Bacon JA, Behrouz B, Melrose HL, Hentati E, Puschmann A, Evans DM, Conibear E, Wasserman WW, Aasly JO, Burkhard PR, Djaldetti R, Ghika J, Hentati F, Krygowska-Wajs A, Lynch T, Melamed E, Rajput A, Rajput AH, Solida A, Wu RM, Uitti RJ, et al. (**2011**). VPS35 mutations in Parkinson disease. **American journal of human genetics** 89(1): 162-167.

22. Chartier-Harlin MC, Dachsel JC, Vilarino-Guell C, Lincoln SJ, Lepretre F, Hulihan MM, Kachergus J, Milnerwood AJ, Tapia L, Song MS, Le Rhun E, Mutez E, Larvor L, Duflot A, Vanbesien-Mailliot C, Kreisler A, Ross OA, Nishioka K, Soto-Ortolaza AI, Cobb SA, Melrose HL, Behrouz B, Keeling BH, Bacon JA, Hentati E, Williams L, Yanagiya A, Sonenberg N, Lockhart PJ, Zubair AC, et al. (**2011**). Translation initiator EIF4G1 mutations in familial Parkinson disease. **American journal of human genetics** 89(3): 398-406.

23. Dhungel N, Eleuteri S, Li LB, Kramer NJ, Chartron JW, Spencer B, Kosberg K, Fields JA, Stafa K, Adame A, Lashuel H, Frydman J, Shen K, Masliah E, Gitler AD (**2015**). Parkinson's disease genes VPS35 and EIF4G1 interact genetically and converge on alpha-synuclein. **Neuron** 85(1): 76-87.

24. Alami NH, Smith RB, Carrasco MA, Williams LA, Winborn CS, Han SS, Kiskinis E, Winborn B, Freibaum BD, Kanagaraj A, Clare AJ, Badders NM, Bilican B, Chaum E, Chandran S, Shaw CE, Eggan KC, Maniatis T, Taylor JP (**2014**). Axonal transport of TDP-43 mRNA granules is impaired by ALS-causing mutations. **Neuron** 81(3): 536-543.

25. Geser F, Martinez-Lage M, Kwong LK, Lee VM, Trojanowski JQ (**2009**). Amyotrophic lateral sclerosis, frontotemporal dementia and beyond: the TDP-43 diseases. **Journal of neurology** 256(8): 1205-1214.

26. Johnson BS, McCaffery JM, Lindquist S, Gitler AD (**2008**). A yeast TDP-43 proteinopathy model: Exploring the molecular determinants of TDP-43 aggregation and cellular toxicity. **Proceedings of the National Academy of Sciences of the United States of America** 105(17): 6439-6444.

27. Johnson BS, Snead D, Lee JJ, McCaffery JM, Shorter J, Gitler AD (**2009**). TDP-43 is intrinsically aggregation-prone, and amyotrophic lateral sclerosis-linked mutations accelerate aggregation and increase toxicity. **The Journal of biological chemistry** 284(30): 20329-20339.

28. Braun RJ, Sommer C, Carmona-Gutierrez D, Khoury CM, Ring J, Buttner S, Madeo F (**2011**). Neurotoxic 43-kDa TAR DNA-binding protein (TDP-43) triggers mitochondrion-dependent programmed cell death in yeast. **The Journal of biological chemistry** 286(22): 19958-19972.

29. Elden AC, Kim HJ, Hart MP, Chen-Plotkin AS, Johnson BS, Fang X, Armakola M, Geser F, Greene R, Lu MM, Padmanabhan A, Clay-Falcone D, McCluskey L, Elman L, Juhr D, Gruber PJ, Rub U, Auburger G, Trojanowski JQ, Lee VM, Van Deerlin VM, Bonini NM, Gitler AD (**2010**). Ataxin-2 intermediate-length polyglutamine expansions are associated with increased risk for ALS. **Nature** 466(7310): 1069-1075.

30. Kim HJ, Raphael AR, LaDow ES, McGurk L, Weber RA, Trojanowski JQ, Lee VM, Finkbeiner S, Gitler AD, Bonini NM (**2014**). Therapeutic modulation of eIF2alpha phosphorylation rescues TDP-43 toxicity in amyotrophic lateral sclerosis disease models. **Nature genetics** 46(2): 152-160.

31. Armakola M, Higgins MJ, Figley MD, Barmada SJ, Scarborough EA, Diaz Z, Fang X, Shorter J, Krogan NJ, Finkbeiner S, Farese RV, Jr., Gitler AD (**2012**). Inhibition of RNA lariat debranching enzyme suppresses TDP-43 toxicity in ALS disease models. **Nature genetics** 44(12): 1302-1309.

32. King OD, Gitler AD, Shorter J (**2012**). The tip of the iceberg: RNA-binding proteins with prion-like domains in neurodegenerative disease. **Brain research** 1462:61-80.

33. Couthouis J, Hart MP, Shorter J, DeJesus-Hernandez M, Erion R, Oristano R, Liu AX, Ramos D, Jethava N, Hosangadi D, Epstein J, Chiang A, Diaz Z, Nakaya T, Ibrahim F, Kim HJ, Solski JA, Williams KL, Mojsilovic-Petrovic J, Ingre C, Boylan K, Graff-Radford NR, Dickson DW, Clay-Falcone D, Elman L, McCluskey L, Greene R, Kalb RG, Lee VM, Trojanowski JQ, et al. (**2011**). A yeast functional screen predicts new candidate ALS disease genes. **Proceedings of the National Academy of Sciences of the United States of America** 108(52): 20881-20890.

34. Kim HJ, Kim NC, Wang YD, Scarborough EA, Moore J, Diaz Z, MacLea KS, Freibaum B, Li S, Molliex A, Kanagaraj AP, Carter R, Boylan KB, Wojtas AM, Rademakers R, Pinkus JL, Greenberg SA, Trojanowski JQ, Traynor BJ, Smith BN, Topp S, Gkazi AS, Miller J, Shaw CE, Kottlors M, Kirschner J, Pestronk A, Li YR, Ford AF, Gitler AD, et al. (**2013**). Mutations in prion-like domains in hnRNPA2B1 and hnRNPA1 cause multisystem proteinopathy and ALS. **Nature** 495(7442): 467-473.

35. Figley MD, Bieri G, Kolaitis RM, Taylor JP, Gitler AD (**2014**). Profilin 1 associates with stress granules and ALS-linked mutations alter stress granule dynamics. **The Journal of neuroscience : the official journal of the Society for Neuroscience** 34(24): 8083-8097.

36. Braun RJ, Sommer C, Leibiger C, Gentier RJ, Dumit VI, Paduch K, Eisenberg T, Habernig L, Trausinger G, Magnes C, Pieber T, Sinner F, Dengjel J, van Leeuwen FW, Kroemer G, Madeo F (**2015**). Accumulation of Basic Amino Acids at Mitochondria Dictates the Cytotoxicity of Aberrant Ubiquitin. **Cell reports**.

37. Jackrel ME, Shorter J (**2015**). Engineering enhanced protein disaggregases for neurodegenerative disease. **Prion** 9(2): 90-109.

38. Desantis ME, Shorter J (**2012**). The elusive middle domain of Hsp104 and ClpB: location and function. **Biochimica et biophysica acta** 1823(1): 29-39.

39. Vashist S, Cushman M, Shorter J (**2010**). Applying Hsp104 to protein-misfolding disorders. **Biochemistry and cell biology = Biochimie et biologie cellulaire** 88(1): 1-13.

40. Lo Bianco C, Shorter J, Regulier E, Lashuel H, Iwatsubo T, Lindquist S, Aebischer P (**2008**). Hsp104 antagonizes alpha-synuclein aggregation and reduces dopaminergic degeneration in a rat model of Parkinson disease. **The Journal of clinical investigation** 118(9): 3087-3097.

41. Duennwald ML, Echeverria A, Shorter J (**2012**). Small heat shock proteins potentiate amyloid dissolution by protein disaggregases from yeast and humans. **PLoS biology** 10(6): e1001346.

42. Jackrel ME, DeSantis ME, Martinez BA, Castellano LM, Stewart RM, Caldwell KA, Caldwell GA, Shorter J (**2014**). Potentiated Hsp104 variants antagonize diverse proteotoxic misfolding events. **Cell** 156(1-2): 170-182.

43. Jackrel ME, Shorter J (**2014**). Potentiated Hsp104 variants suppress toxicity of diverse neurodegenerative disease-linked proteins. **Disease models & mechanisms** 7(10): 1175-1184.

44. Dick SA, Megeney LA (**2013**). Cell death proteins: an evolutionary role in cellular adaptation before the advent of apoptosis. **BioEssays : news and reviews in molecular, cellular and developmental biology** 35(11): 974-983.

45. Kuranaga E (**2012**). Beyond apoptosis: caspase regulatory mechanisms and functions in vivo. **Genes to cells : devoted to molecular & cellular mechanisms** 17(2): 83-97.

46. Lee RE, Brunette S, Puente LG, Megeney LA (**2010**). Metacaspase Yca1 is required for clearance of insoluble protein aggregates. **Proceedings of the National Academy of Sciences of the United States of America** 107(30): 13348-13353.

47. Lee RE, Puente LG, Kaern M, Megeney LA (**2008**). A non-death role of the yeast metacaspase: Yca1p alters cell cycle dynamics. **PloS one** 3(8): e2956.

48. Shrestha A, Puente LG, Brunette S, Megeney LA (**2013**). The role of Yca1 in proteostasis. Yca1 regulates the composition of the insoluble proteome. **Journal of proteomics** 81:24-30.

49. Hill SM, Hao X, Liu B, Nystrom T (**2014**). Life-span extension by a metacaspase in the yeast Saccharomyces cerevisiae. **Science** 344(6190): 1389-1392.

50. Vacher C, Garcia-Oroz L, Rubinsztein DC (**2005**). Overexpression of yeast hsp104 reduces polyglutamine aggregation and prolongs survival of a transgenic mouse model of Huntington's disease. **Human molecular genetics** 14(22): 3425-3433.

51. Perrin V, Regulier E, Abbas-Terki T, Hassig R, Brouillet E, Aebischer P, Luthi-Carter R, Deglon N (**2007**). Neuroprotection by Hsp104 and Hsp27 in lentiviral-based rat models of Huntington's disease. **Molecular therapy : the journal of the American Society of Gene Therapy** 15(5): 903-911.

52. Shimohama S, Tanino H, Fujimoto S (**1999**). Changes in caspase expression in Alzheimer's disease: comparison with development and aging. **Biochemical and biophysical research communications** 256(2): 381-384.

53. LeBlanc A, Liu H, Goodyer C, Bergeron C, Hammond J (**1999**). Caspase-6 role in apoptosis of human neurons, amyloidogenesis, and Alzheimer's disease. **The Journal of biological chemistry** 274(33): 23426-23436.

54. LeBlanc AC (**2013**). Caspase-6 as a novel early target in the treatment of Alzheimer's disease. **The European journal of neuroscience** 37(12): 2005-2018.

55. D'Amelio M, Sheng M, Cecconi F (**2012**). Caspase-3 in the central nervous system: beyond apoptosis. **Trends in neurosciences** 35(11): 700-709.

56. McLaughlin B, Hartnett KA, Erhardt JA, Legos JJ, White RF, Barone FC, Aizenman E (**2003**). Caspase 3 activation is essential for neuroprotection in preconditioning. **Proceedings of the National Academy of Sciences of the United States of America** 100(2): 715-720.

57. Suzuki H, Lee K, Matsuoka M (**2011**). TDP-43-induced death is associated with altered regulation of BIM and Bcl-xL and attenuated by caspase-mediated TDP-43 cleavage. **The Journal of biological chemistry** 286(15): 13171-13183.