Supplemental Information

Supplementary methods

Liquid chromatography/Mass spectrometry

NanoLC-MS/MS was performed using a nanoACQUITY ultra performance liquid chromatography (UPLC®) system (Waters, Milford, MA, USA) coupled to a maXis 4G Q-TOF mass spectrometer (BrukerDaltonics, Bremen, Germany). The system was fully controlled by HyStar 3.2 (BrukerDaltonics). The UPLC system was equipped with a Symmetry C18 precolumn (20 x 0.18 mm, 5 µm particle size, Waters, Milford, USA) and an ACQUITY UPLC® BEH130 C18 separation column (75 µm × 200 mm, 1.7 µm particle size, Waters). The solvent system consisted of 0.1 % formic acid in water (solvent A) and 0.1 % formic acid in acetonitrile (solvent B). 3 µL of each sample was injected. Peptides were trapped during 1 min at 15 µL/min with 99 % A and 1 % B. Elution was performed at 60 °C at a flow rate of 450 nL/min, using a linear gradient of 6-35 % B over 28 minutes. The mass spectrometer was operating in positive mode, with the following settings: source temperature was set to 160°C while dry gas flow was at 5 liter per minute. The nanoelectrospray voltage was optimized to −5000 V. External mass calibration of the TOF was achieved before each set of analyses using Tuning Mix (Agilent Technologies, Paolo Alto, USA) in the mass range of 322-2722 m/z. Mass correction was achieved by recalibration of acquired spectra to the applied lock masses (methylstearate ($[M+H]^+$ 299.2945 m/z) and hexakis(2,2,3,3,-tetrafluoropropoxy) phosphazine ($[M+H]^+$ 922.0098 m/z)). For tandem MS experiments, the system was operated with automatic switching between MS and MS/MS modes in the range of 100-2500 m/z (MS acquisition time of 0.4 s, MS/MS acquisition time between 0.05 s (intensity > 250000) and 1.25 s (intensity <5000)). The 6 most abundant ions (absolute intensity threshold of 1500, were selected from each MS spectrum for further isolation and CID fragmentation using nitrogen as collision gas. Ions were excluded after acquisition of one MS/MS spectrum and the exclusion was released after 0.2 minutes.

MS/MS data interpretation

The peak list has been searched against a Swiss Prot-derived combined target-decoy database created 2012-07-18, containing 7901 target sequences plus the same number of reversed decoy sequences) using Mascot (version 2.4.1, Matrix science, London, England). The database contained sequences of human proteins including common contaminants (human keratins and porcine trypsin) and was created using an in-house database generation toolbox (http://msda.u-strasbg.fr). During database search, up to one missed cleavage by trypsin and three variable modifications (oxidation of Methionine (+16 Da), carbamidomethylation of Cysteine (+57 Da) and acetylation n-ter (+42 Da), were considered. The search window was set to 10 ppm for precursor ions and 0.02 Da for fragment ions. Mascot result files (.dat) were imported into Scaffold 3 software (version 3.6.5; Proteome Software Inc., Portland, OR, USA) and filtering criteria based on probability-based scoring of the identified peptides were taken into account: peptide having an ion score > minus identity score above -40 and a Mascot Ion score > 25 were validated. The false discovery rate (FDR) was calculated to be <1 % based on the number of decoy hits.

Supplemental Tables

Table S1: Yeast strains used in this study.

Name	Genotype	Ref
Y131	MATa ura3-1 trp1-1 leu2-3_112 his3-11_15 ade2-1 can1-100 *hta1-htb1*::*LEU2 hta2-htb2*::URA3 pRS426-*HTA1-HTB1*	(Robzyk et al. 2000)
Y133	isogenic to Y131, pRS426-*hta1-htb1-K123R*	(Robzyk et al. 2000)
Y131 Prp42-HA	isogenic to Y131, *PRP42-HA-HIS*	This study
Y133 Prp42-HA	isogenic to Y133, *PRP42-HA-HIS*	This study
Y131 Lea1-HA	isogenic to Y131, *LEA1-HA-HIS*	This study
Y133 Lea1-HA	isogenic to Y133, *LEA1-HA-HIS*	This study
Y131 Cbc2-TAP	isogenic to Y131, *CBC2-TAP-TRP*	This study
Y133 Cbc2-TAP	isogenic to Y133, *CBC2-TAP-TRP*	This study
Y131 Cbc2-TAP Prp42-HA	isogenic to Y131, *CBC2-TAP-TRP, PRP42-HA-HIS*	This study
Y133 Cbc2-TAP Prp42-HA	isogenic to Y133, *CBC2-TAP-TRP, PRP42-HA-HIS*	This study
Y131 Cbc2-TAP Lea1-HA	isogenic to Y131, *CBC2-TAP-TRP, LEA1-HA-HIS*	This study
Y133 Cbc2-TAP Lea1-HA	isogenic to Y133, *CBC2-TAP-TRP, LEA1-HA-HIS*	This study
W303	MATa ura3-52 trp1D2 leu2-3_112 his3-11 ade2-1 can1-100	
W303 *set1Δ*	isogenic to W303, *set1::KANMX*	This study
W303 *set2Δ*	isogenic to W303, *set2::KANMX*	This study
W303 *bre1Δ*	isogenic to W303*, bre1::KANMX*	This study
W303 Prp42-HA	isogenic to W303*, PRP42-HA-HIS*	This study
W303 *set1Δ* Prp42-HA	isogenic to W303, *set1::KANMX, PRP42-HA-HIS*	This study
W303 *set2Δ* Prp42-HA	isogenic to W303, *set2::KANMX, PRP42-HA-HIS*	This study
W303 *dot1Δ* Prp42-HA	isogenic to W303, *dot1::KANMX, PRP42-HA-HIS*	This study
W303 Cbc2-TAP Prp42-HA	isogenic to W303, *CBC2-TAP-TRP, PRP42-HA-HIS*	This study
W303 *set1Δ* Cbc2-TAP Prp42-HA	isogenic to W303, *set1::KANMX, CBC2-TAP-TRP, PRP42-HA-HIS*	This study

Table S2: Oligonucleotides used in this study.

Name	Sequences	Ref
RPS21B5'UTRf s1	CGAATCTCGGCTCTGTATAATG	(Kress et al. 2008)
RPS21Bexon1r s1	CCATTTTGGCTTATTGATATTCTTTT	(Kress et al. 2008)
RPS21BIntronF3s2	TCCGAATTAGTGGGTTTCCA	(Kress et al. 2008)
RPS21BIntronR3s2	TCAATGTTAGTACATTTGCGCTTA	(Kress et al. 2008)
RPS21BIntronF1s3	AATCATCAAAGCCGATGACC	(Kress et al. 2008)
RPS21BIntronR1s3	CATCGGATTCACCTCTGGAT	(Kress et al. 2008)
RPS21bExon2-2s4	ATCCAGAGGTGAATCCGATG	(Kress et al. 2008)
RPS21b3'UTR-2s4	AACGACTTCCCCTCTTCTTTTT	(Kress et al. 2008)
HNT1 5' s1 F	GCACGCCTTCCAGACTTTTA	this study
HNT1 5' s1 R	TACAGGCAGCATCAAGCGTA	this study
HNT1 Int s2 F	CTTACACTCACACCAATGATGG	this study
HNT1 Intr s2 R	AGGATGGAATTTCGCCTGTT	this study
HNT1 Ex s3 F	ATCCCGGACGAATTCCTTAC	this study
HNT1 Ex s3 R	AAATGGAAGTGGACGTGGTC	this study
RPL14B intron f	AGGGCCGGAGATGTTTCTAT	this study
RPL14B intron r	TGGCAATTGAGGAGGTATGG	this study
RPL14B exon f	ATGGTCCAAAAGCTGGTGTC	this study
RPL14B exon r	GATGAAGCAGCCCACTTTTC	this study
RPL34B intron f	GTTAAAAGGCGAACGAGTGC	this study
RPL34B intron r	CTGGATACTGTTCGTTCATGCT	this study
RPL34B exon f	CTTTGAGACCAAGACAATACGC	this study
RPL34B exon r	GCAGCCTCAGTTTGTTCCTT	this study
Intergenic IV F	CGCATTACCAGACGGAGATGT	(Vitaliano-Prunier et al. 2012)
Intergenic IV R	CAAGCAAGCCTTGTGCATAAGA	(Vitaliano-Prunier et al. 2012)

Supplementary Table 3 - Results of Splicing Microarrays

Log2 change in indicated genotype versus isogenic wild-type for each gene feature

Genotype:		*bre1*Δ	*bre1*Δ	*bre1*Δ
Strains compared:		W303 *bre1*Δ vs W303	W303 *bre1*Δ vs W303	W303 *bre1*Δ vs W303
Feature:		Exon	Intron	Junction
Systematic Name	Common Name			
SNR17A	SNR17A	0,034982246	0,863646606	1,161525056
SNR17B	SNR17B	0,290145197	0,877674138	1,161525056
YAL001C	TFC3: transcription initiation from RNA polymerase III promoter	0,202851075	0,049569878	0,073828287
YAL003W	EFB1: translational elongation	-0,324738575	0,541959398	-0,02859616
YAL030W	SNC1: endocytosis	-0,141626155	-0,021987833	-0,644917808
YBL018C	POP8: rRNA processing	-0,057776011	-0,088204903	-0,409384719
YBL026W	LSM2: nuclear mRNA splicing, via spliceosome	0,568674706	0,802601822	0,053133311
YBL027W	RPL19B: protein biosynthesis	-0,488533725	0,128093386	0,031888437
YBL040C	ERD2: protein retention in ER	0,111929436	0,427157871	-0,144240846
YBL050W	SEC17: ER to Golgi transport	0,036537983	0,609634501	-0,22935552
YBL059C-A	YBL059C-A: biological process unknown	0,278681258	0,436697317	0,09452826
YBL059W	YBL059W: biological process unknown	0,387898479	0,1974097	0,092071388
YBL072C	RPS8A: protein biosynthesis	-0,632281443	0,151712384	-0,616208134
YBL087C	RPL23A: protein biosynthesis	-0,76915381	0,110983962	-1,083003564
YBL091C-A	SCS22: biological process unknown	-0,032450816	0,439274829	-0,126928129
YBL092W	RPL32: protein biosynthesis	-0,565354945	0,044278553	-0,711860814
YBR048W	RPS11B: protein biosynthesis	-0,476540003	0,104889838	-0,343149672
YBR078W	ECM33: cell wall organization and biogenesis	0,43388661	0,370796912	0,040686244
YBR082C	UBC4: response to stress	-0,098765558	0,919426428	-0,063851368
YBR084C-A	RPL19A: protein biosynthesis	-0,636063743	0,019975356	-0,007029668

YBR089C-A	NHP6B: regulation of transcription from RNA polymerase II promot	1,012671733	0,290547787	-0,023258089
YBR119W	MUD1: nuclear mRNA splicing, via spliceosome	-0,36142838	-0,026043544	-0,280156774
YBR181C	RPS6B: protein biosynthesis	-0,210363308	-0,054158193	-1,432990494
YBR186W	PCH2: regulation of meiosis	0,552096385	0,123849745	0,03789808
YBR189W	RPS9B: protein biosynthesis	-0,958802875	-0,371199444	-0,516377294
YBR191W	RPL21A: protein biosynthesis	-1,197163767	-0,177777577	-0,068520524
YBR219C	YBR219C: biological process unknown	0,576713108	0,125288709	0,109121695
YBR230C	YBR230C: biological process unknown	-0,791137462	0,255542929	-0,388830773
YCR028C-A	RIM1: mitochondrial genome maintenance	-0,544484803	-0,006549073	-0,485101308
YCR031C	RPS14A: protein biosynthesis	-0,304467775	-0,555447491	-1,310566198
YCR097W	HMRA1: regulation of transcription, mating-type specific	0,150843777	-0,04312638	0,072480249
YCR097W_2	HMRA1: regulation of transcription, mating-type specific	0,150843777	0,016672004	-0,074764503
YDL012C	YDL012C: biological process unknown	0,519821891	0,826075074	0,059971686
YDL029W	ARP2: actin filament organization	-0,335583362	0,692434787	0,046119329
YDL061C	RPS29B: protein biosynthesis	-0,226830934	-0,131933571	0,039898141
YDL064W	UBC9: G2/M transition of mitotic cell cycle	-0,250954339	-0,028594333	0,132096346
YDL075W	RPL31A: protein biosynthesis	-0,997624656	-0,175862947	-1,006865584
YDL079C	MRK1: protein amino acid phosphorylation	0,054832447	-0,282604346	0,066384582
YDL082W	RPL13A: protein biosynthesis	-0,793204574	-0,268003895	-0,068315536
YDL083C	RPS16B: protein biosynthesis	-0,846493744	-0,445057033	-0,397537957
YDL108W	KIN28: protein amino acid phosphorylation	0,121565052	0,004544094	0,152929926
YDL115C	IWR1: meiosis	0,219957355	0,180821876	0,072151391
YDL125C	HNT1: nucleotide metabolism	0,572389318	0,935682952	-0,081409964
YDL130W	RPP1B: translational elongation	-0,010048775	-0,16478897	0,132929029
YDL136W	RPL35B: protein biosynthesis	-0,722275514	-0,108704229	-0,066405723
YDL137W	ARF2: ER to Golgi transport	-0,122399914	0,585368517	-0,913947099
YDL189W	RBS1: galactose metabolism	-0,331837738	-0,321978985	0,040116261
YDL191W	RPL35A: protein biosynthesis	-0,545011228	-0,094207261	0,014899093
YDL219W	DTD1: translation	-0,160998698	0,240805319	-0,634319088
YDR005C	MAF1: negative regulation of transcription from RNA polymerase II	0,284646447	0,305578391	0,038764566

YDR025W	RPS11A: protein biosynthesis	0,178973103	-0,068685405	-0,076143528
YDR059C	UBC5: endocytosis	0,48582988	0,383371258	-0,031605937
YDR064W	RPS13: protein biosynthesis	-0,628692093	-0,539268754	-1,006233353
YDR092W	UBC13: protein monoubiquitination	0,151128421	0,357215284	0,03137802
YDR129C	SAC6: endocytosis	0,461827561	0,314573346	0,063065069
YDR139C	RUB1: protein deneddylation	0,327719093	-0,05404045	-0,056496807
YDR305C	HNT2: nucleoside catabolism	0,16067356	0,280318191	-0,210011758
YDR367W	YDR367W: biological process unknown	-0,294011024	-0,127845124	-0,081470914
YDR381W	YRA1: mRNA-nucleus export	0,730726427	0,434352123	-0,431939533
YDR397C	NCB2: negative regulation of transcription from RNA polymerase II	-0,346112293	-0,172262787	0,156246563
YDR424C	DYN2: microtubule-based process	0,093066621	0,265574883	-0,004309983
YDR424C_2	DYN2: microtubule-based process	0,093066621	0,132976724	0,095770992
YDR447C	RPS17B: protein biosynthesis	-0,42604652	0,02274138	-0,61802476
YDR450W	RPS18A: protein biosynthesis	-0,790696423	-0,0825671	-0,051147076
YDR471W	RPL27B: protein biosynthesis	-0,466208755	0,103327298	-0,549157557
YDR500C	RPL37B: protein biosynthesis	-0,183125949	-0,122217448	-0,032947287
YEL012W	UBC8: protein monoubiquitination	0,239707881	0,097118251	0,002297743
YER003C	PMI40: protein amino acid glycosylation	-0,031928549	0,171840295	0,033342481
YER007C-A	RBF20: biological process unknown	-0,50867327	-0,07400885	-0,603375098
YER044C-A	MEI4: sporulation (sensu Fungi)	0,037441601	0,250868519	0,024009735
YER056C-A	RPL34A: protein biosynthesis	0,228368048	0,439986197	-0,125488032
YER074W	RPS24A: protein biosynthesis	0,234757582	-0,084677252	-0,171535609
YER074W-A	YOS1: ER to Golgi transport	-0,2143673	0,101990039	0,000742495
YER074W-A_2	YOS1: ER to Golgi transport	-0,2143673	-0,020512176	0,057623318
YER093C-A	YER093C-A: biological process unknown	-0,093310191	0,121888674	-0,20506316
YER102W	RPS8B: protein biosynthesis	-0,558659852	-0,054229516	-0,739914375
YER117W	RPL23B: protein biosynthesis	-0,302266576	-0,459996827	-0,030698701
YER131W	RPS26B: protein biosynthesis	-0,454730659	0,288285167	0,186031669
YER133W	GLC7: 35S primary transcript processing	0,193126354	0,867965806	-0,392807086
YER179W	DMC1: meiosis	0,399818521	-0,057091204	0,226869605

YFL034C-A	RPL22B: protein biosynthesis	-0,252040671	-0,261266761	-0,385308025
YFL034C-B	MOB2: protein amino acid phosphorylation	0,20335105	0,210858162	-0,07188022
YFL039C	ACT1: cell wall organization and biogenesis	0,633181522	1,221989781	0,306566377
YFR024C-A	LSB3: actin filament organization	0,155768669	-0,042789755	-0,118063131
YFR031C-A	RPL2A: protein biosynthesis	-0,52290442	-0,079796008	-0,400995542
YFR032C-A	RPL29: protein biosynthesis	0,024306205	0,271602023	-0,086252233
YGL030W	RPL30: protein biosynthesis	-0,356521511	-0,295890368	-0,747657995
YGL031C	RPL24A: protein biosynthesis	-0,535579126	-0,051786396	0,059403077
YGL033W	HOP2: synapsis	-0,043903077	-0,11461041	-0,035532777
YGL076C	RPL7A: protein biosynthesis	-0,258970605	0,051449697	-0,21503872
YGL076C_2	RPL7A: protein biosynthesis	-0,258970605	-0,032113518	-0,477779643
YGL087C	MMS2: DNA repair	-0,009543289	0,122333345	-0,380168355
YGL103W	RPL28: protein biosynthesis	-0,190443788	-0,089496657	-0,04280824
YGL137W	SEC27: ER to Golgi transport	-0,197793325	0,528380111	-0,674805399
YGL178W	MPT5: cell wall organization and biogenesis	0,640521747	1,128423452	0,561167511
YGL187C	COX4: aerobic respiration	-0,55788755	-0,220795103	0,108381754
YGL189C	RPS26A: protein biosynthesis	-0,732115951	-0,002292711	-0,337322251
YGL226C-A	OST5: protein amino acid N-linked glycosylation	0,357544873	0,286775101	0,032451295
YGL232W	TAN1: tRNA modification	-0,032100848	-0,052782221	-0,308099599
YGL251C	HFM1: meiosis	-0,234951988	-0,033836236	0,061361767
YGR001C	YGR001C: biological process unknown	0,049993787	-0,065084934	-0,320054449
YGR001C_2	YGR001C: biological process unknown	0,049993787	-0,027380515	-0,487001651
YGR027C	RPS25A: protein biosynthesis	-0,648496906	-0,035947752	-0,073200899
YGR029W	ERV1: mitochondrion organization and biogenesis	-0,143470845	0,076663575	-0,094470468
YGR118W	RPS23A: protein biosynthesis	-0,606221506	0,010388407	0,02520582
YGR148C	RPL24B: protein biosynthesis	-0,650076569	-0,105598259	-1,123716334
YGR183C	QCR9: aerobic respiration	0,23048141	0,518217507	-0,61961539
YGR214W	RPS0A: protein biosynthesis	0,031575218	-0,006129183	-1,158292234
YGR225W	AMA1: sporulation (sensu Fungi)	0,213049344	0,285393939	0,121140308
YHL001W	RPL14B: protein biosynthesis	-0,434961975	0,283798982	-0,037697456

YHR001W-A	QCR10: aerobic respiration	1,137864375	0,198835774	-0,527691849
YHR010W	RPL27A: protein biosynthesis	-0,130488207	0,226675566	-0,317585999
YHR012W	VPS29: retrograde transport, endosome to Golgi	-0,124701535	-0,093776526	0,0572504
YHR016C	YSC84: endocytosis	0,209726096	0,371093405	0,283315651
YHR021C	RPS27B: protein biosynthesis	-0,230059557	0,064764491	-0,12517346
YHR039C-A	VMA10: vacuolar acidification	-0,061426108	0,235714629	-0,271970281
YHR041C	SRB2: transcription from RNA polymerase II promoter	-0,090537189	0,568304975	0,165794861
YHR077C	NMD2: mRNA catabolism	0,207610995	0,057508119	0,503269585
YHR097C	YHR097C: biological process unknown	0,556152881	0,510529631	0,024909601
YHR101C	BIG1: cell wall biosynthesis (sensu Fungi)	0,208969094	-0,002340069	0,067797803
YHR123W	EPT1: phosphatidylethanolamine biosynthesis	0,19836488	0,40066612	-0,735758313
YHR141C	RPL42B: protein biosynthesis	-0,575117786	-0,071643512	-0,84297566
YHR203C	RPS4B: protein biosynthesis	-0,298809225	-0,257121936	-0,298789015
YIL004C	BET1: ER to Golgi transport	-0,160445789	-0,168163818	-0,126439735
YIL018W	RPL2B: protein biosynthesis	-0,163310923	-0,158577373	-0,153260503
YIL052C	RPL34B: protein biosynthesis	-0,349858729	0,167194036	-0,137291286
YIL069C	RPS24B: protein biosynthesis	-0,357965238	-0,251406372	-0,648859561
YIL106W	MOB1: protein amino acid phosphorylation	0,191409135	0,288419994	-0,074397375
YIL111W	COX5B: mitochondrial electron transport, cytochrome c to oxygen	0,277266045	0,419940738	-0,336878122
YIL133C	RPL16A: protein biosynthesis	-0,144619218	-0,033866301	-0,043555785
YIL148W	RPL40A: protein biosynthesis	-0,574949777	-0,385355146	-1,472426961
YJL001W	PRE3: response to stress	0,001143531	0,03538539	-0,493770551
YJL024C	APS3: vesicle-mediated transport	-0,309275934	0,089123289	0,093230166
YJL041W	NSP1: mRNA-nucleus export	0,282291152	0,266139993	0,272069283
YJL136C	RPS21B: protein biosynthesis	-0,649677445	-0,251878766	-0,057621892
YJL177W	RPL17B: protein biosynthesis	-0,342177925	-0,111520448	0,088754135
YJL189W	RPL39: protein biosynthesis	-0,279694534	-0,220939505	-0,341104461
YJL191W	RPS14B: protein biosynthesis	0,44883612	0,561881587	0,293536392
YJL205C	NCE1: biological process unknown	0,091381169	0,327352493	-0,069415941
YJR021C	REC107: meiotic recombination	0,162227044	0,023448037	0,040569078

YJR094W-A	RPL43B: protein biosynthesis	-0,699311792	0,064878683	-0,832144377
YJR145C	RPS4A: protein biosynthesis	-0,82421542	-0,090673729	-0,355244708
YKL002W	DID4: protein retention in Golgi	0,179274369	0,235416417	0,109303261
YKL006C-A	SFT1: intra-Golgi transport	0,176660683	0,120969058	0,097998494
YKL006W	RPL14A: protein biosynthesis	0,058088724	-0,068771539	-0,27500143
YKL081W	TEF4: translational elongation	-0,360324016	0,197922329	-0,012161548
YKL156W	RPS27A: protein biosynthesis	-0,408824866	0,012779556	-0,210687526
YKL157W	APE2: peptide metabolism	0,446502298	-0,400962291	-0,035610003
YKL180W	RPL17A: protein biosynthesis	-1,109373551	0,069243604	-1,122000999
YKL186C	MTR2: poly(A)+ mRNA-nucleus export	-0,047876992	-0,031981152	-0,053805179
YKL186C_2	MTR2: poly(A)+ mRNA-nucleus export	-0,047876992	0,05502392	0,05334635
YKL186C_3	MTR2: poly(A)+ mRNA-nucleus export	-0,047876992	-0,003306155	0,061339762
YKL186C_4	MTR2: poly(A)+ mRNA-nucleus export	-0,047876992	-0,032320646	-0,124985271
YKL186C_5	MTR2: poly(A)+ mRNA-nucleus export	-0,047876992	0,026791703	0,034890922
YKL186C_6	MTR2: poly(A)+ mRNA-nucleus export	-0,047876992	-0,064290673	-0,029831231
YKL190W	CNB1: cell wall organization and biogenesis	-0,255355584	0,243069933	0,060360423
YKR057W	RPS21A: protein biosynthesis	-1,009820462	0,076128831	-0,308976708
YKR094C	RPL40B: protein biosynthesis	-0,505300079	-0,310522605	-0,29528474
YLL050C	COF1: actin filament organization	-0,644712931	-0,040033145	0,147511112
YLR048W	RPS0B: protein biosynthesis	-0,509679713	-0,008085021	-0,081213785
YLR061W	RPL22A: protein biosynthesis	-0,323307377	-0,012220097	-0,119661069
YLR078C	BOS1: ER to Golgi transport	-0,18011104	-0,113453788	-0,048193038
YLR093C	NYV1: vesicle fusion	0,009077876	0,484638863	-0,159636041
YLR128W	DCN1: protein neddylation	-0,069242451	0,460019903	0,041906816
YLR185W	RPL37A: protein biosynthesis	-1,029617971	-0,193289405	-1,114781542
YLR211C	YLR211C: biological process unknown	0,070155212	0,158846174	0,021071101
YLR275W	SMD2: nuclear mRNA splicing, via spliceosome	-0,154295199	-0,226017382	-0,127884714
YLR287C-A	RPS30A: protein biosynthesis	0,764719371	-0,090508849	-0,239800462
YLR306W	UBC12: protein monoubiquitination	-0,158528378	-0,003409689	-0,134554141
YLR316C	TAD3: tRNA modification	0,144843476	0,009486721	0,114776128

YLR316C_2	TAD3: tRNA modification	0,144843476	-0,017154677	0,068462634
YLR333C	RPS25B: protein biosynthesis	-0,414927812	0,045845477	-0,023561075
YLR344W	RPL26A: protein biosynthesis	-0,975764317	0,135752687	-0,024227098
YLR367W	RPS22B: protein biosynthesis	-0,03782353	-0,088072224	-0,357199728
YLR367W_2	RPS22B: protein biosynthesis	-0,03782353	-0,466114863	-0,843073862
YLR388W	RPS29A: protein biosynthesis	-0,306744291	-0,069124134	-0,661950439
YLR406C	RPL31B: protein biosynthesis	-0,641334812	0,033536592	-1,248135496
YLR426W	YLR426W: biological process unknown	0,398333653	0,348537533	-0,070140422
YLR448W	RPL6B: protein biosynthesis	-0,942963589	-0,20068512	-0,774808761
YML024W	RPS17A: protein biosynthesis	-0,63980227	0,135706951	-0,622338199
YML025C	YML6: protein biosynthesis	-0,103016771	0,027600125	0,019201119
YML026C	RPS18B: protein biosynthesis	-0,50680937	-0,074686431	-0,500272485
YML034W	SRC1: mitotic sister chromatid segregation	0,303567009	0,144168728	-0,068670678
YML034W_2	SRC1: mitotic sister chromatid segregation	0,303567009	0,053313611	0,004279062
YML056C	IMD4: biological process unknown	-0,216141406	0,124921437	-0,483141051
YML067C	ERV41: ER to Golgi transport	0,017477862	0,094332517	-0,846296769
YML073C	RPL6A: protein biosynthesis	-0,990685083	-0,023253422	-0,741328314
YML085C	TUB1: mitotic sister chromatid segregation	-0,172564455	0,258079008	-0,242845938
YML094W	GIM5: tubulin folding	-0,055308907	0,146258954	-0,521991784
YML124C	TUB3: mitotic sister chromatid segregation	0,234045597	0,371645694	-0,236340737
YMR033W	ARP9: chromatin remodeling	0,194822882	0,268047822	-0,326235686
YMR079W	SEC14: sporulation (sensu Fungi)	-0,232627028	-0,126441112	-0,011919236
YMR116C	ASC1: biological process unknown	-1,041718025	-0,054062101	-0,968667324
YMR125W	STO1: nuclear mRNA splicing, via spliceosome	0,082940782	0,250166402	0,033906475
YMR133W	REC114: meiotic recombination	0,158670074	0,178539244	0,061351288
YMR142C	RPL13B: protein biosynthesis	-1,401511223	-0,241755008	-1,645354798
YMR143W	RPS16A: protein biosynthesis	-1,441683052	-0,128970551	-1,14341496
YMR194W	RPL36A: protein biosynthesis	-0,09908923	0,186882598	-0,539447498
YMR201C	RAD14: nucleotide-excision repair, DNA damage recognition	0,056819119	-0,036694366	-0,019784258
YMR225C	MRPL44: protein biosynthesis	-0,191881657	0,09978866	-0,480831679

YMR230W	RPS10B: protein biosynthesis	-0,917903972	-0,220319567	-0,935114845
YMR292W	GOT1: ER to Golgi transport	0,298858546	0,996109885	-0,016227626
YNL012W	SPO1: meiosis	0,50471612	-0,102839961	-0,188651923
YNL044W	YIP3: ER to Golgi transport	0,308966037	0,373021443	-0,019834918
YNL050C	YNL050C: biological process unknown	0,132252864	-0,090101452	0,028910293
YNL069C	RPL16B: protein biosynthesis	-0,556251391	0,005786373	-0,014167879
YNL096C	RPS7B: protein biosynthesis	0,176025306	0,3655022	-0,344091047
YNL112W	DBP2: mRNA catabolism, nonsense-mediated decay	0,282894262	0,529809043	0,562207703
YNL130C	CPT1: phosphatidylcholine biosynthesis	-0,008528604	0,47480777	-0,067035282
YNL147W	LSM7: nuclear mRNA splicing, via spliceosome	0,112899214	0,118747912	-0,174423749
YNL162W	RPL42A: protein biosynthesis	-0,1933077	-0,11001455	-0,899082261
YNL246W	VPS75: protein-vacuolar targeting	-0,021168341	0,130182009	-0,280765425
YNL265C	IST1: protein biosynthesis	-0,100692267	-0,030062461	-0,542470198
YNL301C	RPL18B: protein biosynthesis	-0,272665709	-0,273192875	-0,153572455
YNL302C	RPS19B: protein biosynthesis	-1,224017575	-0,092729353	-0,892021592
YNL312W	RFA2: DNA recombination	0,073537454	0,015063308	-0,00661734
YNR053C	NOG2: ribosome assembly	0,269651309	1,050662924	0,02975042
YOL047C	YOL047C: biological process unknown	0,948555168	0,665820898	0,413123626
YOL048C	YOL048C: biological process unknown	0,07686342	0,064048109	0,431210289
YOL120C	RPL18A: protein biosynthesis	-0,888065163	-0,303770915	-0,310236295
YOL121C	RPS19A: protein biosynthesis	-0,75757508	0,029516485	-0,062676929
YOL127W	RPL25: protein biosynthesis	-0,558037054	0,085394632	-0,513726285
YOR096W	RPS7A: protein biosynthesis	-0,83888377	0,01672735	-1,014154686
YOR122C	PFY1: response to osmotic stress	-0,230853125	0,59638779	0,037127469
YOR182C	RPS30B: protein biosynthesis	-0,117594616	-0,179306173	-0,242277733
YOR234C	RPL33B: protein biosynthesis	-0,133594344	0,232016964	-0,092884312
YOR293W	RPS10A: protein biosynthesis	-0,674476637	0,135221918	-0,674323458
YOR312C	RPL20B: protein biosynthesis	-1,120037724	-0,477230848	-1,436287566
YPL031C	PHO85: protein amino acid phosphorylation	-0,0452194	0,277745652	-0,582385808
YPL075W	GCR1: positive regulation of transcription from RNA polymerase II	0,186955297	-0,309873829	0,016540285

YPL079W	RPL21B: protein biosynthesis	-0,873861365	-0,14067805	-0,061735157
YPL081W	RPS9A: protein biosynthesis	0,019454253	0,083631847	-0,018921872
YPL090C	RPS6A: protein biosynthesis	-0,526854683	-0,181511363	-1,011065718
YPL129W	TAF14: chromatin remodeling	-0,044597021	-0,128541779	-0,024336372
YPL143W	RPL33A: protein biosynthesis	-0,583280709	-0,116895903	-0,01652646
YPL175W	SPT14: GPI anchor biosynthesis	-0,047440799	-0,122927316	-0,035873592
YPL198W	RPL7B: protein biosynthesis	-0,370898149	0,2178283	-0,173180489
YPL198W_2	RPL7B: protein biosynthesis	-0,370898149	0,342334446	-0,221431823
YPL218W	SAR1: ER to Golgi transport	-0,475770339	0,596545805	-0,375767098
YPL241C	CIN2: microtubule-based process	0,255322119	0,209662941	0,072280269
YPL249C-A	RPL36B: protein biosynthesis	-0,843593637	0,367091486	-0,17007721
YPR028W	YOP1: vesicle-mediated transport	-0,3325031	1,290492778	-0,095385103
YPR043W	RPL43A: protein biosynthesis	-0,846806779	0,001810849	-0,551509841
YPR063C	YPR063C: biological process unknown	-0,659284799	0,028645296	-1,255909347
YPR098C	YPR098C: biological process unknown	0,052837743	0,76024146	-0,094743768
YPR132W	RPS23B: protein biosynthesis	-0,156691488	-0,004123436	-1,109517
YPR187W	RPO26: transcription from RNA polymerase II promoter	0,070175415	-0,02626417	0,028208447

Genotype:		*htb1K123R*	*htb1K123R*	*htb1K123R*
Strains compared:		Y133 vs Y131	Y133 vs Y131	Y133 vs Y131
Feature:		Exon	Intron	Junction
Systematic Name	Common Name			
SNR17A	SNR17A	0,036549804	0,633105941	0,22353502
SNR17B	SNR17B	0,02727521	0,843829809	0,22353502
YAL001C	TFC3: transcription initiation from RNA polymerase III promoter	0,183963462	0,10844419	0,059184514
YAL003W	EFB1: translational elongation	-0,269499233	0,188971	0,029484719
YAL030W	SNC1: endocytosis	0,106701516	0,181329543	-0,176351994

YBL018C	POP8: rRNA processing	0,078593703	0,043213854	-0,035426901
YBL026W	LSM2: nuclear mRNA splicing, via spliceosome	0,119524809	0,271702715	-0,013377785
YBL027W	RPL19B: protein biosynthesis	-0,338174837	-0,217775189	0,072440536
YBL040C	ERD2: protein retention in ER	0,110420553	0,209168211	0,189937269
YBL050W	SEC17: ER to Golgi transport	-0,002680909	0,290772004	0,153411658
YBL059C-A	YBL059C-A: biological process unknown	0,067624312	0,192399599	0,169690193
YBL059W	YBL059W: biological process unknown	0,166781509	0,102905692	-0,006985976
YBL072C	RPS8A: protein biosynthesis	-0,343230955	0,010969716	-0,350340054
YBL087C	RPL23A: protein biosynthesis	-0,373106641	-0,154626676	-0,383418509
YBL091C-A	SCS22: biological process unknown	0,083956745	0,405992484	-0,119394247
YBL092W	RPL32: protein biosynthesis	-0,402828422	-0,003229225	-0,5128709
YBR048W	RPS11B: protein biosynthesis	-0,315821882	-0,086435318	-0,15585055
YBR078W	ECM33: cell wall organization and biogenesis	-0,105642154	0,108234499	0,221328248
YBR082C	UBC4: response to stress	-0,159650069	0,205421553	0,329157578
YBR084C-A	RPL19A: protein biosynthesis	-0,187213553	-0,135796514	0,023644601
YBR089C-A	NHP6B: regulation of transcription from RNA polymerase II promot	0,455739761	0,060204286	0,048891486
YBR119W	MUD1: nuclear mRNA splicing, via spliceosome	-0,077658707	-0,004492688	-0,13444343
YBR181C	RPS6B: protein biosynthesis	-0,099360289	-0,206249303	-0,47418038
YBR186W	PCH2: regulation of meiosis	-0,019373384	0,070663109	0,111957604
YBR189W	RPS9B: protein biosynthesis	-0,486986115	-0,315608826	-0,329595628
YBR191W	RPL21A: protein biosynthesis	-0,347924728	-0,329233217	0,098275565
YBR219C	YBR219C: biological process unknown	0,088333276	-0,098743507	0,241094959
YBR230C	YBR230C: biological process unknown	0,103860703	0,340346897	-0,251803196
YCR028C-A	RIM1: mitochondrial genome maintenance	-0,012570058	-0,202443905	0,015734808
YCR031C	RPS14A: protein biosynthesis	0,066902002	-0,539855233	-0,291748222
YCR097W	HMRA1: regulation of transcription, mating-type specific	0,239571548	0,055329974	0,218416364
YCR097W_2	HMRA1: regulation of transcription, mating-type specific	0,239571548	0,145627974	-0,021774606
YDL012C	YDL012C: biological process unknown	0,251284344	0,24872668	0,160873619
YDL029W	ARP2: actin filament organization	0,052777648	0,160142676	0,192510619
YDL061C	RPS29B: protein biosynthesis	-0,03026936	-0,165070422	0,012931044

YDL064W	UBC9: G2/M transition of mitotic cell cycle	-0,134763952	0,186793847	0,231960388
YDL075W	RPL31A: protein biosynthesis	-0,442341131	-0,073384532	-0,360247053
YDL079C	MRK1: protein amino acid phosphorylation	-0,068640841	-0,043771524	0,112884915
YDL082W	RPL13A: protein biosynthesis	-0,368229581	-0,014873773	0,040636698
YDL083C	RPS16B: protein biosynthesis	-0,316021073	-0,29283382	-0,176768731
YDL108W	KIN28: protein amino acid phosphorylation	-0,002179	-0,112438684	0,113607232
YDL115C	IWR1: meiosis	0,215358926	0,131103936	0,165286489
YDL125C	HNT1: nucleotide metabolism	0,279705779	0,594603882	-0,13044429
YDL130W	RPP1B: translational elongation	0,075696278	-0,073041172	-0,018367124
YDL136W	RPL35B: protein biosynthesis	-0,23283701	-0,107568086	0,025790744
YDL137W	ARF2: ER to Golgi transport	0,056061757	0,271434702	0,846087812
YDL189W	RBS1: galactose metabolism	-0,109389279	-0,085160853	0,103722699
YDL191W	RPL35A: protein biosynthesis	-0,150536859	-0,221069356	-0,059436096
YDL219W	DTD1: translation	-0,291167552	0,02630324	-0,56573435
YDR005C	MAF1: negative regulation of transcription from RNA polymerase II	0,097882203	0,123372633	0,210341601
YDR025W	RPS11A: protein biosynthesis	-0,086227278	0,043359234	-0,033120688
YDR059C	UBC5: endocytosis	0,274373236	0,228114751	0,079321184
YDR064W	RPS13: protein biosynthesis	-0,157767931	-0,210965124	-0,324116163
YDR092W	UBC13: protein monoubiquitination	0,114746269	0,315098455	0,157869786
YDR129C	SAC6: endocytosis	0,292356289	0,278235761	0,092956473
YDR139C	RUB1: protein deneddylation	0,255978932	0,034489496	0,066434876
YDR305C	HNT2: nucleoside catabolism	-0,005785712	0,127796309	-0,120392699
YDR367W	YDR367W: biological process unknown	-0,159660519	0,083328425	0,153004461
YDR381W	YRA1: mRNA-nucleus export	0,3413275	0,164806849	-0,227086856
YDR397C	NCB2: negative regulation of transcription from RNA polymerase II	-0,0022658	0,234402193	0,046874508
YDR424C	DYN2: microtubule-based process	0,115374371	0,15666389	0,03685928
YDR424C_2	DYN2: microtubule-based process	0,115374371	0,168942861	0,133418536
YDR447C	RPS17B: protein biosynthesis	-0,041325976	0,036132597	-0,026803176
YDR450W	RPS18A: protein biosynthesis	-0,267425253	-0,034803078	-0,050559691
YDR471W	RPL27B: protein biosynthesis	0,007591309	0,212209154	-0,162981941

YDR500C	RPL37B: protein biosynthesis	-0,115520629	-0,069702747	-0,044917409
YEL012W	UBC8: protein monoubiquitination	0,207977882	0,092504352	0,139159352
YER003C	PMI40: protein amino acid glycosylation	0,035958647	0,115010652	0,202751673
YER007C-A	RBF20: biological process unknown	-0,054539131	0,206784153	-0,266709489
YER044C-A	MEI4: sporulation (sensu Fungi)	0,014969013	0,059255833	0,009254499
YER056C-A	RPL34A: protein biosynthesis	-0,166721674	-0,28806445	-0,012154903
YER074W	RPS24A: protein biosynthesis	0,073211683	-0,26916449	-0,115903021
YER074W-A	YOS1: ER to Golgi transport	0,050942795	0,2414827	-0,046243191
YER074W-A_2	YOS1: ER to Golgi transport	0,050942795	-0,054429222	-0,135580852
YER093C-A	YER093C-A: biological process unknown	-0,077721968	0,02183537	-0,272728843
YER102W	RPS8B: protein biosynthesis	-0,255366913	-0,161623649	-0,414734598
YER117W	RPL23B: protein biosynthesis	-0,016263425	-0,200082926	-0,007370448
YER131W	RPS26B: protein biosynthesis	-0,221330624	0,172242745	0,112142328
YER133W	GLC7: 35S primary transcript processing	0,113663137	0,296954173	-0,143778804
YER179W	DMC1: meiosis	0,25913456	0,013953693	0,478128723
YFL034C-A	RPL22B: protein biosynthesis	-0,109044747	-0,128057979	-0,204263044
YFL034C-B	MOB2: protein amino acid phosphorylation	0,244052465	-0,013594864	-0,046702254
YFL039C	ACT1: cell wall organization and biogenesis	0,170315972	0,415351624	0,144654566
YFR024C-A	LSB3: actin filament organization	-0,076911657	-0,119778629	0,174684727
YFR031C-A	RPL2A: protein biosynthesis	-0,212360022	-0,099341153	-0,163709335
YFR032C-A	RPL29: protein biosynthesis	-0,092560756	0,06547577	-0,178494957
YGL030W	RPL30: protein biosynthesis	-0,168802502	-0,203145042	-0,318297151
YGL031C	RPL24A: protein biosynthesis	-0,211995209	-0,161657336	-0,027918023
YGL033W	HOP2: synapsis	0,008982209	-0,030971905	0,072027004
YGL076C	RPL7A: protein biosynthesis	-0,156727472	-0,000473268	-0,051513406
YGL076C_2	RPL7A: protein biosynthesis	-0,156727472	0,089443963	-0,241530979
YGL087C	MMS2: DNA repair	0,041785304	0,073401984	-0,182256325
YGL103W	RPL28: protein biosynthesis	-0,099456236	-0,081275216	-0,016715981
YGL137W	SEC27: ER to Golgi transport	0,024431827	0,284421185	-0,112268625
YGL178W	MPT5: cell wall organization and biogenesis	0,094713379	0,332339135	0,226832625

YGL187C	COX4: aerobic respiration	-0,073387416	-0,050489331	0,100654343
YGL189C	RPS26A: protein biosynthesis	-0,296926598	-0,117388382	0,284422348
YGL226C-A	OST5: protein amino acid N-linked glycosylation	0,126534155	0,354700774	-0,006882638
YGL232W	TAN1: tRNA modification	0,103294604	-0,080604228	-0,255840396
YGL251C	HFM1: meiosis	-0,439170954	-0,030396905	0,047733749
YGR001C	YGR001C: biological process unknown	0,028981605	0,054440236	-0,228874828
YGR001C_2	YGR001C: biological process unknown	0,028981605	-0,011648484	-0,32077652
YGR027C	RPS25A: protein biosynthesis	-0,277807086	-0,018606683	0,095872607
YGR029W	ERV1: mitochondrion organization and biogenesis	0,023703541	0,031237835	-0,110263503
YGR118W	RPS23A: protein biosynthesis	-0,261901083	0,098795176	0,00244516
YGR148C	RPL24B: protein biosynthesis	-0,310121486	-0,083118369	-0,606738926
YGR183C	QCR9: aerobic respiration	0,232169854	0,142861237	0,106074921
YGR214W	RPS0A: protein biosynthesis	-0,186689234	-0,309701924	-0,240048571
YGR225W	AMA1: sporulation (sensu Fungi)	0,137038354	-0,014381919	0,126672198
YHL001W	RPL14B: protein biosynthesis	-0,267574212	0,418687801	-0,135679942
YHR001W-A	QCR10: aerobic respiration	0,17853558	0,226563974	0,058639676
YHR010W	RPL27A: protein biosynthesis	0,015150867	-0,005082465	0,090062012
YHR012W	VPS29: retrograde transport, endosome to Golgi	-0,026835097	-0,080320871	0,011352747
YHR016C	YSC84: endocytosis	0,087833554	0,074419021	0,319888837
YHR021C	RPS27B: protein biosynthesis	-0,241830433	-0,065739063	0,006547711
YHR039C-A	VMA10: vacuolar acidification	0,0856885	0,136183895	0,143500859
YHR041C	SRB2: transcription from RNA polymerase II promoter	0,055339409	0,359442227	0,214214204
YHR077C	NMD2: mRNA catabolism	0,150523545	0,160793544	0,487468174
YHR097C	YHR097C: biological process unknown	0,272356781	0,188015234	-0,060450002
YHR101C	BIG1: cell wall biosynthesis (sensu Fungi)	-0,009167023	0,288435374	0,033649236
YHR123W	EPT1: phosphatidylethanolamine biosynthesis	-0,189829015	0,232078761	-0,352818317
YHR141C	RPL42B: protein biosynthesis	-0,177121723	0,075772079	-0,270166255
YHR203C	RPS4B: protein biosynthesis	-0,076849723	-0,038107045	-0,064099796
YIL004C	BET1: ER to Golgi transport	0,026647557	0,024808659	0,066743549
YIL018W	RPL2B: protein biosynthesis	0,06734508	-0,219282157	-0,184509077

YIL052C	RPL34B: protein biosynthesis	-0,11992513	0,245509248	-0,083330462
YIL069C	RPS24B: protein biosynthesis	-0,13080098	-0,263852842	-0,088258351
YIL106W	MOB1: protein amino acid phosphorylation	0,037317707	0,154346317	-0,068264114
YIL111W	COX5B: mitochondrial electron transport, cytochrome c to oxygen	-0,138836977	0,105417821	-0,093310951
YIL133C	RPL16A: protein biosynthesis	-0,195700665	0,020963049	0,148280525
YIL148W	RPL40A: protein biosynthesis	-0,059831908	-0,124425069	-0,102645223
YJL001W	PRE3: response to stress	0,011974921	0,164968978	-0,220629544
YJL024C	APS3: vesicle-mediated transport	-0,141092416	-0,019395125	-0,003201849
YJL041W	NSP1: mRNA-nucleus export	0,179392746	0,156191153	0,324002669
YJL136C	RPS21B: protein biosynthesis	-0,181921747	-0,316463235	-0,006613365
YJL177W	RPL17B: protein biosynthesis	-0,296602559	-0,0357092	0,067982928
YJL189W	RPL39: protein biosynthesis	-0,125274545	-0,093225744	-0,16916053
YJL191W	RPS14B: protein biosynthesis	0,028430038	-0,090726757	-0,0618906
YJL205C	NCE1: biological process unknown	0,163908867	0,372852332	0,017226747
YJR021C	REC107: meiotic recombination	0,209128406	0,081634409	0,156806767
YJR094W-A	RPL43B: protein biosynthesis	-0,171711737	0,043198572	-0,103608034
YJR145C	RPS4A: protein biosynthesis	-0,365381444	0,042969524	-0,263778443
YKL002W	DID4: protein retention in Golgi	0,245810577	0,128693255	0,258220087
YKL006C-A	SFT1: intra-Golgi transport	0,119874271	0,265536357	0,015141741
YKL006W	RPL14A: protein biosynthesis	-0,06478349	-0,230181062	-0,17175318
YKL081W	TEF4: translational elongation	-0,197157723	0,259630286	-0,163888945
YKL156W	RPS27A: protein biosynthesis	-0,258013218	0,012611594	-0,073160782
YKL157W	APE2: peptide metabolism	0,353636902	-0,511775451	0,073606281
YKL180W	RPL17A: protein biosynthesis	-0,417662856	0,04541195	-0,456482546
YKL186C	MTR2: poly(A)+ mRNA-nucleus export	-0,136919971	0,029196454	-0,041570521
YKL186C_2	MTR2: poly(A)+ mRNA-nucleus export	-0,136919971	0,032699758	0,000568213
YKL186C_3	MTR2: poly(A)+ mRNA-nucleus export	-0,136919971	0,03612347	0,137747431
YKL186C_4	MTR2: poly(A)+ mRNA-nucleus export	-0,136919971	-0,130711491	0,178653729
YKL186C_5	MTR2: poly(A)+ mRNA-nucleus export	-0,136919971	0,012731491	0,033598608
YKL186C_6	MTR2: poly(A)+ mRNA-nucleus export	-0,136919971	0,019450659	0,102628481

YKL190W	CNB1: cell wall organization and biogenesis	-0,156444929	0,015021153	0,060857471
YKR057W	RPS21A: protein biosynthesis	-0,316770373	-0,068338312	-0,201149611
YKR094C	RPL40B: protein biosynthesis	-0,194008711	-0,008305486	-0,20300148
YLL050C	COF1: actin filament organization	-0,247352476	-0,054575289	0,260690151
YLR048W	RPS0B: protein biosynthesis	-0,208874599	0,013337137	-0,141314211
YLR061W	RPL22A: protein biosynthesis	-0,289160947	0,144577879	-0,175018227
YLR078C	BOS1: ER to Golgi transport	-0,14352168	0,041546687	-0,039844558
YLR093C	NYV1: vesicle fusion	0,101608134	0,134047997	-0,005869866
YLR128W	DCN1: protein neddylation	0,113959944	0,252650455	0,260023466
YLR185W	RPL37A: protein biosynthesis	-0,257871564	-0,105937339	-0,356967571
YLR211C	YLR211C: biological process unknown	0,001182316	0,048209075	0,010656979
YLR275W	SMD2: nuclear mRNA splicing, via spliceosome	-0,010877107	-0,114678107	-0,589106875
YLR287C-A	RPS30A: protein biosynthesis	0,420854835	-0,277024577	-0,141569361
YLR306W	UBC12: protein monoubiquitination	0,036632544	0,222725611	-0,074490119
YLR316C	TAD3: tRNA modification	0,134483461	0,041180082	-0,048538599
YLR316C_2	TAD3: tRNA modification	0,134483461	0,17717076	0,025145557
YLR333C	RPS25B: protein biosynthesis	-0,330687115	-0,059298985	-0,162705952
YLR344W	RPL26A: protein biosynthesis	-0,298491954	-0,095278316	0,420781292
YLR367W	RPS22B: protein biosynthesis	0,200386855	0,196613381	0,075721844
YLR367W_2	RPS22B: protein biosynthesis	0,200386855	0,074168735	-0,010867023
YLR388W	RPS29A: protein biosynthesis	-0,146692764	0,01168338	-0,374288382
YLR406C	RPL31B: protein biosynthesis	-0,371014069	-0,032577891	-0,637062533
YLR426W	YLR426W: biological process unknown	0,065496342	0,113222886	-0,026166361
YLR448W	RPL6B: protein biosynthesis	-0,422506516	-0,093616237	-0,391890363
YML024W	RPS17A: protein biosynthesis	-0,043737145	-0,235599929	-0,325054516
YML025C	YML6: protein biosynthesis	0,065773944	0,225432344	-0,060472659
YML026C	RPS18B: protein biosynthesis	-0,149351967	-0,114585042	-0,267115824
YML034W	SRC1: mitotic sister chromatid segregation	0,396429054	0,279111499	-0,033185413
YML034W_2	SRC1: mitotic sister chromatid segregation	0,396429054	0,191070917	0,099788941
YML056C	IMD4: biological process unknown	-0,011998119	0,389854692	-0,095737718

YML067C	ERV41: ER to Golgi transport	-0,046079453	0,049063943	-0,320693644
YML073C	RPL6A: protein biosynthesis	-0,325931707	-0,077285324	-0,230190183
YML085C	TUB1: mitotic sister chromatid segregation	-0,044035907	-0,075566511	0,02906762
YML094W	GIM5: tubulin folding	0,021570528	0,058383986	-0,157705025
YML124C	TUB3: mitotic sister chromatid segregation	0,044187712	0,218599232	0,035902084
YMR033W	ARP9: chromatin remodeling	0,206784681	0,273728512	0,040049623
YMR079W	SEC14: sporulation (sensu Fungi)	-0,064857429	0,090245731	-0,005638476
YMR116C	ASC1: biological process unknown	-0,302347911	0,282864973	-0,310941984
YMR125W	STO1: nuclear mRNA splicing, via spliceosome	0,260681944	0,200969948	0,13677097
YMR133W	REC114: meiotic recombination	-0,002275969	-0,037049588	-0,010373262
YMR142C	RPL13B: protein biosynthesis	-0,412415567	-0,279924292	-0,367445838
YMR143W	RPS16A: protein biosynthesis	-0,443150772	-0,199404205	-0,28802686
YMR194W	RPL36A: protein biosynthesis	-0,090232699	-0,056322671	-0,200890034
YMR201C	RAD14: nucleotide-excision repair, DNA damage recognition	0,077552565	0,21362246	0,080116059
YMR225C	MRPL44: protein biosynthesis	-0,022084739	0,235779198	-0,05270847
YMR230W	RPS10B: protein biosynthesis	-0,268688614	-0,074116765	-0,250840735
YMR292W	GOT1: ER to Golgi transport	-0,18508454	0,192013909	-0,070969959
YNL012W	SPO1: meiosis	0,049350907	-0,020328333	0,027190952
YNL044W	YIP3: ER to Golgi transport	0,453403524	0,299572237	-0,162777126
YNL050C	YNL050C: biological process unknown	0,086234977	-0,087851389	-0,017376709
YNL069C	RPL16B: protein biosynthesis	-0,09125503	0,109388377	0,064083445
YNL096C	RPS7B: protein biosynthesis	-0,202724971	0,081128399	-0,385805331
YNL112W	DBP2: mRNA catabolism, nonsense-mediated decay	-0,09491678	0,168169964	-0,122729502
YNL130C	CPT1: phosphatidylcholine biosynthesis	-0,009297224	0,180149537	-0,025259842
YNL147W	LSM7: nuclear mRNA splicing, via spliceosome	0,035852421	0,134941764	-0,044847111
YNL162W	RPL42A: protein biosynthesis	-0,199472281	-0,252107334	-0,323167425
YNL246W	VPS75: protein-vacuolar targeting	0,121335601	0,054168825	-0,123052727
YNL265C	IST1: protein biosynthesis	0,155878728	0,050436773	-0,118982949
YNL301C	RPL18B: protein biosynthesis	-0,150537954	-0,329689157	0,043513514
YNL302C	RPS19B: protein biosynthesis	-0,401116764	-0,341838799	-0,279517207

YNL312W	RFA2: DNA recombination	0,015660161	0,041239373	0,026318188
YNR053C	NOG2: ribosome assembly	0,148017916	0,372780028	0,031252891
YOL047C	YOL047C: biological process unknown	0,120794867	0,133446021	0,007706455
YOL048C	YOL048C: biological process unknown	0,196949696	0,075208325	0,133255191
YOL120C	RPL18A: protein biosynthesis	-0,469560929	-0,46309681	-0,044387819
YOL121C	RPS19A: protein biosynthesis	-0,303291904	0,066885611	0,227968971
YOL127W	RPL25: protein biosynthesis	-0,409930398	-0,07829018	-0,407171159
YOR096W	RPS7A: protein biosynthesis	-0,131711493	-0,162966371	-0,252978785
YOR122C	PFY1: response to osmotic stress	0,061493299	0,316592939	-0,033939209
YOR182C	RPS30B: protein biosynthesis	0,184563005	-0,071160542	-0,076847137
YOR234C	RPL33B: protein biosynthesis	-0,092636687	0,106501876	-0,008251032
YOR293W	RPS10A: protein biosynthesis	-0,258223019	0,07863109	-0,181006143
YOR312C	RPL20B: protein biosynthesis	-0,393196105	-0,516393961	-0,398218219
YPL031C	PHO85: protein amino acid phosphorylation	-0,192945824	0,094582421	-0,231638901
YPL075W	GCR1: positive regulation of transcription from RNA polymerase II	0,051448227	-0,12325667	0,009172164
YPL079W	RPL21B: protein biosynthesis	-0,231716686	-0,097987503	0,023242071
YPL081W	RPS9A: protein biosynthesis	-0,108003489	0,051178644	-0,061136556
YPL090C	RPS6A: protein biosynthesis	-0,162793232	-0,069786529	-0,361691746
YPL129W	TAF14: chromatin remodeling	-0,141061245	-0,219927243	-0,025023623
YPL143W	RPL33A: protein biosynthesis	-0,273012379	-0,276845304	0,120630661
YPL175W	SPT14: GPI anchor biosynthesis	-0,257187158	-0,14043484	0,173970377
YPL198W	RPL7B: protein biosynthesis	-0,161574608	0,176808373	-0,057186457
YPL198W_2	RPL7B: protein biosynthesis	-0,161574608	0,190577861	-0,19102129
YPL218W	SAR1: ER to Golgi transport	-0,032495154	0,204890077	-0,061341475
YPL241C	CIN2: microtubule-based process	0,091687674	-0,057702964	0,122007489
YPL249C-A	RPL36B: protein biosynthesis	-0,399606573	-0,088399739	-0,180609451
YPR028W	YOP1: vesicle-mediated transport	-0,127075493	0,476678939	0,049871239
YPR043W	RPL43A: protein biosynthesis	-0,408916766	-0,271724709	-0,307638641
YPR063C	YPR063C: biological process unknown	-0,436869457	0,21341946	-0,701044666
YPR098C	YPR098C: biological process unknown	-0,014619757	0,492965376	-0,041704585

YPR132W	RPS23B: protein biosynthesis	-0,005199764	-0,031749198	-0,414453006
YPR187W	RPO26: transcription from RNA polymerase II promoter	-0,027199607	0,1268478	0,064732477

Genotype:		*set1*Δ	*set1*Δ	*set1*Δ
Strains compared:		W303 *set1*Δ vs W303	W303 *set1*Δ vs W303	W303 *set1*Δ vs W303
Feature:		Exon	Intron	Junction
Systematic Name	Common Name			
SNR17A	SNR17A	0,197678103	0,366134636	0,363915327
SNR17B	SNR17B	0,157475607	0,434131696	0,363915327
YAL001C	TFC3: transcription initiation from RNA polymerase III promoter	0,198053274	0,048591336	0,037155555
YAL003W	EFB1: translational elongation	-0,403082333	0,239880352	-0,13814561
YAL030W	SNC1: endocytosis	0,017656027	-0,040981588	0,148775282
YBL018C	POP8: rRNA processing	-0,123329223	-0,262793156	-0,079708912
YBL026W	LSM2: nuclear mRNA splicing, via spliceosome	0,081403196	0,222408935	0,07153594
YBL027W	RPL19B: protein biosynthesis	-0,446358813	0,04749079	0,185561632
YBL040C	ERD2: protein retention in ER	0,072192981	0,121066528	-0,121193426
YBL050W	SEC17: ER to Golgi transport	-0,159654535	0,154414037	-0,150980358
YBL059C-A	YBL059C-A: biological process unknown	-0,05871412	-0,059074441	-0,141462426
YBL059W	YBL059W: biological process unknown	0,060917672	-0,041707288	-0,088971325
YBL072C	RPS8A: protein biosynthesis	-0,213852796	0,149321922	-0,158955808
YBL087C	RPL23A: protein biosynthesis	-0,282204392	0,15213857	-0,336129704
YBL091C-A	SCS22: biological process unknown	-0,072879607	0,422830454	0,009705717
YBL092W	RPL32: protein biosynthesis	0,017133483	-0,080457648	-0,268946597
YBR048W	RPS11B: protein biosynthesis	-0,06506507	0,092557598	-0,104049499
YBR078W	ECM33: cell wall organization and biogenesis	0,164212183	0,668086782	0,315077495
YBR082C	UBC4: response to stress	0,173979101	0,044063246	-0,071096143

YBR084C-A	RPL19A: protein biosynthesis	-0,128367571	0,003626174	0,100252191
YBR089C-A	NHP6B: regulation of transcription from RNA polymerase II promot	0,023833399	-0,020766341	0,231217614
YBR119W	MUD1: nuclear mRNA splicing, via spliceosome	-0,306619124	0,031781606	-0,026079388
YBR181C	RPS6B: protein biosynthesis	-0,083486497	-0,059928236	-0,555320938
YBR186W	PCH2: regulation of meiosis	0,419694192	-0,104837764	0,467024864
YBR189W	RPS9B: protein biosynthesis	-0,303079668	0,079859054	-0,278499582
YBR191W	RPL21A: protein biosynthesis	-0,102300045	0,029370606	0,003879928
YBR219C	YBR219C: biological process unknown	0,091683605	-0,153275193	0,102128593
YBR230C	YBR230C: biological process unknown	-0,156957689	0,114343741	-0,203194569
YCR028C-A	RIM1: mitochondrial genome maintenance	-0,223600925	0,115804936	-0,217127866
YCR031C	RPS14A: protein biosynthesis	0,230967428	-0,110252352	-0,44793901
YCR097W	HMRA1: regulation of transcription, mating-type specific	0,031171325	-0,245626962	0,192482033
YCR097W_2	HMRA1: regulation of transcription, mating-type specific	0,031171325	0,017171794	0,31174947
YDL012C	YDL012C: biological process unknown	0,131806307	0,237918949	0,300287053
YDL029W	ARP2: actin filament organization	-0,311326487	0,103634022	0,010325526
YDL061C	RPS29B: protein biosynthesis	0,312780751	-0,010624818	0,054580116
YDL064W	UBC9: G2/M transition of mitotic cell cycle	-0,064772725	-0,030699814	0,207088024
YDL075W	RPL31A: protein biosynthesis	-0,338444839	-0,248283428	-0,509138911
YDL079C	MRK1: protein amino acid phosphorylation	0,044377767	-0,161377786	0,014594704
YDL082W	RPL13A: protein biosynthesis	-0,092411182	-0,231747212	0,029760003
YDL083C	RPS16B: protein biosynthesis	-0,286718345	-0,072218542	-0,114078315
YDL108W	KIN28: protein amino acid phosphorylation	0,05670332	-0,146329565	0,200464402
YDL115C	IWR1: meiosis	0,136027776	0,043787647	0,164392342
YDL125C	HNT1: nucleotide metabolism	0,286169071	0,587605087	-0,078969466
YDL130W	RPP1B: translational elongation	0,144432259	-0,049249679	-0,147707316
YDL136W	RPL35B: protein biosynthesis	-0,24729918	-0,183963772	-0,035032457
YDL137W	ARF2: ER to Golgi transport	-0,177959321	0,296578165	-0,490412597
YDL189W	RBS1: galactose metabolism	-0,01793081	-0,136142403	-0,005040698
YDL191W	RPL35A: protein biosynthesis	-0,119651815	0,07545395	-0,001050748
YDL219W	DTD1: translation	-0,164344405	0,113113477	-0,282483038

YDR005C	MAF1: negative regulation of transcription from RNA polymerase II	-0,058697231	0,166070367	0,024615238
YDR025W	RPS11A: protein biosynthesis	0,244092215	0,027965795	-0,051877743
YDR059C	UBC5: endocytosis	0,482132968	0,023147253	-0,031997036
YDR064W	RPS13: protein biosynthesis	-0,360055802	-0,382944061	-0,474889835
YDR092W	UBC13: protein monoubiquitination	0,018387636	0,219902878	-0,00322117
YDR129C	SAC6: endocytosis	-0,252632533	0,09873979	0,120698335
YDR139C	RUB1: protein deneddylation	0,406423068	-0,098768759	-0,042235706
YDR305C	HNT2: nucleoside catabolism	0,114157046	-0,055072488	-0,229680878
YDR367W	YDR367W: biological process unknown	-0,122194667	-0,103846234	-0,047365496
YDR381W	YRA1: mRNA-nucleus export	0,017598738	0,079214393	-0,317363951
YDR397C	NCB2: negative regulation of transcription from RNA polymerase II	-0,144795323	-0,113921577	0,220222184
YDR424C	DYN2: microtubule-based process	0,140621493	0,273993889	0,14576819
YDR424C_2	DYN2: microtubule-based process	0,140621493	0,073664737	0,106816793
YDR447C	RPS17B: protein biosynthesis	-0,032423913	-0,005956276	-0,206356443
YDR450W	RPS18A: protein biosynthesis	-0,232594203	0,034475454	0,133242115
YDR471W	RPL27B: protein biosynthesis	-0,144534965	-0,020657812	-0,166820805
YDR500C	RPL37B: protein biosynthesis	-0,014258244	-0,04240468	-0,040868318
YEL012W	UBC8: protein monoubiquitination	0,207939155	-0,079353129	0,078128766
YER003C	PMI40: protein amino acid glycosylation	0,102173085	0,069896137	0,408089012
YER007C-A	RBF20: biological process unknown	-0,293239191	-0,182999682	-0,369953115
YER044C-A	MEI4: sporulation (sensu Fungi)	-0,051266132	-0,120623688	0,04536331
YER056C-A	RPL34A: protein biosynthesis	-0,203890741	0,233979482	0,037047131
YER074W	RPS24A: protein biosynthesis	0,004963889	0,166410082	-0,106381825
YER074W-A	YOS1: ER to Golgi transport	-0,201211607	0,01221744	0,004934393
YER074W-A_2	YOS1: ER to Golgi transport	-0,201211607	-0,007805203	-0,029607077
YER093C-A	YER093C-A: biological process unknown	-0,127056976	0,128037272	-0,059578998
YER102W	RPS8B: protein biosynthesis	-0,025076171	-0,000960958	-0,000796998
YER117W	RPL23B: protein biosynthesis	-0,1671257	-0,136645214	0,029442488
YER131W	RPS26B: protein biosynthesis	0,066654471	0,039499518	0,268864978
YER133W	GLC7: 35S primary transcript processing	0,022199037	0,365694361	-0,181104715

YER179W	DMC1: meiosis	0,158714553	-0,341176962	0,297640966
YFL034C-A	RPL22B: protein biosynthesis	0,10153239	0,141911511	0,019605646
YFL034C-B	MOB2: protein amino acid phosphorylation	0,153951677	0,198721238	0,0353909
YFL039C	ACT1: cell wall organization and biogenesis	0,3297276	0,219402303	0,264135326
YFR024C-A	LSB3: actin filament organization	0,107946716	-0,104070721	0,20562296
YFR031C-A	RPL2A: protein biosynthesis	0,015116962	0,21336488	-0,103386988
YFR032C-A	RPL29: protein biosynthesis	-0,130912646	0,283757553	-0,201747866
YGL030W	RPL30: protein biosynthesis	-0,021645238	-0,077898757	-0,260954234
YGL031C	RPL24A: protein biosynthesis	-0,341174902	0,120625429	0,103987177
YGL033W	HOP2: synapsis	0,628310631	0,409384225	0,093291164
YGL076C	RPL7A: protein biosynthesis	0,076622952	0,116719254	-0,059162911
YGL076C_2	RPL7A: protein biosynthesis	0,076622952	0,216427061	-0,120924528
YGL087C	MMS2: DNA repair	0,27238546	-0,069992449	0,220014897
YGL103W	RPL28: protein biosynthesis	-0,015256478	-0,028465305	0,00281107
YGL137W	SEC27: ER to Golgi transport	-0,17333038	-0,031550414	-0,399077442
YGL178W	MPT5: cell wall organization and biogenesis	0,257582385	0,232122417	0,52716317
YGL187C	COX4: aerobic respiration	-0,036016152	-0,10857019	0,151819668
YGL189C	RPS26A: protein biosynthesis	-0,124294234	0,282792476	0,760776797
YGL226C-A	OST5: protein amino acid N-linked glycosylation	-0,181453669	-0,05752587	0,08345953
YGL232W	TAN1: tRNA modification	0,012310726	0,102364197	-0,161861149
YGL251C	HFM1: meiosis	-0,220755662	-0,130259941	-0,069310179
YGR001C	YGR001C: biological process unknown	-0,360674024	-0,108840044	-0,209766731
YGR001C_2	YGR001C: biological process unknown	-0,360674024	-0,164179391	-0,659829307
YGR027C	RPS25A: protein biosynthesis	-0,289333207	0,100311506	0,051209413
YGR029W	ERV1: mitochondrion organization and biogenesis	-0,186444333	-0,033579561	0,016793298
YGR118W	RPS23A: protein biosynthesis	-0,217815832	-0,052397804	0,093016913
YGR148C	RPL24B: protein biosynthesis	-0,243949989	0,192937201	-0,272377151
YGR183C	QCR9: aerobic respiration	0,160267889	0,150808298	0,055137059
YGR214W	RPS0A: protein biosynthesis	-0,023554448	-0,034882493	-0,031864084
YGR225W	AMA1: sporulation (sensu Fungi)	0,103012914	0,292076579	0,067172973

YHL001W	RPL14B: protein biosynthesis	-0,250200183	0,136937978	-0,045259459
YHR001W-A	QCR10: aerobic respiration	0,535789519	-0,091484728	0,090132198
YHR010W	RPL27A: protein biosynthesis	0,081133185	0,176589354	0,106454037
YHR012W	VPS29: retrograde transport, endosome to Golgi	-0,157693071	-0,140882775	0,085919511
YHR016C	YSC84: endocytosis	0,08911571	0,193283404	0,169083269
YHR021C	RPS27B: protein biosynthesis	0,055867219	0,064834998	-0,032255949
YHR039C-A	VMA10: vacuolar acidification	-0,155045877	0,077343402	-0,169718636
YHR041C	SRB2: transcription from RNA polymerase II promoter	0,016589983	0,108458654	0,052748906
YHR077C	NMD2: mRNA catabolism	0,014956196	-0,194984858	0,210443668
YHR097C	YHR097C: biological process unknown	0,359450514	0,248262014	0,074995948
YHR101C	BIG1: cell wall biosynthesis (sensu Fungi)	-0,070221082	-0,041682746	0,192197648
YHR123W	EPT1: phosphatidylethanolamine biosynthesis	-0,312426127	0,003945712	-0,477405152
YHR141C	RPL42B: protein biosynthesis	-0,163359241	-0,010617813	-0,182953069
YHR203C	RPS4B: protein biosynthesis	-0,027435739	-0,059901355	-0,081599181
YIL004C	BET1: ER to Golgi transport	-0,173321897	-0,207580706	-0,061363296
YIL018W	RPL2B: protein biosynthesis	-0,018001426	0,140906255	-0,00923819
YIL052C	RPL34B: protein biosynthesis	0,058236246	0,079003582	0,040306751
YIL069C	RPS24B: protein biosynthesis	0,032337523	-0,111223543	-0,269682785
YIL106W	MOB1: protein amino acid phosphorylation	0,227128622	0,217308281	0,438537737
YIL111W	COX5B: mitochondrial electron transport, cytochrome c to oxygen	0,016160513	-0,022530418	-0,188639307
YIL133C	RPL16A: protein biosynthesis	0,374221046	-0,092071456	0,136315382
YIL148W	RPL40A: protein biosynthesis	-0,049321182	-0,17868769	-0,23950284
YJL001W	PRE3: response to stress	-0,136872482	0,076177513	-0,093617543
YJL024C	APS3: vesicle-mediated transport	-0,254182622	-0,028985773	0,073137015
YJL041W	NSP1: mRNA-nucleus export	0,067444511	0,246695689	0,326259831
YJL136C	RPS21B: protein biosynthesis	-0,155948347	-0,074639246	-0,045973142
YJL177W	RPL17B: protein biosynthesis	-0,139043959	-0,109768188	0,011576646
YJL189W	RPL39: protein biosynthesis	-0,111646037	-0,002898734	-0,016518733
YJL191W	RPS14B: protein biosynthesis	0,424487315	0,089095116	0,267286414
YJL205C	NCE1: biological process unknown	0,029231168	0,19839181	0,048702453

YJR021C	REC107: meiotic recombination	0,220873834	0,081966152	0,139409662
YJR094W-A	RPL43B: protein biosynthesis	0,214700051	0,12972512	0,132480478
YJR145C	RPS4A: protein biosynthesis	-0,353961555	0,021332198	-0,17025924
YKL002W	DID4: protein retention in Golgi	-0,063019626	-0,144306816	0,136719788
YKL006C-A	SFT1: intra-Golgi transport	-0,112444776	0,006699636	0,079153816
YKL006W	RPL14A: protein biosynthesis	0,012419857	0,149657792	-0,016597235
YKL081W	TEF4: translational elongation	0,225570903	0,097199652	0,259001926
YKL156W	RPS27A: protein biosynthesis	0,062374453	0,064822059	-0,151326759
YKL157W	APE2: peptide metabolism	0,18634009	-0,610981821	0,048401752
YKL180W	RPL17A: protein biosynthesis	-0,259010296	0,031286508	-0,388125158
YKL186C	MTR2: poly(A)+ mRNA-nucleus export	-0,131103132	-0,053739445	-0,116836018
YKL186C_2	MTR2: poly(A)+ mRNA-nucleus export	-0,131103132	-0,08691001	0,10872715
YKL186C_3	MTR2: poly(A)+ mRNA-nucleus export	-0,131103132	-0,060871118	-0,014639836
YKL186C_4	MTR2: poly(A)+ mRNA-nucleus export	-0,131103132	-0,082304137	0,222240532
YKL186C_5	MTR2: poly(A)+ mRNA-nucleus export	-0,131103132	-0,137477945	0,042451414
YKL186C_6	MTR2: poly(A)+ mRNA-nucleus export	-0,131103132	0,028412258	-0,049620407
YKL190W	CNB1: cell wall organization and biogenesis	-0,230584996	-0,051558138	-0,03425145
YKR057W	RPS21A: protein biosynthesis	-0,387684661	0,088275829	-0,157735097
YKR094C	RPL40B: protein biosynthesis	-0,025471893	-0,210424693	0,031707345
YLL050C	COF1: actin filament organization	-0,412207162	0,012496669	0,432516927
YLR048W	RPS0B: protein biosynthesis	0,080405886	0,042159257	0,144257557
YLR061W	RPL22A: protein biosynthesis	-0,003349876	0,231290049	0,097871036
YLR078C	BOS1: ER to Golgi transport	-0,266450477	-0,132418072	0,068243847
YLR093C	NYV1: vesicle fusion	-0,112240851	0,096472663	-0,186550775
YLR128W	DCN1: protein neddylation	0,002792523	0,293605151	-0,02449166
YLR185W	RPL37A: protein biosynthesis	-0,049713597	-0,041559832	-0,231081115
YLR211C	YLR211C: biological process unknown	0,019207922	-0,063863223	-0,051172349
YLR275W	SMD2: nuclear mRNA splicing, via spliceosome	-0,083803451	-0,010941132	2,190639048
YLR287C-A	RPS30A: protein biosynthesis	0,399449212	-0,173799039	-0,004499621
YLR306W	UBC12: protein monoubiquitination	-0,017905752	0,095136099	0,006553045

YLR316C	TAD3: tRNA modification	0,149412408	-0,149358651	0,271407175
YLR316C_2	TAD3: tRNA modification	0,149412408	-0,166590681	-0,020981802
YLR333C	RPS25B: protein biosynthesis	-0,226084459	-0,067377016	-0,057570419
YLR344W	RPL26A: protein biosynthesis	-0,280853443	0,025025627	-0,004055588
YLR367W	RPS22B: protein biosynthesis	0,230235625	0,146274495	-0,133466947
YLR367W_2	RPS22B: protein biosynthesis	0,230235625	-0,288701002	0,139671868
YLR388W	RPS29A: protein biosynthesis	-0,195411853	-0,088257503	-0,154950591
YLR406C	RPL31B: protein biosynthesis	-0,270174443	-0,026275296	-0,313056961
YLR426W	YLR426W: biological process unknown	0,027998716	0,169057673	-0,174023315
YLR448W	RPL6B: protein biosynthesis	-0,353233492	0,003847758	-0,306359412
YML024W	RPS17A: protein biosynthesis	-0,416670472	0,048485861	-0,250874401
YML025C	YML6: protein biosynthesis	0,033227168	-0,048680903	-0,037632138
YML026C	RPS18B: protein biosynthesis	-0,014258821	0,027518438	-0,154560048
YML034W	SRC1: mitotic sister chromatid segregation	0,104853359	-0,069531574	0,028363806
YML034W_2	SRC1: mitotic sister chromatid segregation	0,104853359	-0,099127384	0,128167573
YML056C	IMD4: biological process unknown	-0,235154839	0,177778769	-0,34600952
YML067C	ERV41: ER to Golgi transport	-0,226820686	-0,157134737	-0,565738554
YML073C	RPL6A: protein biosynthesis	-0,284512367	0,048565004	-0,425014772
YML085C	TUB1: mitotic sister chromatid segregation	0,027532741	0,011023156	-0,143016452
YML094W	GIM5: tubulin folding	-0,061815997	-0,128743561	-0,12500357
YML124C	TUB3: mitotic sister chromatid segregation	0,306225763	0,083417522	-0,069991556
YMR033W	ARP9: chromatin remodeling	0,117638222	-0,038407743	-0,196784734
YMR079W	SEC14: sporulation (sensu Fungi)	0,141631967	-0,099246422	0,043498617
YMR116C	ASC1: biological process unknown	-0,030271177	0,093124162	0,020023902
YMR125W	STO1: nuclear mRNA splicing, via spliceosome	0,039477455	-0,021326542	0,146783007
YMR133W	REC114: meiotic recombination	-0,006141121	0,037024641	0,204632862
YMR142C	RPL13B: protein biosynthesis	-0,39502383	-0,073610585	-0,409886478
YMR143W	RPS16A: protein biosynthesis	-0,034429846	-0,120306751	-0,246549112
YMR194W	RPL36A: protein biosynthesis	-0,081613943	0,082567591	-0,168750853
YMR201C	RAD14: nucleotide-excision repair, DNA damage recognition	-0,130736011	-0,106844434	-0,060093896

YMR225C	MRPL44: protein biosynthesis	-0,138655486	0,101058583	-0,108274354
YMR230W	RPS10B: protein biosynthesis	-0,182267899	-0,034422629	-0,249445204
YMR292W	GOT1: ER to Golgi transport	-0,038659879	0,00572857	-0,108432453
YNL012W	SPO1: meiosis	-0,047066699	-0,204510059	-0,176185218
YNL044W	YIP3: ER to Golgi transport	0,186621009	0,190634523	-0,079164171
YNL050C	YNL050C: biological process unknown	0,124625822	-0,050054776	-0,104658925
YNL069C	RPL16B: protein biosynthesis	0,110972302	0,131567163	0,1539242
YNL096C	RPS7B: protein biosynthesis	0,376115417	0,356461544	0,228074745
YNL112W	DBP2: mRNA catabolism, nonsense-mediated decay	0,172192763	0,47810543	0,082900563
YNL130C	CPT1: phosphatidylcholine biosynthesis	0,157196266	-0,102966843	-0,006200541
YNL147W	LSM7: nuclear mRNA splicing, via spliceosome	-0,028357146	-0,080606669	0,056168017
YNL162W	RPL42A: protein biosynthesis	0,029675557	-0,187790527	-0,413689217
YNL246W	VPS75: protein-vacuolar targeting	-0,053885516	0,049382849	0,056380119
YNL265C	IST1: protein biosynthesis	-0,119750072	0,295016654	-0,115044071
YNL301C	RPL18B: protein biosynthesis	-0,081352927	-0,142767771	0,006049504
YNL302C	RPS19B: protein biosynthesis	-0,561474224	0,200984104	-0,29325763
YNL312W	RFA2: DNA recombination	0,162549723	0,002696706	0,135842384
YNR053C	NOG2: ribosome assembly	0,358684178	0,978411768	0,14939881
YOL047C	YOL047C: biological process unknown	0,52133722	0,188864579	0,410400099
YOL048C	YOL048C: biological process unknown	0,028248936	-0,047886582	-0,043651918
YOL120C	RPL18A: protein biosynthesis	-0,085249825	-0,237999758	0,000684845
YOL121C	RPS19A: protein biosynthesis	-0,135413668	0,162688543	0,191483511
YOL127W	RPL25: protein biosynthesis	-0,215369099	0,113575067	-0,086099377
YOR096W	RPS7A: protein biosynthesis	-0,551081993	0,056673601	-0,488638203
YOR122C	PFY1: response to osmotic stress	-0,117360469	0,003712806	-0,028927615
YOR182C	RPS30B: protein biosynthesis	-0,155351888	-0,039603184	-0,001608946
YOR234C	RPL33B: protein biosynthesis	0,164032592	0,050555375	-0,019071277
YOR293W	RPS10A: protein biosynthesis	-0,157100901	0,140098375	-0,126238236
YOR312C	RPL20B: protein biosynthesis	-0,166360295	-0,164758832	-0,242254789
YPL031C	PHO85: protein amino acid phosphorylation	0,06674175	0,198651297	-0,265553385

YPL075W	GCR1: positive regulation of transcription from RNA polymerase II	-0,112873363	-0,376567748	0,049949976
YPL079W	RPL21B: protein biosynthesis	-0,027296548	-0,00149601	-0,121342827
YPL081W	RPS9A: protein biosynthesis	0,194746024	-0,024418418	0,079423838
YPL090C	RPS6A: protein biosynthesis	-0,390242719	-0,16089062	-0,372471952
YPL129W	TAF14: chromatin remodeling	-0,220213948	-0,165996381	0,056360621
YPL143W	RPL33A: protein biosynthesis	-0,138066462	0,115977791	-0,01502695
YPL175W	SPT14: GPI anchor biosynthesis	0,012786296	-0,16001701	-0,018318743
YPL198W	RPL7B: protein biosynthesis	0,31864225	-0,004318114	0,135648439
YPL198W_2	RPL7B: protein biosynthesis	0,31864225	0,141214716	0,08640419
YPL218W	SAR1: ER to Golgi transport	0,172631397	0,1078415	-0,125241107
YPL241C	CIN2: microtubule-based process	0,003125145	-0,080859488	0,173144336
YPL249C-A	RPL36B: protein biosynthesis	-0,304636567	0,074714787	-0,295881321
YPR028W	YOP1: vesicle-mediated transport	-0,31515637	0,033176794	0,131735392
YPR043W	RPL43A: protein biosynthesis	-0,238551767	0,140938558	-0,250701476
YPR063C	YPR063C: biological process unknown	-0,313458094	0,058945915	-0,506260009
YPR098C	YPR098C: biological process unknown	-0,191336941	0,071994088	-0,110815157
YPR132W	RPS23B: protein biosynthesis	-0,235462691	-0,013740111	-0,347694788
YPR187W	RPO26: transcription from RNA polymerase II promoter	-0,055221332	-0,175758111	0,128236102

Genotype:		*set2*Δ	*set2*Δ	*set2*Δ
Strains compared:		W303 *set2*Δ vs W303	W303 *set2*Δ vs W303	W303 *set2*Δ vs W303
Feature:		Exon	Intron	Junction
Systematic Name	Common Name			
SNR17A	SNR17A	0,179532366	0,409513139	0,475160914
SNR17B	SNR17B	0,120026884	0,119309126	0,475160914
YAL001C	TFC3: transcription initiation from RNA polymerase III promoter	0,165071499	0,430577299	0,054720882
YAL003W	EFB1: translational elongation	0,211736715	0,304137702	0,132134784

YAL030W	SNC1: endocytosis	-0,082878968	0,096100317	-0,189253701
YBL018C	POP8: rRNA processing	-0,212412238	0,058167124	-0,206129316
YBL026W	LSM2: nuclear mRNA splicing, via spliceosome	-0,029191752	0,113811577	-0,138439947
YBL027W	RPL19B: protein biosynthesis	-0,022073083	0,007295409	-0,124172181
YBL040C	ERD2: protein retention in ER	0,323995887	0,131494076	0,396040843
YBL050W	SEC17: ER to Golgi transport	-0,095915906	0,253684667	-0,286196087
YBL059C-A	YBL059C-A: biological process unknown	-0,013927938	0,010030269	-0,143533861
YBL059W	YBL059W: biological process unknown	0,152449468	0,162161261	-0,066297146
YBL072C	RPS8A: protein biosynthesis	-0,532730657	0,026612668	-0,452866309
YBL087C	RPL23A: protein biosynthesis	-0,357007438	0,166006248	-0,224690234
YBL091C-A	SCS22: biological process unknown	-0,097880351	-0,104211451	-0,111723188
YBL092W	RPL32: protein biosynthesis	-0,395009641	0,014446788	-0,343364834
YBR048W	RPS11B: protein biosynthesis	-0,102572706	0,188638221	0,027336907
YBR078W	ECM33: cell wall organization and biogenesis	-0,311801837	0,425897026	0,189227605
YBR082C	UBC4: response to stress	-0,077356406	0,040574631	0,203699913
YBR084C-A	RPL19A: protein biosynthesis	0,01775962	0,229785276	-0,012751235
YBR089C-A	NHP6B: regulation of transcription from RNA polymerase II promot	-0,156755966	-0,099036393	-0,077709065
YBR119W	MUD1: nuclear mRNA splicing, via spliceosome	-0,333332655	0,133563668	0,183185186
YBR181C	RPS6B: protein biosynthesis	-0,217504038	-0,100770562	-0,260333796
YBR186W	PCH2: regulation of meiosis	0,079603241	-0,174501391	0,03507107
YBR189W	RPS9B: protein biosynthesis	-0,300905171	0,189303655	-0,110252744
YBR191W	RPL21A: protein biosynthesis	-0,003689024	0,037097052	-0,105298012
YBR219C	YBR219C: biological process unknown	0,302167042	0,109727243	-0,2371085
YBR230C	YBR230C: biological process unknown	-0,20846058	-0,028946609	-0,112208349
YCR028C-A	RIM1: mitochondrial genome maintenance	-0,235131762	0,168255756	-0,303605098
YCR031C	RPS14A: protein biosynthesis	0,01769516	-0,001457289	-0,325028519
YCR097W	HMRA1: regulation of transcription, mating-type specific	-0,087480186	-0,125252808	0,210237546
YCR097W_2	HMRA1: regulation of transcription, mating-type specific	-0,087480186	0,257660297	-0,090208054
YDL012C	YDL012C: biological process unknown	0,170019487	0,22542085	-0,027902817
YDL029W	ARP2: actin filament organization	-0,237036321	-0,013686696	-0,104101314

YDL061C	RPS29B: protein biosynthesis	-0,58300051	0,047462424	-0,173908988
YDL064W	UBC9: G2/M transition of mitotic cell cycle	-0,091390691	0,311697893	-0,017512547
YDL075W	RPL31A: protein biosynthesis	-0,439347825	-0,024871062	-0,316132645
YDL079C	MRK1: protein amino acid phosphorylation	0,01126874	-0,188513328	-0,070998494
YDL082W	RPL13A: protein biosynthesis	0,036307718	-0,159309322	-0,201672696
YDL083C	RPS16B: protein biosynthesis	-0,270206753	0,035178519	-0,191822659
YDL108W	KIN28: protein amino acid phosphorylation	0,115394148	0,35559232	-0,010479963
YDL115C	IWR1: meiosis	-0,027822684	0,222452107	0,01794767
YDL125C	HNT1: nucleotide metabolism	0,150979749	0,417441272	0,107370516
YDL130W	RPP1B: translational elongation	0,129329734	0,03361241	0,076925895
YDL136W	RPL35B: protein biosynthesis	-0,051231833	-0,074101242	-0,095743445
YDL137W	ARF2: ER to Golgi transport	0,114437953	0,19562268	-0,111421106
YDL189W	RBS1: galactose metabolism	-0,155225682	-0,230192081	0,10252156
YDL191W	RPL35A: protein biosynthesis	-0,335531952	-0,04203484	0,037336329
YDL219W	DTD1: translation	-0,025014223	0,256736658	-0,1622494
YDR005C	MAF1: negative regulation of transcription from RNA polymerase II	0,36958684	0,651360683	0,075511485
YDR025W	RPS11A: protein biosynthesis	-0,333258131	0,106840218	0,078931102
YDR059C	UBC5: endocytosis	0,044740636	0,076179606	-0,109663304
YDR064W	RPS13: protein biosynthesis	0,032505182	0,009755861	0,032362444
YDR092W	UBC13: protein monoubiquitination	-0,240604013	0,042717895	-0,107661716
YDR129C	SAC6: endocytosis	0,286808619	0,239755444	0,229732137
YDR139C	RUB1: protein deneddylation	-0,058428318	0,007907524	-0,086693717
YDR305C	HNT2: nucleoside catabolism	-0,011522485	0,094690299	-0,040540431
YDR367W	YDR367W: biological process unknown	-0,292927214	0,012127248	0,074555654
YDR381W	YRA1: mRNA-nucleus export	0,550962968	0,456143251	-0,255556976
YDR397C	NCB2: negative regulation of transcription from RNA polymerase II	-0,149254033	-0,107014295	0,089139706
YDR424C	DYN2: microtubule-based process	-0,083286781	0,262615324	-0,122498251
YDR424C_2	DYN2: microtubule-based process	-0,083286781	0,007003889	-0,076188462
YDR447C	RPS17B: protein biosynthesis	-0,635093887	0,016247829	-0,819300614
YDR450W	RPS18A: protein biosynthesis	-0,55362253	-0,087052182	0,170002635

YDR471W	RPL27B: protein biosynthesis	-0,290350138	-0,13498606	-0,489307995
YDR500C	RPL37B: protein biosynthesis	-0,361847829	-0,010202131	-0,008431309
YEL012W	UBC8: protein monoubiquitination	-0,044346909	0,147182557	-0,146529149
YER003C	PMI40: protein amino acid glycosylation	0,052801052	0,011636771	-0,088184102
YER007C-A	RBF20: biological process unknown	-0,2384693	-0,07145492	-0,325631185
YER044C-A	MEI4: sporulation (sensu Fungi)	-0,351592518	-0,151701928	0,004865552
YER056C-A	RPL34A: protein biosynthesis	-0,541585896	0,062414969	0,050464645
YER074W	RPS24A: protein biosynthesis	0,054557473	0,04254055	-0,158452727
YER074W-A	YOS1: ER to Golgi transport	-0,559045826	-0,026018851	-0,057991832
YER074W-A_2	YOS1: ER to Golgi transport	-0,559045826	0,143401446	-0,248652569
YER093C-A	YER093C-A: biological process unknown	-0,159774285	-0,064668218	0,038038981
YER102W	RPS8B: protein biosynthesis	-0,101317784	-0,009448429	-0,191203564
YER117W	RPL23B: protein biosynthesis	-0,343887992	0,003791542	-0,134028889
YER131W	RPS26B: protein biosynthesis	-0,384974972	0,162040904	-0,130140918
YER133W	GLC7: 35S primary transcript processing	0,488999656	0,236534248	0,082432211
YER179W	DMC1: meiosis	-0,077642648	-0,105373732	0,357317828
YFL034C-A	RPL22B: protein biosynthesis	0,324879329	0,402568729	-0,197716867
YFL034C-B	MOB2: protein amino acid phosphorylation	0,234690017	0,577697233	0,099536544
YFL039C	ACT1: cell wall organization and biogenesis	0,236173598	0,140061395	0,078830332
YFR024C-A	LSB3: actin filament organization	0,04653254	-0,057232498	0,058374103
YFR031C-A	RPL2A: protein biosynthesis	-0,174390656	0,064448372	-0,230923826
YFR032C-A	RPL29: protein biosynthesis	-0,293105611	-0,055738995	-0,159028407
YGL030W	RPL30: protein biosynthesis	-0,523551067	0,035883236	-0,565817743
YGL031C	RPL24A: protein biosynthesis	-0,573106514	0,00759704	-0,09224415
YGL033W	HOP2: synapsis	-0,407610449	0,034895609	0,043312635
YGL076C	RPL7A: protein biosynthesis	-0,523500125	0,30510027	-0,29597994
YGL076C_2	RPL7A: protein biosynthesis	-0,523500125	0,09264352	-0,301119457
YGL087C	MMS2: DNA repair	-0,054127804	0,061023129	0,01956173
YGL103W	RPL28: protein biosynthesis	-0,658331337	0,556380583	-0,041083503
YGL137W	SEC27: ER to Golgi transport	0,2304621	0,155470087	0,074681811

YGL178W	MPT5: cell wall organization and biogenesis	0,478425212	0,644742746	0,25831711
YGL187C	COX4: aerobic respiration	-0,240699973	-0,294815613	0,246817074
YGL189C	RPS26A: protein biosynthesis	-0,4843175	0,081345507	0,25190775
YGL226C-A	OST5: protein amino acid N-linked glycosylation	-0,512263906	0,042623346	0,121035265
YGL232W	TAN1: tRNA modification	-0,112768072	0,120412147	0,15920514
YGL251C	HFM1: meiosis	0,29428327	0,077227942	0,118149666
YGR001C	YGR001C: biological process unknown	0,180729454	0,073570806	-0,264761282
YGR001C_2	YGR001C: biological process unknown	0,180729454	-0,165710343	-0,104290382
YGR027C	RPS25A: protein biosynthesis	-0,390831241	-0,040467717	0,055085204
YGR029W	ERV1: mitochondrion organization and biogenesis	0,098741562	-0,015056609	-0,02525258
YGR118W	RPS23A: protein biosynthesis	-0,516751313	-0,095622996	-0,051671919
YGR148C	RPL24B: protein biosynthesis	-0,238955496	-0,079261842	-0,422580706
YGR183C	QCR9: aerobic respiration	0,032723672	-0,060734858	-0,108525958
YGR214W	RPS0A: protein biosynthesis	-0,39341884	0,342565718	-0,136665302
YGR225W	AMA1: sporulation (sensu Fungi)	-0,154748502	-0,175855287	-0,028387253
YHL001W	RPL14B: protein biosynthesis	-0,173527858	-0,114484976	-0,089159422
YHR001W-A	QCR10: aerobic respiration	0,500101571	0,164103448	-0,502539169
YHR010W	RPL27A: protein biosynthesis	-0,105507403	0,038751596	0,281551015
YHR012W	VPS29: retrograde transport, endosome to Golgi	-0,202999004	0,106197888	0,06133366
YHR016C	YSC84: endocytosis	0,118339863	0,060767752	-0,05979998
YHR021C	RPS27B: protein biosynthesis	-0,328457957	-0,131050951	-0,032800257
YHR039C-A	VMA10: vacuolar acidification	-0,451720434	-0,116528501	-0,549439815
YHR041C	SRB2: transcription from RNA polymerase II promoter	-0,26576945	-0,169070051	-0,095489774
YHR077C	NMD2: mRNA catabolism	0,081519098	0,007536556	0,138011929
YHR097C	YHR097C: biological process unknown	0,182334105	0,202783885	0,10161465
YHR101C	BIG1: cell wall biosynthesis (sensu Fungi)	0,171000266	0,431671966	0,111503133
YHR123W	EPT1: phosphatidylethanolamine biosynthesis	-0,043605697	0,121007413	-0,464252977
YHR141C	RPL42B: protein biosynthesis	-0,540535649	-0,274271281	-0,600623573
YHR203C	RPS4B: protein biosynthesis	-0,103996623	0,032387954	-0,224720955
YIL004C	BET1: ER to Golgi transport	0,02907017	0,048018935	-0,174416338

YIL018W	RPL2B: protein biosynthesis	-0,41644019	0,005619808	-0,292759628
YIL052C	RPL34B: protein biosynthesis	-0,731564511	-0,12076533	-0,015426966
YIL069C	RPS24B: protein biosynthesis	-0,201454361	0,048051958	-0,064640103
YIL106W	MOB1: protein amino acid phosphorylation	-0,121324231	-0,054374021	-0,197041382
YIL111W	COX5B: mitochondrial electron transport, cytochrome c to oxygen	0,099982167	0,327240401	0,0908799
YIL133C	RPL16A: protein biosynthesis	-0,251214774	-0,097466482	-0,3370084
YIL148W	RPL40A: protein biosynthesis	-0,1919781	0,127434381	-0,226908273
YJL001W	PRE3: response to stress	-0,341033844	0,232347516	-0,452269642
YJL024C	APS3: vesicle-mediated transport	-0,19594778	0,274562041	0,031802453
YJL041W	NSP1: mRNA-nucleus export	0,258476587	0,488949133	0,610972012
YJL136C	RPS21B: protein biosynthesis	-0,120122912	0,050712625	-0,084405035
YJL177W	RPL17B: protein biosynthesis	-0,006949745	0,084940173	0,006876683
YJL189W	RPL39: protein biosynthesis	-0,157433909	0,021886607	-0,49504713
YJL191W	RPS14B: protein biosynthesis	0,095334272	0,433868503	-0,232488671
YJL205C	NCE1: biological process unknown	0,156264067	0,287747695	-0,016459377
YJR021C	REC107: meiotic recombination	0,028394042	0,14655537	-0,059785042
YJR094W-A	RPL43B: protein biosynthesis	-0,433153985	-0,042239623	-0,412471985
YJR145C	RPS4A: protein biosynthesis	-0,064592237	0,048380437	-0,172854273
YKL002W	DID4: protein retention in Golgi	0,056836662	0,17038086	-0,148848825
YKL006C-A	SFT1: intra-Golgi transport	-0,367363693	-0,261921072	-0,082282097
YKL006W	RPL14A: protein biosynthesis	0,245189767	0,114471644	-0,101605882
YKL081W	TEF4: translational elongation	0,318428133	-0,084866769	0,222711061
YKL156W	RPS27A: protein biosynthesis	-0,113990404	0,005874608	-0,146567069
YKL157W	APE2: peptide metabolism	0,131962408	-0,044048226	1,34E-05
YKL180W	RPL17A: protein biosynthesis	-0,112870169	0,169752162	-0,310062078
YKL186C	MTR2: poly(A)+ mRNA-nucleus export	-0,196426382	-0,032466935	0,052571996
YKL186C_2	MTR2: poly(A)+ mRNA-nucleus export	-0,196426382	-0,11506968	0,076571733
YKL186C_3	MTR2: poly(A)+ mRNA-nucleus export	-0,196426382	-0,132076687	0,050745236
YKL186C_4	MTR2: poly(A)+ mRNA-nucleus export	-0,196426382	-0,199668771	0,13878537
YKL186C_5	MTR2: poly(A)+ mRNA-nucleus export	-0,196426382	-0,218927749	0,026629702

YKL186C_6	MTR2: poly(A)+ mRNA-nucleus export	-0,196426382	-0,035295841	-0,045712278
YKL190W	CNB1: cell wall organization and biogenesis	0,018632689	0,121907613	0,01247367
YKR057W	RPS21A: protein biosynthesis	-0,064280783	0,139072879	-0,248542205
YKR094C	RPL40B: protein biosynthesis	-0,380341492	-0,0025212	-0,083890006
YLL050C	COF1: actin filament organization	-0,374555593	0,120059357	-0,150050427
YLR048W	RPS0B: protein biosynthesis	-0,280549271	0,286520514	0,259100852
YLR061W	RPL22A: protein biosynthesis	-0,053262229	-0,052871432	-0,041674086
YLR078C	BOS1: ER to Golgi transport	-0,04100539	-0,115519178	-0,013845596
YLR093C	NYV1: vesicle fusion	0,071605015	0,197976986	-0,120434598
YLR128W	DCN1: protein neddylation	0,134214168	-0,071357575	-0,060682918
YLR185W	RPL37A: protein biosynthesis	-0,346025638	0,076913033	-0,569390667
YLR211C	YLR211C: biological process unknown	-0,100542819	0,111169281	-0,145489603
YLR275W	SMD2: nuclear mRNA splicing, via spliceosome	-0,075677457	0,051683575	0,043212068
YLR287C-A	RPS30A: protein biosynthesis	-0,136500517	0,262867308	-0,179007171
YLR306W	UBC12: protein monoubiquitination	0,066098776	0,019770951	0,08905016
YLR316C	TAD3: tRNA modification	0,21277497	0,265574056	-0,079374707
YLR316C_2	TAD3: tRNA modification	0,21277497	0,213672166	-0,039923129
YLR333C	RPS25B: protein biosynthesis	-0,679388975	-0,132827947	0,047418037
YLR344W	RPL26A: protein biosynthesis	-0,192751819	0,149627519	0,155221857
YLR367W	RPS22B: protein biosynthesis	-0,481715585	0,294014117	0,099886033
YLR367W_2	RPS22B: protein biosynthesis	-0,481715585	0,424195873	0,063337962
YLR388W	RPS29A: protein biosynthesis	-0,32412403	0,232534411	-0,457136834
YLR406C	RPL31B: protein biosynthesis	-0,29374143	0,002025023	-0,335471363
YLR426W	YLR426W: biological process unknown	0,299696721	0,58852354	-0,064227054
YLR448W	RPL6B: protein biosynthesis	-0,059144815	-0,130226118	-0,005997687
YML024W	RPS17A: protein biosynthesis	-0,410800908	0,068634088	-0,420158321
YML025C	YML6: protein biosynthesis	0,183101984	-0,000963124	-0,001612649
YML026C	RPS18B: protein biosynthesis	-0,088179071	0,161351807	-0,169729476
YML034W	SRC1: mitotic sister chromatid segregation	0,078325759	0,14347996	-0,020922901
YML034W_2	SRC1: mitotic sister chromatid segregation	0,078325759	-0,012813756	0,014342849

YML056C	IMD4: biological process unknown	-0,064110239	0,450136979	0,230102269
YML067C	ERV41: ER to Golgi transport	0,153872572	0,049103314	-0,20692026
YML073C	RPL6A: protein biosynthesis	-0,045743132	0,038767145	-0,16221568
YML085C	TUB1: mitotic sister chromatid segregation	0,044944226	-0,012022957	0,031399587
YML094W	GIM5: tubulin folding	-0,027851617	0,059103183	-0,136539682
YML124C	TUB3: mitotic sister chromatid segregation	-0,001367455	0,178492665	-0,039825627
YMR033W	ARP9: chromatin remodeling	-0,007161559	-0,00326674	0,124652883
YMR079W	SEC14: sporulation (sensu Fungi)	0,04734132	0,118170617	-0,075361557
YMR116C	ASC1: biological process unknown	-0,100389833	-0,10968707	-0,168893301
YMR125W	STO1: nuclear mRNA splicing, via spliceosome	-0,192808517	0,104010762	-0,222966871
YMR133W	REC114: meiotic recombination	0,027931046	-0,006828412	-0,153774649
YMR142C	RPL13B: protein biosynthesis	-0,050931975	0,011331668	-0,09761018
YMR143W	RPS16A: protein biosynthesis	-0,145465569	-0,20776743	-0,178107884
YMR194W	RPL36A: protein biosynthesis	-0,526897933	0,085680581	-0,673340057
YMR201C	RAD14: nucleotide-excision repair, DNA damage recognition	0,065803068	-0,108555966	-0,230933198
YMR225C	MRPL44: protein biosynthesis	-0,207267357	-0,080505433	-0,281391564
YMR230W	RPS10B: protein biosynthesis	-0,315827182	-0,181853393	-0,416527879
YMR292W	GOT1: ER to Golgi transport	0,395680166	0,235327068	0,267001967
YNL012W	SPO1: meiosis	0,317676548	0,149692891	-0,158101839
YNL044W	YIP3: ER to Golgi transport	0,266010698	0,127013105	-0,110717121
YNL050C	YNL050C: biological process unknown	-0,092014812	-0,061411027	-0,036278201
YNL069C	RPL16B: protein biosynthesis	0,091378726	-0,135264444	-0,002114395
YNL096C	RPS7B: protein biosynthesis	-0,238203949	0,083692303	-0,225981675
YNL112W	DBP2: mRNA catabolism, nonsense-mediated decay	0,509731286	0,375543615	0,716208333
YNL130C	CPT1: phosphatidylcholine biosynthesis	-0,456175613	-0,141571238	-0,139367482
YNL147W	LSM7: nuclear mRNA splicing, via spliceosome	-0,160343398	0,06834648	-0,058624779
YNL162W	RPL42A: protein biosynthesis	-0,327004242	0,282000991	-0,497914829
YNL246W	VPS75: protein-vacuolar targeting	0,098638841	0,078704722	-0,085567106
YNL265C	IST1: protein biosynthesis	-0,114163189	0,237795096	-0,222332646
YNL301C	RPL18B: protein biosynthesis	0,052267758	-0,114560918	0,161017595

YNL302C	RPS19B: protein biosynthesis	-0,134381587	0,070768214	-0,369847065
YNL312W	RFA2: DNA recombination	0,027831574	0,117989476	0,177354786
YNR053C	NOG2: ribosome assembly	0,344442025	0,115926397	0,329089998
YOL047C	YOL047C: biological process unknown	0,043635494	0,094064798	-0,068402406
YOL048C	YOL048C: biological process unknown	-0,22206719	-0,015941327	0,328960247
YOL120C	RPL18A: protein biosynthesis	0,009382878	0,232163528	-0,030374388
YOL121C	RPS19A: protein biosynthesis	-0,485548202	0,019246889	-0,085204367
YOL127W	RPL25: protein biosynthesis	-0,296754918	0,003206396	-0,183708236
YOR096W	RPS7A: protein biosynthesis	-0,331257373	0,046435356	-0,3536696
YOR122C	PFY1: response to osmotic stress	-0,125457242	-0,001914688	0,096776311
YOR182C	RPS30B: protein biosynthesis	-0,253537014	-0,008241416	0,037253301
YOR234C	RPL33B: protein biosynthesis	-0,255602965	0,030629677	-0,111498515
YOR293W	RPS10A: protein biosynthesis	-0,344459105	0,131671851	-0,543732734
YOR312C	RPL20B: protein biosynthesis	-0,051300782	0,072986662	-0,283438501
YPL031C	PHO85: protein amino acid phosphorylation	0,020527707	-0,040126573	-0,181273331
YPL075W	GCR1: positive regulation of transcription from RNA polymerase II	0,400593784	0,225056062	-0,194031252
YPL079W	RPL21B: protein biosynthesis	-0,444807033	-0,11407887	-0,107836711
YPL081W	RPS9A: protein biosynthesis	0,101261192	0,159630657	-0,003467385
YPL090C	RPS6A: protein biosynthesis	-0,35746377	-0,003382894	-0,086927872
YPL129W	TAF14: chromatin remodeling	0,201419531	0,059354029	0,150049519
YPL143W	RPL33A: protein biosynthesis	-0,003484575	0,32311519	-0,120116427
YPL175W	SPT14: GPI anchor biosynthesis	0,134281087	0,194258801	-0,147419633
YPL198W	RPL7B: protein biosynthesis	0,404684292	0,317858122	0,050041172
YPL198W_2	RPL7B: protein biosynthesis	0,404684292	0,269744975	-0,002186439
YPL218W	SAR1: ER to Golgi transport	0,482701801	0,243593735	0,141814872
YPL241C	CIN2: microtubule-based process	0,036789594	0,056902273	-0,098695054
YPL249C-A	RPL36B: protein biosynthesis	-0,218848101	0,259284601	-0,175530062
YPR028W	YOP1: vesicle-mediated transport	-0,024420094	0,07035215	0,157289199
YPR043W	RPL43A: protein biosynthesis	-0,08066806	0,185530709	-0,058821312
YPR063C	YPR063C: biological process unknown	-0,18297896	-0,171442604	-0,465171235

YPR098C	YPR098C: biological process unknown	-0,481972973	0,068130516	-0,190351173
YPR132W	RPS23B: protein biosynthesis	-0,539123591	-0,104889576	-0,640414606
YPR187W	RPO26: transcription from RNA polymerase II promoter	0,038260748	0,061583442	-0,141577996

Supplementary Table S4: Complete identification table referring to Figure 2a

sample name	Protein name	Protein accession numbers	Protein molecular weight (Da)	Percentage sequence coverage	Peptide sequence	Variable modifications identified by spectrum	Total number of peptide	Number of shared peptide	Number of discriminant peptide
htb1K123R	Heat shock protein SSB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSB1 PE=1 SV=3	sp|P11484	66602,8	56%	AADEAFAK-ARFEDLNAALFK-AVITVPAYFNDAQR-DAGAISGLNVLR-ENTLLGEFDLK-FEDLNAALFK-IEAALSDALAALQIEDPSADELRK-IINEPTAAAIAYGLGAGK-KTGLDISDDAR-LESYVASIEQTVTDPVLSSK-LIGDAA		28	0	28
htb1K123R	Keratin, type II cytoskeletal 1 - Homo sapiens	sp|P04264	66019,2	33%	AEAESLYQSK-DVDGAYMTK-FLEQQNQVLQTK-GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR-IEISELNR-LALDLEIATYR-LNDLEDALQQAK-NMQDMVEDYR-QISNLQQSISDAEQR-SKAEAESLYQSK-SLDLDSIIAEVK-		19	0	19
htb1K123R	Histone H1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HHO1 PE=1 SV=1	sp|P53551	27805,3	22%	ASSPSSLTYK-cVENGELVQPK-ELIIEGLTALK-GVEAGDFEQPK-TSSNFDYLFNSAIK		5	0	5
htb1K123R	THO complex subunit THP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=THP2 PE=1 SV=1	sp|O13539	30300,7	17%	DVAAGVQNPK-ELINSSIR-SISEYYSTFEHLNR-SSDDLLTESLK		4	0	4
htb1K123R	60S ribosomal protein L9-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL9B PE=1 SV=1	sp|P51401	21657	40%	FIEVR-FLDGIYVSHK-HIDVTFTK-SLVDNmITGVTK-VNNQLIK-YIQTEQQIEIPEGVTVSIK-YVYAHFPINVNIVEK		7	6	1
htb1K123R	40S ribosomal protein S9-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS9A PE=1 SV=3	sp|O13516,sp|P05755	22443,9	40%	ISFQLSK-KLDYVLALK-LAGEFGLK-LDAELK-LDYVLALK-lFEGNALIR-LQTQVYK-QIVNIPSFMVR-VEDFLER-VGVLSEDK-VGVLSEDKK-VLITQR		12	0	12
htb1K123R	Heat shock protein SSA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSA2 PE=1 SV=3	sp|P10592	69471,8	53%	ARFEELcADLFR-ATAGDTHLGGEDFDNR-AVGIDLGTTYScVAHFSNDR-DAGTIAGLNVLR-ELQEVANPIMSK-ETAESYLGAK-FEELcADLFR-FELSGIPPAPR-IINEPTAAAIAYGLDK-IINEPTAAAIAYGLDKK-IT	c7: Carbamidome	29	22	7
htb1K123R	Heat shock protein SSA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSA1 PE=1 SV=4	sp|P10591	69659,4	47%	ARFEELcADLFR-ATAGDTHLGGEDFDNR-AVGIDLGTTYScVAHFANDR-DAGTIAGLNVLR-ELQDIANPIMSK-ETAESYLGAK-FEELcADLFR-FELSGIPPAPR-IINEPTAAAIAYGLDK-IINEPTAAAIAYGLDKK-IT	c7: Carbamidome	26	1	25
htb1K123R	Hexokinase-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HXK2 PE=1 SV=4	sp|P04807	53944,7	5%	IFTVPTETLQAVTK-INEGILQR		2	0	2
htb1K123R	Protein OPY1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=OPY1 PE=1 SV=1	sp|P38271	37741,3	2%	mFDPR	m1: Oxidation (+	1	0	1
htb1K123R	Pentafunctional AROM polypeptide OS=Saccharomyces cerevisiae (strain YJM789) GN=ARO1 PE=3 SV=1	sp|A6ZY89,sp|B3LGE9,sp|C7GIN5,sp	174810,3	1%	ITQTATSTTVSGPPVGTLKPLK		1	0	1
htb1K123R	ATP-dependent RNA helicase SUB2 OS=Saccharomyces cerevisiae (strain YJM789) GN=SUB2 PE=3 SV=1	sp|A6ZXP4	50280,1	10%	DVQEIFR-LTLHGLQQYYIK-NKDTAPHIVVATPGR-TAVFYGGTPISK		4	0	4
htb1K123R	60S ribosomal protein L14-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL14B PE=1 SV=1	sp|P38754	15153,2	41%	AALTDFER-FQVMVLR-KVLIDGPK-LAAIVEIIDQK-LVEVGR-VLIDGPK-WAAAGVcEK-WAASSWAK		8	0	8
htb1K123R	Keratin, type I cytoskeletal 14 - Homo sapiens	sp|P02533	51622,6	5%	LAADDFR-LASYLDK-VTMQNLNDR		3	3	0
htb1K123R	Trypsin precursor - Sus scrofa	sp|P00761	24409,3	29%	APVLSDSScK-IITHPNFNGNTLDNDImLIK-IITHPNFNGNTLDNDIMLIKLSSPATLNSR-LGEHNIDVLEGNEQFINAAK-LSSPATLNSR-VATVSLPR	c9: Carbamidome	6	0	6
htb1K123R	Regulator of V-ATPase in vacuolar membrane protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RAV1 PE=1 SV=1	sp|P47104	154939,8	0%	VETRLK		1	0	1
htb1K123R	FACT complex subunit SPT16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPT16 PE=1 SV=1	sp|P32558	118636	42%	AIDLFKDPESK-ALADVVQQDK-DFNKPVTHINTVPIESLDFLK-DLGFQGVPNR-DSNFILNVK-DSQSANNYALQLADTVQIPLDETEPPR-DVNEQAFLSVSSK-EASDMSVDETGGGR-EIVTNILKPGR-ENEFNVIDISLGLSK-EVYES		39	0	39
htb1K123R	NADPH-dependent aldose reductase GRE3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GRE3 PE=1 SV=1	sp|P38715	37120,2	10%	SIGVSNFQGSLIQDLLR-VSQNHPGSTTSQVLLR		2	0	2
htb1K123R	Nuclear segregation protein BFR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BFR1 PE=1 SV=1	sp|P38934	54641,7	38%	ADFDNEFK-DLVNIEPIR-DLVNIEPIRK-DVSNQFEENQQK-EELNGLNPK-FKRPDVSVR-IDTEIGLIR-INQLKEELNGLNPK-IQADLK-ITVEQLK-KDDFVNVAPSK-KIDTEIGLIR-KLDTLNVQLK-KNILPDLSSNALETKPAR-KQID		24	0	24
htb1K123R	Eukaryotic initiation factor 4F subunit p130 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TIF4632 PE=1 SV=1	sp|P39936	103901,5	17%	AQPISDIYEFAYPENVERPDIK-DTLTETSNEK-EAPKPTGEANEVVIDGK-EATPVLPANEAVK-EEIAPLVPSANR-FRPDPAWVEAVSSK-IEITTK-IVIEQIFHK-LFLEQVR-LVLHYLVAR-TIQQIHQEEEQLR-WEDDGETLK-YTYGPTF		13	3	10
htb1K123R	Eukaryotic initiation factor 4F subunit p150 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TIF4631 PE=1 SV=2	sp|P39935	107103,8	30%	ADAEWVQSTASK-ASSEENISEAEK-AVIEQIFLK-DATPIEDVFSFNYPEGIEGPDIK-DSFITTR-EDDKPKEEVAPLVPSANR-EEVAPLVPSANR-ELNPDITDETNEGK-EQLEGSSGNNNIPMK-EVPVQEETK-FIGFLYR-IEITTK-IVIPPG		24	0	24
htb1K123R	60S ribosomal protein L32 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL32 PE=1 SV=1	sp|P38061	14771,8	33%	DLETLTmHTK-TFLVANVK-TYAAEIAHNISAK-VAENWR-VVILAR	m7: Oxidation (+	5	0	5
htb1K123R	Nuclear cap-binding protein complex subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STO1 PE=1 SV=2	sp|P34160	100023,3	61%	AFEDDIK-AGIFTEPGESIAQLIATYEENPLAPTFK-AIAPVFGR-EmMPDIR-EYNGEPPYEMVELVR-FFYSHLDSLDFELK-FIANIDNAIPHESTR-FLSEAImNEYGHEDYFNNALLSTLNAVVVEQPQK-FLSILSPmFLVDELINIYK-FVII		47	0	47
htb1K123R	60S ribosomal protein L34-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL34B PE=1 SV=1	sp|P40525,sp|P87262	13641,1	26%	AFLIEEQK-cGDcGSALQGISTLRPR-TPGGILR		3	0	3
htb1K123R	Nuclear polyadenylated RNA-binding protein NAB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAB2 PE=1 SV=1	sp|P32505	58319,6	11%	FGALcSNPScPFGHPTPANEDAK-FGVNcK-IKEVKPISQK-KPVQTGIVLcK-NLTcDNPEcR	c5: Carbamidome	5	0	5
htb1K123R	V-type proton ATPase catalytic subunit A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VMA1 PE=1 SV=3	sp|P17255	118639,8	13%	ANELVESYR-DLSLLGSHVR-FHLTIEGPK-FTcNATHELVVR-IVELVK-LADSTGDVK-LSADYPLLTGQR-NIPSFLSTDNIGTR-NVSmIADSSSR-SLGLVVSVNAEPAK-SYPISEGPER-TTLVANTSNMPVAAR-TVNLYSK		13	0	13
htb1K123R	ATP-dependent molecular chaperone HSP82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP82 PE=1 SV=1	sp|P02829	81410,2	30%	AELINNLGTIAK-AILFIPK-APFDLFESK-DSGIGMTK-EILGDQVEK-ELISNASDALDK-GVVDSEDLPLNLSR-HSEFVAYPIQLVVTK-KTFEISPK-LGVHEDTQNR-LLDAPAAIR-NIYYITGESLK-NPSDITQEEYNAFYK-QLETEPDLI		22	0	22
htb1K123R	ATP-dependent molecular chaperone HSC82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSC82 PE=1 SV=4	sp|P15108	80903,4	30%	AELINNLGTIAK-AILFIPK-APFDLFESK-DSGIGMTK-ELISNASDALDK-GVVDSEDLPLNLSR-HSEFVAYPIQLLVTK-KTFEISPK-LGVHEDTQNR-LLDAPAAIR-NIYYITGESLK-NPSDITQEEYNAFYK-QLETEPDLFIR-RAPFDLF		22	20	2
htb1K123R	60S ribosomal protein L27-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL27A PE=1 SV=1	sp|P0C2H6,sp|P0C2H7	15531,2	54%	KVVIVKPHDEGSK-NQWFFSK-SHPFGHALVAGIER-SVVSTETFEQPSQR-VAVVVR-VVIVKPHDEGSK-VVNYNHLLPTR-YTLDVEAFK		8	0	8
htb1K123R	Heat shock protein 26 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP26 PE=1 SV=3	sp|P15992	23880,2	40%	EVARPNNYAGALYDPR-LLGEGGLR-NQILVSGEIPSTLNEESK-NQILVSGEIPSTLNEESKDK-SVAVPVDILDHDNNYELK-VITLPDYPGVDADNIK-VVVPGVK		7	0	7
htb1K123R	RNA annealing protein YRA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YRA1 PE=1 SV=2	sp|Q12159	24956,3	35%	EFFASQVGGVQR-FNGSPIDGGR-GQSTGmANITFK-LLDTTR-LNLIVDPNQRPVK-SLDEIIGSNK-VLLSYNER-VNVEGLPR		8	0	8
htb1K123R	Isocitrate dehydrogenase [NADP], mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IDP1 PE=1 SV=1	sp|P21954	48192,8	8%	ITQDAAEAIKK-LILPYLDVDLK-TFESEAAHGTVTR		3	0	3
htb1K123R	Guanine nucleotide-binding protein subunit beta-like protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ASC1 PE=1 SV=4	sp|P38011	34805,9	46%	ASMIISGSR-aSNEVLVLR-DGEImLWNLAAK-DKTLISWK-FGVPVR-GQcLATLLGHNDWVSQVR-GTLEGHNGWVTSLATSAGQPNLLLSASR-KAmYTLSAQDEVFSLAFSPNR-lWDVATGETYQR-SDVmSVDIDKK-TLISWK-YW		12	0	12
htb1K123R	Heat shock protein SSA4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSA4 PE=1 SV=3	sp|P22202	69652,7	28%	ARFEELcADLFR-AVGIDLGTTYScVAHFANDR-DAGTIAGLNVLR-FEELcADLFR-FELSGIPPAPR-IINEPTAAAIAYGLDK-IINEPTAAAIAYGLDKK-ITITNDK-KSEVFSTYADNQPGVLIQVFEGER-LIGDAAK-LVN	c7: Carbamidome	17	11	6
htb1K123R	UTP--glucose-1-phosphate uridylyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UGP1 PE=1 SV=1	sp|P32861	55989,9	47%	DGHEINVLQLETAcGAAIR-EGNTFLDLSVR-EHIDEFK-FGPNPLIK-FTNFNTNNLWINLK-GGTLISYDGQVR-GTVIIVcSDGHK-HFDGAHGVVVPR-ILNHmIETGAEYIMELTDK-IVELDHLTITGNVFLGK-LIESSN	c14: Carbamidom	20	0	20
htb1K123R	Glucokinase-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GLK1 PE=1 SV=1	sp|P17709	55379,1	2%	LPTTPTER		1	0	1
htb1K123R	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MET6 PE=	sp|P05694	85862,4	14%	AVDVTALEMVK-FINSEIEK-ITVDELFK-LDAEIK-NVSGQDVAAALEANAK-QTLSVGIVDGR-VFNLPLFPTTTIGSFPQTK-VIQVDEPALR-VVVATSSSLLHTPVDLNNETK		9	1	8
htb1K123R	Nascent polypeptide-associated complex subunit alpha OS=Saccharomyces cerevisiae (strain YJM789) GN=EGD2 PE=3 SV=1	sp|A6ZT99,sp|P38879	18709,1	7%	SAGGNYVVFGEAK		1	0	1
htb1K123R	Protein NRD1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NRD1 PE=1 SV=1	sp|P53617	63860,4	31%	AYLDETR-cFAMDISNNTANTASQQLSLDPK-DGALPLR-HEAENVLQNFNK-IISLIIDYSR-KLTTYALDHIDIESK-KSPPLNLNISLPTDLTSTDPAK-LGSLYIIDSIGR-LTTYALDHIDIESK-MLLDIWDR-QILSNLK-QILSNLKK-QQAAL		18	0	18
htb1K123R	60S ribosomal protein L4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL4A PE=1 SV=4	sp|P10664	39092	56%	AGHQTSAESWGTGR-AVGAHSDLLK-FVIWTEAAFTK-GPLVVYAEDNGIVK-IINSSEIQSAIRPAGQATQK-IPEIPLVVSTDLESIQK-LDQVWGSETVASSK-MFAPTK-NVPGVETANVASLNLLQLAPGAHLGR-QAYAVSEK-RGPLVV		15	0	15
htb1K123R	Proteasome component PRE6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE6 PE=1 SV=1	sp|P40303	28438,7	9%	YTQSGGVRPFGVSTLIAGFDPR		1	0	1
htb1K123R	Transcription elongation factor SPT5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPT5 PE=1 SV=1	sp|P27692	115651,4	24%	AAAQDGYVPQR-EGAVDLTSVSQSIK-EGGEGITYDELVNR-EVTITANNLSK-FDEIDPTTQQR-FLLPSVDTATIWGVR-GQLGIVK-IEVLNGEQR-IGDTIVEK-IVENAGVFVVNPSNVEAVASK-KIVENAGVFVVNPSNVEAVASK-LD		22	0	22
htb1K123R	Nuclear cap-binding protein subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CBC2 PE=1 SV=1	sp|Q08920	23775,7	43%	FDFDASR-gGFAIPFAER-IIMGLDR-LDTPSR-NPNGLQELR-RIIMGLDR-RNPNGLQELR-SGGQVSDELR-sLEEFDEVKYDHSTK-TITIDLDPGFEDGR-YLSDTKLDEK		11	0	11
htb1K123R	Elongation factor 1-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TEF1 PE=1 SV=1	sp|P02994	50032,6	52%	EHALLAFTLGVR-ETSNFIK-FDELLEK-FQEIVK-FVPSKPmcVEAFSEYPPLGR-IGGIGTVPVGR-LPLQDVYK-QLIVAVNK-QLIVAVNKmDSVK-QTVAVGVIK-sGDAALVK-SHINVVVIGHVDSGK-SVEMHHEQLEQGVPGDNVGF		19	0	19
htb1K123R	60S ribosomal protein L24-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL24A PE=1 SV=1	sp|P04449	17614,4	20%	AQRPITGASLDLIK-IAWTVLFR-KGITEEVAK		3	0	3
htb1K123R	Protein URA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=URA2 PE=1 SV=5	sp|P07259	245044,8	24%	AIMGLPLTPYPVEK-ALKEEGIYTILINPNIATIQTSK-ATGYPLAYTAAK-cIVNPSPASITASAELQSTSAK-DSLPLLLAAVEEGK-EELPSLVLR-EHPTQAFLDLFTIR-EIGFPVIVR-ELVAPGAIQNLIR-FLDSNEVAIR-FNSPEEYAR-HIEL		42	0	42
htb1K123R	60S ribosomal protein L16-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL16B PE=1 SV=3	sp|P26785	22249,9	39%	AEALNISGEFFR-IFEGIPPPYDK-KVSSASAAASESDVAK-LSTSVGWK-sQPVVVIDAK-VSSASAAASESDVAK-VVVPQALR-YEDVVAK-YTTLGK		9	0	9
htb1K123R	60S ribosomal protein L16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL16A PE=1 SV=3	sp|P26784	22201,6	44%	AEELNISGEFFR-LSTSVGWK-SVEPVVVIDGK-VASANATAAESDVAK-VFEGIPPPYDK-VSSAEYYAK-VVVPQALR-YEDVVAK-YTTLGK		9	4	5
htb1K123R	C-1-tetrahydrofolate synthase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADE3 PE=1 SV=1	sp|P07245	102207,3	38%	AALEAGAFEAVTSNHWAEGGK-ANVTIEGSR-AVIEASNQPVDFHFLYDVNSSVEDK-cVGDVEFNEAIK-DIASYLHDADIVVVAIGQPEFVK-DVDGFGPTNIGELNK-EQGFGNLPIcIAK-GIIELLHK-GVPTGFTFPIR-LLTPVPSDIDIS		28	0	28
htb1K123R	Alcohol dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADH1 PE=1 SV=5	sp|P00330	36848,7	58%	aNELLINVK-ANGTTVLVGmPAGAK-ATDGGAHGVINVSVSEAAIEASTR-ccSDVFNQVVK-EALDFFAR-EELFR-EKDIVGAVLK-GVIFYESHGK-IGDYAGIK-LPLVGGHEGAGVVVGmGENVK-SANLmAGHWVA	n-term: Acetyl (+	16	0	16
htb1K123R	Heat shock protein SSB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSB2 PE=1 SV=2	sp|P40150	66595,7	54%	AADEAFAK-ARFEDLNAALFK-AVITVPAYFNDAQR-DAGAISGLNVLR-ENTLLGEFDLK-FEDLNAALFK-IEAALSDALAALQIEDPSADELRK-IINEPTAAAIAYGLGAGK-KTGLDISDDAR-LESYVASIEQTVTDPVLSSK-LIGDAA		27	26	1
htb1K123R	Uncharacterized protein YNL134C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YNL134C PE=1 SV=1	sp|P53912	41165,7	22%	DKLPEGPVK-FPSNGAFAEYSAISSETAYKPAR-IGPQGALLGcDAAGQIVK-IIVVASR-LGPNVDAAR-LPEGPVK-LVAVLK-TVAVAGNPTDWK		8	0	8
htb1K123R	Serine hydroxymethyltransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SHM1 PE=1 SV=2	sp|P37292	53688	48%	ALELYGLDPAK-AVmDLLGSELQNK-EIPYELEK-GAmIFFR-HSITLIPSENFTSK-IGTPAMTTR-KLcNESSEVAALSGEISK-LAENLK-LmGLDLPDGGHLSHGYQLK-LVSGGTDNHLIVIDLSGTQVDGAR-SALFPSGLR-SESLcQAR-S		19	0	19
htb1K123R	GU4 nucleic-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARC1 PE=1 SV=2	sp|P46672	42084,5	3%	APEKPKPSAIDFR		1	0	1
htb1K123R	60S ribosomal protein L3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL3 PE=1 SV=4	sp|P14126	43757,9	34%	AGmTTIVR-AHLAEIQLNGGSISEK-ALEEVSLK-FQTPAEK-GHGFEGVTHR-HGHLGFLPR-SKPVALTSFLGYK-SLTTVWAEHLSDEVK-TITPMGGFVHYGEIK-VLVHTQIR-WIDTASK-YAQDGAGIER-YASVVR	m3: Oxidation (+	13	0	13
htb1K123R	40S ribosomal protein S0-B OS=Saccharomyces cerevisiae (strain YJM789) GN=RPS0B PE=3 SV=1	sp|A7A0V3,sp|B3LT19,sp|P46654	27962,3	31%	FAAHTGATPIAGR-FTPGSFTNYITR-IIAAIPNPEDVVAISSR-LDAQAIK-LVIVTDPR-LVLAAR-TQPWSImPDLYFYR		7	0	7
htb1K123R	ISWI chromatin-remodeling complex ATPase ISW1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ISW1 PE=1 SV=2	sp|P38144	131109,5	21%	DALLSMIQHGAADVFK-DIISPLLLNPTK-FVFLLTTR-IAGILADEmGLGK-INWEYIIIDEAHR-IPGPFLVIAPK-IQAIDDYNAPDSK-LLDILEDYcYFR-LQVLDK-LSVNNSQPLTEEEEK-LVTDNSVEEK-MQQEALR-NSIQAIAR-QLH		21	0	21
htb1K123R	Uncharacterized protein YDR179W-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDR179W-A PE=1 SV=2	sp|Q03983,sp|Q3E765	53733,7	1%	LLIYR		1	0	1
htb1K123R	78 kDa glucose-regulated protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KAR2 PE=1 SV=1	sp|P16474	74470,2	35%	ALSSQMSTR-DAGTIAGLNVLR-DGKPAVEVSVK-FASEDASIK-FELTGIPPAPR-HLPFNVVNK-ITPSYVAFTDDER-IVNEPTAAAIAYGLDK-LIGDAAK-LTQEEIDR-NKLENYAHSLK-NQVAANPQNTIFDIK-QIAEDYLGTK-SESITI		21	2	19
htb1K123R	Peroxisomal-coenzyme A synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PCS60 PE=1 SV=1	sp|P38137	60489,9	19%	FVNTNPVK-ISPIELDGImLSHPK-LQSSEILK-mTYEELVNFLK-SSDVALILHTSGTTSTPK-STLNIANTYK-TGDQGYFDPEGFLVLTGR-VGEVSIR-VIAETFAK		9	0	9
htb1K123R	Pre-mRNA-splicing factor CWC21 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CWC21 PE=1 SV=1	sp|Q03375	15762,4	7%	EIEVQVSELR		1	0	1
htb1K123R	Transcription initiation factor TFIID subunit 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF5 PE=1 SV=1	sp|P38129	88970,6	2%	EGNVLISGGADHTVR		1	0	1
htb1K123R	60S ribosomal protein L42-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL42A PE=1 SV=1	sp|P0CX27,sp|P0CX28	12211,5	13%	AQLTLK-HFELGGEK		2	0	2
htb1K123R	Nuclear polyadenylated RNA-binding protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAB3 PE=1 SV=1	sp|P38996	90438,5	28%	ADLSKPITEEEHDR-DAIEcESQEMNFGK-DGTGLETDMIFLKPR-DVDEAIKK-EDLFR-EENDNTHFPTNMENVNYDLLQK-FRDGTGLETDMIFLKPR-HTVScNIFVK-IFSPYGHIMQINIK-LFIGNLPLK-LINDAAYNGVWGVVLVNK		19	1	18
htb1K123R	60S ribosomal protein L4-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL4B PE=1 SV=2	sp|P49626	39062	56%	AGHQTSAESWGTGR-AVGAHSDLLK-FVIWTEAAFTK-GPLVVYAEDNGIVK-IINSSEIQSAIRPAGQATQK-IPEIPLVVSTDLESIQK-LDQVWGSETVASSK-MFAPTK-NVPGVETANVASLNLLQLAPGAHLGR-QAYAVSEK-RGPLVV		15	14	1
htb1K123R	Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IDH1 PE=1 SV=2	sp|P28834	39325,3	9%	DYAVFEPGSR-FTVTLIPGDGVGK-IPDIDLIVIR		3	0	3
htb1K123R	60S ribosomal protein L7-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL7B PE=1 SV=3	sp|Q12213	27697,8	50%	AAGSYYVEAQHK-AIILER-ATLELLK-HFIQGGSFGNR-ILTPESQLKK-INSGTFVK-LIEPYVAYGYPSYSTIR-LSNPSGGWGVPR-LVFVVR-QANNFLWPFK-QRVPLSDNAIIEANLGK-VLQLLR-VPLSDNAIIEANLGK		13	13	0
htb1K123R	Protein MLP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MLP1 PE=1 SV=2	sp|Q02455	218464,7	16%	DLESQVQDLQTR-DYESVITSVDSK-ESLLEQLDLSNSR-ESTENMSLLNK-FDYLQNTILK-IEDLSSQNK-IEELQNAK-IESETVNEAK-ILEAQER-IMVTQLQTLQK-INLTDAYSQIK-ISILQNNNK-LLSNTLDLTK-LNQLNLLR-LSQDS		27	0	27
htb1K123R	60S ribosomal protein L10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL10 PE=1 SV=1	sp|P41805	25362,1	66%	ATVDEFPLcVHLVSNELEQLSSEALEAAR-DAFHLR-DSNKDVVVEGLR-DVVVEGLR-EAGEVKDDGAFVK-GAWGKPHGLAAR-GSLENNIR-IYDLGK-KGSLENNIR-KWGFTNLDRPEYLK-MLScAGADR-vDIG	c9: Carbamidome	16	0	16
htb1K123R	Imidazoleglycerol-phosphate dehydratase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HIS3 PE=1 SV=2	sp|P06633	23833,2	7%	ALAVAIR-ITLHVDcLR		2	0	2
htb1K123R	40S ribosomal protein S3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS3 PE=1 SV=5	sp|P05750	26503	58%	AAYGVVR-ALPDAVTIIEPK-EEEPILAPSVK-ELAEEGYSGVEVR-FADGFLIHSGQPVNDFIDTATR-GcEVVVSGK-GLSAVAQAESmK-INELTLLVQK-QGVLGIK-RINELTLLVQK-TEVIIR-TQDVLGENGR-TQDVLGENGRR-YAPG		15	0	15
htb1K123R	Clustered mitochondria protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CLU1 PE=1 SV=1	sp|Q03690	145171,1	16%	ALEHITVTQGIFTK-ALTNLAILEFSNESPYNATVVYNR-DLTTSTLQDR-ELDSQIVHYEQNLK-FGIQLLNK-FVEPPTTFSLSDLTIIPR-IIELSQK-ILAQTPVPGLLATMGNK-ISELEIVSR-LAEILK-LALYPEAIAFcR-LGNLFAALK-LQ		17	0	17
htb1K123R	60S ribosomal protein L36-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL36B PE=1 SV=3	sp|O14455	11135,9	38%	EIAGLSPYER-LIDLIR-RLIDLIR-TGIAIGLNK-VEEmNNIIAASR		5	0	5
htb1K123R	40S ribosomal protein S6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS6A PE=1 SV=1	sp|P0CX37,sp|P0CX38	26997,2	21%	EAAAEYAQLLAK-FFGLSK-KGEQELEGLTDTTVPK-TFEIDDEHR-VFFDKR		5	0	5
htb1K123R	40S ribosomal protein S4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS4A PE=1 SV=1	sp|P0CX35,sp|P0CX36	29411,2	46%	AILmQR-DSLDNTFVTR-eSLPLIVFLR-GVPYVVTHDGR-IDLASGK-ITDFIK-KGVPYVVTHDGR-LAAPHHWLLDK-lNNVFVIGEQGKPYISLPK-LRESLPLIVFLR-LSIAEER-LVYVTGGR-TDTTYPAGFmDVITLD	m4: Oxidation (+	13	0	13
htb1K123R	40S ribosomal protein S24-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS24A PE=1 SV=1	sp|P0CX31,sp|P0CX32	15329	55%	ANVSKDELR-DAVSVFGFR-KFEPTYR-KQFVVDVLHPNR-KVISNPLLAR-LAEVYK-QFVVDVLHPNR-SVGFGLVYNSVAEAK-VISNPLLAR-YGLAEK		10	0	10
htb1K123R	40S ribosomal protein S23-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS23A PE=1 SV=1	sp|P0CX29,sp|P0CX30	16038,3	12%	LLGTAFK-VSGVSLLALWK		2	0	2
htb1K123R	60S ribosomal protein L9-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL9A PE=1 SV=2	sp|P05738	21568,8	40%	FIEVR-FLDGIYVSHK-HIDVTFTK-SLVDNmITGVTK-VNNQLIK-YIQTEQQIEVPEGVTVSIK-YVYAHFPINVNIVEK		7	0	7
htb1K123R	60S ribosomal protein L7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL7A PE=1 SV=3	sp|P05737	27639,6	54%	AAGSYYVEAQHK-AIILER-ATLELLK-HFIQGGSFGNR-ILTPESQLKK-INSGTFVK-LIEPYVAYGYPSYSTIR-LSNPSGGWGVPR-LVFVVR-QANNFLWPFK-QRVPLSDNAIIEANLGK-TAEQVAAER-VLQLLR-VPLSDNAIIEANLGK		14	0	14
htb1K123R	60S ribosomal protein L20-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL20A PE=1 SV=1	sp|P0CX23,sp|P0CX24	20437,1	48%	ASGEIVSINQINEAHPTK-DLKFPLPHR-EYQVIGR-FPLPHR-IFASNEVIAK-LPTESVPEPK-NFGVWVR-RLPTESVPEPK-SIHILK-VAAVETLYQDMAAR		10	0	10
htb1K123R	Phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARO3 PE=	sp|P14843	41072	4%	ELASGLSFPIGFK		1	0	1
htb1K123R	Acetyl-CoA carboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ACC1 PE=1 SV=2	sp|Q00955	250359,5	27%	ADVDAVWAGWGHASENPLLPEK-AFLASEEAR-AGVLEPQGMVGIK-AIQVEGQPIILTGAPAINK-ALINNVSGYVIK-AYTIGDIR-cDIILR-EILDLNKQELINASIR-EILIQGALPSVK-EPGANAIGMVAFK-FQLPSAAFSTFPTVK-FYF		50	0	50
htb1K123R	DNA topoisomerase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TOP1 PE=1 SV=2	sp|P04786	89998,9	1%	LDPSILNK		1	0	1
htb1K123R	DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB8 PE=1 SV=1	sp|P20436	16512,1	14%	IEAASTTQDQcK-QENAYLLIR	c11: Carbamidom	2	0	2
htb1K123R	DNA-directed RNA polymerase II subunit RPB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPO21 PE=1 SV=2	sp|P04050	191615,1	14%	ALEDIMVHYDNTTR-ATGDADEPELR-DLQENLLVLR-EGLIDTAVK-EITETIAEAK-EVQFGLFSPEEVR-FAAIWTLcK-FDEGTTLLSPK-GFVENSYLR-GLTPQEFFFHAMGGR-IAFGFVDR-LAEVNLK-LLLDEHNELMR-LTQLVR-S		21	1	20
htb1K123R	Nucleoporin NUP53 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP53 PE=1 SV=1	sp|Q03790	52621,2	3%	TTPNTASSEASAGSK		1	0	1
htb1K123R	RNA polymerase II degradation factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DEF1 PE=1 SV=1	sp|P35732	83968,3	11%	EQQHSYVPQQHLPNPEDDITYK-HVPSKPVSNTTSWAAAVSVDTK-QIEQPSLSSK-SSNNSNSFTSTK-TESPLENVAELKK		5	0	5
htb1K123R	60S ribosomal protein L17-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL17B PE=1 SV=2	sp|P46990	20551,6	30%	FNSSIGR-FVQGLLQNAAANAEAK-LYVSHIQVNQAPK-YGATSTNPAK-YLDQVLDHQR		5	0	5
htb1K123R	40S ribosomal protein S16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS16A PE=1 SV=1	sp|P0CX51,sp|P0CX52	15847,9	66%	FSNIDIR-GLVAYHQK-sATAVAHVK-sAVPSVQTFGK-TLLIADSR-VNGSPITLVEPEILR-VTGGGHVSQVYAIR-VYEPLLLVGLDK-YVDEQSKNELK		9	0	9
htb1K123R	ATP synthase subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ATP1 PE=1 SV=5	sp|P07251	58609,4	9%	HALIVYDDLSK-TGNIVDVPVGPGLLGR-VLAVGDGIAR-VVDALGNPIDGK		4	0	4
htb1K123R	ATP-dependent helicase NAM7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAM7 PE=1 SV=1	sp|P30771	109432,6	14%	ANEQQAIGFLR-DGVKPEQIGVITPYEGQR-ILGHQVVDISFDVPLPK-ILVcAPSNVAVDHLAAK-LITPSQISK-LPNSFQDTFTLELKPSK-QVILVGDHQQLGPVILER-TVTSATIVYHLSK-VEVASVDAFQGR		9	0	9
htb1K123R	DNA-directed RNA polymerase I subunit RPA12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA12 PE=1 SV=1	sp|P32529	13660,6	12%	VVTTTADDAFPSSLR		1	0	1
htb1K123R	Nucleolar protein NET1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NET1 PE=1 SV=1	sp|P47035	128535,1	1%	KRPPTGTTTTTTIR		1	0	1
htb1K123R	Protein LUC7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LUC7 PE=1 SV=1	sp|Q07508	30195,1	15%	IGLmGQEIDSLIR-IQQVTEELDVLDVR-NITENVGQSAQQK	m4: Oxidation (+	3	0	3
htb1K123R	Elongator complex protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ELP3 PE=1 SV=1	sp|Q02908	63658,8	7%	GTGLYELWK-ISVISGVGVR-IYPTLVIR-SYSANALVDLVAR		4	0	4
htb1K123R	NADP-specific glutamate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GDH1 PE=1 SV=2	sp|P07262,sp|P39708	49570,2	2%	FLGFEQIFK		1	0	1
htb1K123R	60S ribosomal protein L1-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL1A PE=1 SV=1	sp|P0CX43,sp|P0CX44	24486,3	34%	FPTPVSHNDDLYGK-KNWQNVGSLVVK-NFLETVELQVGLK-NWQNVGSLVVK-ScGVDAmSVDDLK-ScGVDAMSVDDLKK-SSmGPAFR-YNAFIASEVLIK		8	0	8
htb1K123R	Eukaryotic translation initiation factor 2A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YGR054W PE=1 SV=1	sp|P53235	71307,1	4%	FDATNTSVcK-VSLTTGPVHDFTWSPTSR	c9: Carbamidome	2	0	2
htb1K123R	Protein BMH2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BMH2 PE=1 SV=3	sp|P34730	31061,7	18%	DSTLIMQLLR-EDSVYLAK-ISDDILSVLDSHLIPSATTGESK-IVSSIEQK		4	4	0
htb1K123R	Transcription initiation factor TFIID subunit 14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF14 PE=1 SV=1	sp|P35189	27440,7	14%	SGSTEETTANTGTIGK-TQQHILPEVPPVENFPVR		2	0	2
htb1K123R	Saccharopepsin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PEP4 PE=1 SV=1	sp|P07267	44501	4%	VVPPFYNAIQQDLLDEKR		1	0	1
htb1K123R	T-complex protein 1 subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CCT3 PE=1 SV=2	sp|P39077	58814,7	4%	QAQISNITAAK-VTGATIVNR		2	0	2
htb1K123R	Protein SCP160 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SCP160 PE=1 SV=3	sp|P06105	134813,7	33%	ANESLNSLR-APSATYAGYVWGADTR-DKTVEVTLTGLEYNLTHAK-DLPSLGSNAAFANVK-EAADVIINVPR-EVDVPASIYEYVSER-FNMIVGPGGSNIK-FTIEEVGAPTSSEEGDITMR-GALIGPGGIVR-GLEESHPNVK-IFESILNS		35	0	35
htb1K123R	Zinc finger protein ZPR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ZPR1 PE=1 SV=1	sp|P53303	55072,7	2%	LLLTSIPYFR		1	0	1
htb1K123R	Mitochondrial 2-oxodicarboxylate carrier 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ODC2 PE=1 SV=1	sp|Q99297	34007,9	4%	IQSVDAVSSAVK		1	0	1
htb1K123R	Protein transport protein SEC13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEC13 PE=1 SV=1	sp|Q04491	33042,6	5%	LIDTLTGHEGPVWR		1	0	1
htb1K123R	Nicotinamidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PNC1 PE=1 SV=1	sp|P53184	24993,4	6%	ATAISAAELGYK		1	0	1
htb1K123R	Sphingolipid long chain base-responsive protein PIL1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PIL1 PE=1 SV=1	sp|P53252	38350,3	4%	SAAGAFGPELSR		1	0	1
htb1K123R	Isocitrate dehydrogenase [NAD] subunit 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IDH2 PE=1 SV=1	sp|P28241	39740,6	8%	GPLATPIGK-ISIFEAVHGSAPDIAGQDK		2	0	2
htb1K123R	Ketol-acid reductoisomerase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ILV5 PE=1 SV=1	sp|P06168	44369,9	22%	DNGLNVIIGVR-EVNSDLYGER-GINSSYAVWNDVTGK-NALKPVFQDLYESTK-NLFTVEDAIK-SLEFNSQPDYR-TLYFSHGFSPVFK		7	0	7
htb1K123R	DNA-directed RNA polymerase II subunit RPB7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB7 PE=1 SV=1	sp|P34087	19058,4	8%	ILPTDGSAEFNVK		1	0	1

htb1K123R	rRNA biogenesis protein RRP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RRP5 PE=1 SV=1	sp|Q05022	193141,4	4%	IGTELTGLVIDKDTR-KVEAFVPVSK-LLPGAVFLGNITK-SLFEGLVADAPK-VLGYSPVDDIYQLSTDPK		5	0	5
htb1K123R	40S ribosomal protein S2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS2 PE=1 SV=3	sp|P25443	27450,2	19%	GSGIVASPAVK-ITTIEEIFLHSLPVK-LSVIPIR-sAPEAQQQK-TLENTLK		5	0	5
htb1K123R	Protein NAM8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAM8 PE=1 SV=2	sp|Q00539	56972,5	6%	SSSSLNNENVDSR-VGPTSGQQQHVSGNNDYNR		2	0	2
htb1K123R	ARS-binding factor 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ABF2 PE=1 SV=1	sp|Q02486	21563,3	34%	AIQEYNAR-ENPTLRPAEISK-RPTSAYFLYLQDHR-SQVFAQHPDK-WQNLEADIK-WQSLDQSIK		6	0	6
htb1K123R	U2 small nuclear ribonucleoprotein A' OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LEA1 PE=1 SV=1	sp|Q08963	27194,2	6%	QADGDTLGPVNTAIR		1	0	1
htb1K123R	Spermidine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPE3 PE=1 SV=1	sp|Q12074	33324,4	4%	VLVIGGGDGGVLR		1	0	1
htb1K123R	Thioredoxin reductase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TRR1 PE=1 SV=3	sp|P29509,sp|P38816	34239,2	6%	VTIIGSGPAAHTAAIYLAR		1	0	1
htb1K123R	Coatomer subunit delta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RET2 PE=1 SV=3	sp|P43621	60629,3	2%	AFPANDQSLGVLR		1	0	1
htb1K123R	60S ribosomal protein L5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL5 PE=1 SV=4	sp|P26321	33716,1	9%	ADPAFKPTEK-LGLDETYK-VFLDIGLQR		3	0	3
htb1K123R	Peptidyl-prolyl cis-trans isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CPR1 PE=1 SV=3	sp|P14832	17390,7	37%	GFGYAGSPFHR-HVVFGEVVDGYDIVK-KVESLGSPSGATK-VIPDFmLQGGDFTAGNGTGGK		4	0	4
htb1K123R	Diphosphomevalonate decarboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MVD1 PE=1 SV=2	sp|P32377	44116,9	5%	VILTQVGSGPQETNESLIDAK		1	0	1
htb1K123R	Imitation switch two complex protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ITC1 PE=1 SV=1	sp|P53125	145648,7	2%	NVLANSIWGSSLR-VQFNATINPESR		2	0	2
htb1K123R	Eukaryotic peptide chain release factor GTP-binding subunit OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SUP35 PE=1 SV=1	sp|P05453	76550,7	2%	FVAQIAIVELK		1	0	1
htb1K123R	Cell division control protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC10 PE=1 SV=1	sp|P25342	37026,3	32%	LDVEALKR-LNINVIDTPGFGDFIDNSK-LTEIANVIPVIGK-mDPLSSVQPASYVGFDTITNQIEHR-SDTLTLDER-STLINTLFASHLIDSATGDDISALPVTK		6	0	6
htb1K123R	ATP synthase subunit beta, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ATP2 PE=1 SV=2	sp|P00830	54794,7	10%	ETGVINLEGESK-IINVIGEPIDER-TVFIQELINNIAK-VLDTGGPISVPVGR		4	0	4
htb1K123R	40S ribosomal protein S26-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS26A PE=1 SV=1	sp|P39938,sp|P39939	13505	20%	DLSEASVYPEYALPK-NIVEAAAVR		2	0	2
htb1K123R	60S acidic ribosomal protein P0 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP0 PE=1 SV=2	sp|P05317	33717,4	31%	AGAVAPEDIWVR-EYLEEYK-GFLSDLPDFEK-GNVGFVFTNEPLTEIK-GTIEIVSDVK-LREYLEEYK-NVIVSNR-SLFVVGVDNVSSQQMHEVR-TSFFQALGVPTK		9	0	9
htb1K123R	Single-stranded nucleic acid-binding protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SBP1 PE=1 SV=2	sp|P10080	32989,9	7%	IFTSDSANR-SKDTLYINNVPFK		2	0	2
htb1K123R	UPF0202 protein KRE33 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KRE33 PE=1 SV=1	sp|P53914	119353,8	1%	LFVLLPPIDPK		1	0	1
htb1K123R	U1 small nuclear ribonucleoprotein component PRP42 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP42 PE=1 SV=1	sp|Q03776	65149,7	18%	ALLPLAHYDLVWIK-DTVEFVEK-FYALWLQR-GLQAFNQR-LIYFDTSR-LLYSVIcK-LNEYVLLR-SGQEILLNNLVQFYSK-STEPQLLK-YSDSQSNGLLNK		10	0	10
htb1K123R	Nuclear and cytoplasmic polyadenylated RNA-binding protein PUB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PUB1 PE=1 S	sp|P32588	50762	5%	QYFQVGGPIANIK-VLYVGNLDK		2	0	2
htb1K123R	6-phosphofructokinase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PFK2 PE=1 SV=4	sp|P16862	104619,8	9%	AFVVMEGYEGLVR-AIDYVEATANSHSR-ISNEQYER-LAEVITAEADGR-NAVSTKPTPPPAPEASAESGLSSK-SSPDENSTLLSNDSISLK		6	0	6
htb1K123R	Aconitate hydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ACO1 PE=1 SV=2	sp|P19414	85371,6	2%	TIFTVTPGSEQIR		1	0	1
htb1K123R	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RIP1 PE=1 SV=1	sp|P08067	23365,4	6%	VEVNLAAIPLGK		1	0	1
htb1K123R	Histone H3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HHT1 PE=1 SV=2	sp|P61830	15356,8	12%	STELLIR-YKPGTVALR		2	0	2
htb1K123R	Serine hydroxymethyltransferase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SHM2 PE=1 SV=2	sp|P37291	52219,7	22%	AVEFAQQVQQSLPK-GAmIFFR-IGAPAmTTR-ISAVSTYFESFPYR-IVQYINK-LmGLYLPDGGHLSHGYATENR-PYTLSDAHHK-QAATPEFK-VLVAGTSAYcR		9	1	8
htb1K123R	60S ribosomal protein L31-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL31A PE=1 SV=1	sp|P0C2H8	12953,2	53%	AGLKDVVTR-EYTINLHK-LAPELNQAIWK-LHGVSFK-LHMGTDDVR-NPLFSYVEPVLVASAK		6	0	6
htb1K123R	60S ribosomal protein L21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL21A PE=1 SV=1	sp|Q02753	18242	33%	AQGVAVQLK-HGAVHLSTYLK-QEFLER-SSVGVIINK-TGVVYNVTK-VGDIVDIK		6	0	6
htb1K123R	Branched-chain-amino-acid aminotransferase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BAT2 PE=1 SV=1	sp|P47176	41626	7%	ELVTAPLDGTILEGVTR-TLAPLDASK		2	0	2
htb1K123R	40S ribosomal protein S13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS13 PE=1 SV=3	sp|P05756	17029,8	51%	GISSSAIPYSR-GLTPSQIGVLLR-KGLTPSQIGVLLR-LILIESR-LSSESVIEQIVK-NAPAWFK-SNGLAPEIPEDLYYLIK-TVAVLPPNWK		8	0	8
htb1K123R	GTP-binding nuclear protein GSP1/CNR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GSP1 PE=1 SV=1	sp|P32835	24810,6	34%	FDVWDTAGQEK-HLTGEFEK-NLQYYDISAK-sAPAANGEVPTFK-SNYNFEKPFLWLAR-TITFHR-VcENIPIVLcGNK		7	0	7
htb1K123R	60S ribosomal protein L2-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL2A PE=1 SV=1	sp|P0CX45,sp|P0CX46	27408,9	45%	aSGNYVIIIGHNPDENK-ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR-GAGSIFTSHTR-GVIGVIAGGGR-KGAGSIFTSHTR-LREEIFIANEGVHTGQFIYAGK-TLDYAER-VDKPLLK-VRLPSGAK	n-term: Acetyl (+	9	0	9
htb1K123R	ADP-ribosylation factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARF1 PE=1 SV=3	sp|P11076	20530,1	23%	ILMVGLDGAGK-LFSNLFGNK-mLNEDELR-NISFTVWDVGGQDR		4	4	0
htb1K123R	Inorganic phosphate transport protein PHO88 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PHO88 PE=1 SV=1	sp|P38264	21138	15%	APSLFGGmGQTGPK-YTNPLFMQSISPVK	m8: Oxidation (+	2	0	2
htb1K123R	40S ribosomal protein S14-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS14B PE=1 SV=2	sp|P39516	14649,8	62%	ADRDESSPYAAMLAAQDVAAK-cKEVGITAVHVK-DESSPYAAmLAAQDVAAK-DNSQVFGVAR-EVGITAVHVK-IEDVTPVPSDSTR-IYASFNDTFVHVTDLSGK-TPGPGGQAALR		8	0	8
htb1K123R	40S ribosomal protein S7-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS7B PE=1 SV=1	sp|P48164	21634,7	28%	DVQQIDYK-HVIFLAER-ILPKPSR-LESFQAVYNK-VLEDMVFPTEIVGK-YLVGGNK		6	5	1
htb1K123R	DNA-directed RNA polymerase I subunit RPA190 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA190 PE=1 SV=2	sp|P10964	186435,3	10%	EGLIDTAVK-EQLDSPSAR-IFETALNEK-LQEILR-LQTDVANSSSNSK-LTYPEPVTAYNIAELR-NILDTVFR-QGTYLAFNR-SVISPDPNIETNEIGVPPVFAVK-TGSTYILSTEVK-TTGPDIGVAVPR-VIVTETTGTSNTAGGNAAR-VLLS		14	0	14
htb1K123R	ATP-dependent RNA helicase eIF4A OS=Saccharomyces cerevisiae (strain YJM789) GN=TIF1 PE=3 SV=1	sp|A6ZQJ1,sp|P10081	44698,3	38%	AIMPIIEGHDVLAQAQSGTGK-APQALmLAPTR-DAQIVVGTPGR-ELALQIQK-FTVSAIYSDLPQQER-GIDVQQVSLVINYDLPANK-GVFGYGFEEPSAIQQR-ILISTDLLAR-KDELTLEGIK-TGTFSIAALQR-VHAcIGGTSFVEDAE		11	0	11
htb1K123R	High mobility group protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HMO1 PE=1 SV=1	sp|Q03973	27545,1	12%	AGLPPLSSTEITQEISK-AGLPPLSSTEITQEISKK-QAYNVELENYQR		3	0	3
htb1K123R	40S ribosomal protein S22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS22A PE=1 SV=2	sp|P0C0W1,sp|Q3E7Y3	14626,5	25%	FLQVmQK-SSVLADALNAINNAEK-WTANLLPAR	m5: Oxidation (+	3	0	3
htb1K123R	56 kDa U1 small nuclear ribonucleoprotein component OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNU56 PE=1 SV=1	sp|Q03782	56500,3	7%	GQLSQGHYPTTSNDGQR-HAVNKPSNVLNSSNR		2	0	2
htb1K123R	Replication factor A protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RFA1 PE=1 SV=1	sp|P22336	70350,2	20%	ATAFNDFATK-FQSMELQR-ITQSIQMNEYDFR-LFNVNFLDTSGEIR-NANFITLK-QEPGMGGQSAASLTK-TRPIFAIEQLSPYQNVWTIK-VIIAEPAIVR-YDNPTGGVYQVYNTR-YTVANLHSLNYR		10	0	10
htb1K123R	Eukaryotic translation initiation factor 3 subunit B OS=Saccharomyces cerevisiae (strain YJM789) GN=PRT1 PE=3 SV=1	sp|A6ZPJ1,sp|P06103	88330,8	5%	IFNIAGNLVK-MVGDSLIVHDATK-NINDNNDVSASLK		3	0	3
htb1K123R	40S ribosomal protein S25-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS25B PE=1 SV=1	sp|P0C0T4,sp|Q3E792	12009,9	31%	AQHAVILDQEK-AQHAVILDQEKYDR-EGIIKPISK-YVSVSVLVDR		4	0	4
htb1K123R	Hsp90 co-chaperone HCH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HCH1 PE=1 SV=1	sp|P53834	17246,8	8%	LTSLSTVSSDGK		1	0	1
htb1K123R	Nuclear migration protein NUM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUM1 PE=1 SV=2	sp|Q00402	313042,2	0%	LTNLSMEcR	c8: Propionamide	1	0	1
htb1K123R	(DL)-glycerol-3-phosphatase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RHR2 PE=1 SV=3	sp|P41277	27948,2	28%	LcNALNALPK-PLTTKPLSLK-RPEYFITANDVK-VVVFEDAPAGIAAGK-WAVATSGTR-YGEHSIEVPGAVK	c2: Carbamidome	6	0	6
htb1K123R	Proteasome component PRE2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE2 PE=1 SV=3	sp|P30656	31636,9	3%	ILSNLVYQYK		1	0	1
htb1K123R	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=OST3 PE	sp|P48439	39485,6	3%	SPAYPFPLLR		1	0	1
htb1K123R	Small nuclear ribonucleoprotein-associated protein B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMB1 PE=1 SV=1	sp|P40018	22379,9	23%	EIAQPSSSR-GEQILSTVVEDKPLLSK-LANLIDYK-VYIGQLMAFDK		4	0	4
htb1K123R	60S ribosomal protein L18-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL18A PE=1 SV=1	sp|P0CX49,sp|P0CX50	20563,7	16%	INRPPVSVSR-SDNVYLK-TVVVVGTVTDDAR		3	0	3
htb1K123R	60S ribosomal protein L35-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL35A PE=1 SV=1	sp|P0CX84,sp|P0CX85	13910,2	36%	EQLASQLVDLKK-FEASQVTEK-KSIAcVLTVINEQQR-QIAFPQR-SIAcVLTVINEQQR		5	0	5
htb1K123R	40S ribosomal protein S10-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS10B PE=1 SV=1	sp|P46784,sp|Q08745	12738,7	38%	ALQSLTSK-EYLNLPEHIVPGTYIQER-IHQYLFQEGVVVAK		3	0	3
htb1K123R	Uncharacterized protein YHR127W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YHR127W PE=1 SV=1	sp|P38833	27132	5%	LVSSNDVGVLLR		1	0	1
htb1K123R	Transcription elongation factor SPT6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPT6 PE=1 SV=1	sp|P23615	168298,5	11%	AIDFLQSLQR-ATDNNYYASALK-ENLEVPFIYAYR-IHPEDYHLATK-ISLQDIYDLEDLKK-LAIDTVQK-LDQAPFIPNVR-LLNEMTSSEK-LNEPLLAR-MVEAESLNLLSVK-QPTQITGLSSDK-QQLITHNILHK-TPMHFR-VLIVDNQ		16	0	16
htb1K123R	Nucleoporin NUP85 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP85 PE=1 SV=1	sp|P46673	84902,3	1%	LLNQLVLR		1	0	1
htb1K123R	Eukaryotic translation initiation factor 3 subunit G OS=Saccharomyces cerevisiae (strain YJM789) GN=TIF35 PE=3 SV=1	sp|A6ZZ25,sp|Q04067	30474,6	7%	GSPAGPSAVTAR-LGEEVELR		2	0	2
htb1K123R	Myosin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MYO2 PE=1 SV=1	sp|P19524	180687	13%	AcGVLETIR-AINAVVISESLPGFSAGETSGFLNK-ASTNETLINILEGLEK-ILAALLHIGNIEIK-ILATNPIMEAFGNAK-IScAGFPSR-ITVDALTLVGITK-IVSNLNYSQALVAK-KPTLGSMFK-LGILSLLDEESR-LYQTL	c2: Carbamidome	16	0	16
htb1K123R	RNA annealing protein YRA2 OS=Saccharomyces cerevisiae (strain YJM789) GN=YRA2 PE=3 SV=1	sp|A7A075,sp|B3LQP5,sp|B5VLV2,s	23836,6	35%	AFDEIIGNSHTDSSSNHK-EFGSPIFSK-IEVEIYQPQR-IFDNKEDR-IPLDVSDYTLDDmIK-LGFAPSDAASR		6	0	6
htb1K123R	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GFA1 PE=1 SV	sp|P14742	80048,7	14%	AFLSEDGSPTPVEFFVSSDAASVVK-EFEAGSQNANLLPIAANEFNLR-GYQFAAALEGALK-HGVLALVDENLPIIAFGTR-SDPEDQFVVVHNGIITNFR		5	0	5
htb1K123R	Nucleolar protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NPL3 PE=1 SV=1	sp|Q01560	45407,3	17%	ENSLETTFSSVNTR-GSVITVERDDNPPPIR-LNNIEFR-NLPEGcSWQDLK-QEGELSNTR-SFANQPLEVVYSK		6	0	6
htb1K123R	40S ribosomal protein S1-A OS=Saccharomyces cerevisiae (strain YJM789) GN=RPS1A PE=3 SV=1	sp|A7A1W1,sp|B3RHV0,sp|B5VNY0	28743,8	58%	APSTFENR-DIFPLQNIHVR-EVQGSTLAQLTSK-FDVGALMALHGEGSGEEK-hSYAQSSHIR-IFAIAFTR-KEWFDIK-KVISEILTK-LIPEVINK-LRVDEVQGK-NLLTNFHGmDFTTDK-TSDDYVLR-VISEILTK-VVDPFTR-VVEVcLAI		15	12	3
htb1K123R	Eukaryotic translation initiation factor 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TIF6 PE=1 SV=1	sp|Q12522	26457,4	7%	GLLVPTQTTDQELQHLR		1	0	1
htb1K123R	C-1-tetrahydrofolate synthase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MIS1 PE=1 SV=1	sp|P09440	106220,5	6%	IEVSPEAQK-LNINPDTITIR-QITIGEAATEK-QPSLGPTLGVK-TFGIPVVVAINR-VVDINDR		6	2	4
htb1K123R	Nucleoporin NIC96 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NIC96 PE=1 SV=2	sp|P34077	96180,3	5%	AQDFSNLDDNIVK-FANILANYTK-LNVNENNILR-NAQLLESWK		4	0	4
htb1K123R	H/ACA ribonucleoprotein complex subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GAR1 PE=1 SV=1	sp|P28007	21481,3	6%	IPYFNAPIYLENK		1	0	1
htb1K123R	Mannan polymerase complexes subunit MNN9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MNN9 PE=1 SV=3	sp|P39107	45956,7	3%	ELIELGFITPR		1	0	1
htb1K123R	Orotate phosphoribosyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=URA5 PE=1 SV=2	sp|P13298	24666	5%	GQVVGSIIALDR		1	0	1
htb1K123R	Uncharacterized membrane protein YGR016W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YGR016W PE=1 SV=1	sp|P53209	22228	5%	NIEDEIADLR		1	0	1
htb1K123R	Bifunctional purine biosynthetic protein ADE5,7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADE5,7 PE=1 SV=1	sp|P07244	86068,6	3%	VINWDITPDVANFAR-VLSVTSTAQDLR		2	0	2
htb1K123R	Transcription elongation factor S-II OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DST1 PE=1 SV=4	sp|P07273	34843,6	4%	QNLYNAQGATIER		1	0	1
htb1K123R	Magnesium-activated aldehyde dehydrogenase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ALD6 PE=1 SV=4	sp|P54115	54415,5	17%	GYFIRPTVFYDVNEDMR-IVKEEIFGPVVTVAK-SAHLVFDDANIKK-SVAVDSSESNLK-TVGAALTNDPR-VGIPAGVVNIVPGPGR		6	0	6
htb1K123R	Transcriptional regulatory protein RCO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RCO1 PE=1 SV=1	sp|Q04779	78840,6	3%	IFINNSMATLK-VSVTGLPLNK		2	0	2
htb1K123R	Transketolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TKL1 PE=1 SV=4	sp|P23254	73807,9	14%	FFGFTPEGVAER-HTPSIIALSR-ILAVDTVSK-LGNLIAIYDDNK-MNPTNPDWINR-QNLPQLEGSSIESASK-SFVVPQEVYDHYQK-VVSLPDFFTFDK		8	0	8
htb1K123R	U1 small nuclear ribonucleoprotein A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MUD1 PE=1 SV=1	sp|P32605	34379,9	4%	LQNNDVTIGFAK		1	0	1
htb1K123R	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Saccharomyces cerevisiae (strain AT	sp|P12695	51819,7	25%	ADIESYLEK-AQPAEPQAEK-FKNVDVSVAVATPTGLLTPIVK-IFASPLAK-ILVPEGTK-LLQSTQGIPSYIVSSK-LSINDLLVK-NVDVSVAVATPTGLLTPIVK-QSLNATANDK-QSLNATANDKYK-RVPDANAYWLPNENVIR-TVIENPL		13	0	13
htb1K123R	Valyl-tRNA synthetase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VAS1 PE=1 SV=2	sp|P07806	125774,7	2%	ILVSLDDPALK-SLGNVIDPLDVITGIK		2	0	2
htb1K123R	Ribosomal RNA small subunit methyltransferase NEP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EMG1 PE=1 SV=1	sp|Q06287	27896,2	4%	GILIEVNPTVR		1	0	1
htb1K123R	Transcription initiation factor TFIID subunit 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF12 PE=1 SV=1	sp|Q03761	61072,1	19%	FLQESTQQQR-IPGYSADEIR-LQSITSDK-QTEPAIPISENISTK-QVYDALTLNR-SNRPTITGGSAmNASALNTPATTK-SQQQQQNTITATNNPR-TPAPVAYR		8	0	8
htb1K123R	ISWI one complex protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IOC3 PE=1 SV=1	sp|P43596	90901,4	3%	LQEFFLGR-STTDNNPSINTNPLPK		2	0	2
htb1K123R	DNA-directed RNA polymerase I subunit RPA135 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA135 PE=1 SV=1	sp|P22138	135745,4	16%	EIFDGIIGNDVK-IGSISTVccR-ISTQQSDVSR-LLNSSDYTQASVcR-LQTGQTPIVK-LSVSVEQVSIAKPmSNDGVSSAVER-QTMGTPGVALcHR-STGPVNSLTMQPVK-TPGLPIDLEIGYVPPSTR-TQVLQYLGDK-VIFDGKPLNSEDE		13	0	13
htb1K123R	Translationally-controlled tumor protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TMA19 PE=1 SV=1	sp|P35691	18741,3	19%	EDGTTPFVAIWK-LQETNPEEVPK-LQQTAFDKK		3	0	3
htb1K123R	Transcriptional modulator WTM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=WTM1 PE=1 SV=1	sp|Q12363	48383,6	3%	TSDKPIWVLGEPK		1	0	1
htb1K123R	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=COR1 PE=1 SV=1	sp|P07256	50229	18%	AAFLGSEVR-EGLALSSNISR-HEDLVNSIESK-LQLGQLYESGNPVNDANLLGAEVLIK-LTISVTDTEVER-QVQDFEENDHPNR		6	0	6
htb1K123R	Homoaconitase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LYS4 PE=1 SV=1	sp|P49367	75152,1	2%	IVQSYAVNLPEGK		1	0	1
htb1K123R	Carbamoyl-phosphate synthase arginine-specific large chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CPA2 PE=1 SV=1	sp|P03965	123919,7	7%	ATGYPLAYTAAK-LAGADPFLGVEMASTGEVASFGR-VLAIGQALIHENYTVER-VLGTPIK-VLGVNFIEIAVK-VPQFSFTR		6	1	5
htb1K123R	Transposon Ty1-PR1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-PR1 PE=3 SV=1	sp|P0C2I9,sp|Q03612	198575,8	8%	AHNVSTSNNSPSTDNDSISK-DILSVDYTDIMK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-KYVRPPPmLTSPNDFPNWVK-LNNNGIHINNK-SDGTVLAPIVK-STTEPIQLNNK-VAcQLIMR-VTNIIDR-YVRPPPMLTSPN		11	0	11
htb1K123R	RNA-binding protein SGN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SGN1 PE=1 SV=1	sp|P40561	28955	10%	GYGYIEFESPAYR-LSIEGTPQVSQK		2	0	2
htb1K123R	Pre-mRNA-splicing factor CEF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CEF1 PE=1 SV=1	sp|Q03654	67732,9	2%	VESIEQLQR		1	0	1
htb1K123R	60S ribosomal protein L30 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL30 PE=1 SV=3	sp|P14120	11416	11%	LIIIAANTPVLR		1	0	1
htb1K123R	Histone deacetylase HOS3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HOS3 PE=1 SV=1	sp|Q02959	79201,4	12%	AAAQIPESAK-AMIPEFDDIIFK-ATVEPASTSTIAQR-AVVVLSPYSLQHVFPR-QFQAFVQNNPNVISAAR-TVEDITIDDISR		6	0	6
htb1K123R	ATP-dependent RNA helicase DED1 OS=Saccharomyces cerevisiae (strain YJM789) GN=DED1 PE=3 SV=1	sp|A6ZP47,sp|P06634	65554,5	10%	GcDLLVATPGR-SGAATLLVATAVAAR-TGPSPQPESQGSFYQR-VGSTSENITQK-YLVLDEADR	c2: Carbamidome	5	0	5
htb1K123R	Exosome complex component RRP4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RRP4 PE=1 SV=1	sp|P38792	39427,8	4%	STGPTGAVSLNPSITR		1	0	1
htb1K123R	Nucleoporin NUP188 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP188 PE=1 SV=1	sp|P52593	188591	3%	DQLIISSSANK-LVTNVVDPK-SSILTVLQK-VLPETcLFVSYFGK		4	0	4
htb1K123R	60S ribosomal protein L15-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL15A PE=1 SV=3	sp|P05748	24422,6	28%	GATYGKPTNQGVNELK-QGFVIYR-QNTLSLWR-VLNSYWVNQDSTYK-YFEVILVDPQHK		5	0	5
htb1K123R	Elongation factor 3B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HEF3 PE=1 SV=2	sp|P53978	115871,6	10%	ATETVDNKDIER-DSLGALSK-EALASGQFR-IAVIGPNGAGK-LSSAELR-QINENDAEAMNK-STLINVLTGELLPTSGEVYTHENcR-TPSEYIQWR-WVPMMSVDNAWLPR		9	8	1
htb1K123R	Threonyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=THS1 PE=1 SV=2	sp|P04801	84522,6	4%	IYNTLVDLLR-QVLVVPVGVK-VPDGGATTVYR		3	0	3
htb1K123R	40S ribosomal protein S15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS15 PE=1 SV=1	sp|Q01855	16002,2	30%	LAAPENEKPAPVR-LLEmSTEDFVK-NmIIVPEmIGSVVGIYNGK		3	0	3
htb1K123R	Protein FAF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FAF1 PE=1 SV=1	sp|P40546	38890,9	3%	ISGGERSGK		1	0	1
htb1K123R	Probable inosine-5'-monophosphate dehydrogenase IMD3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IMD3 PE=1 SV=1	sp|P50095	56586,2	21%	EQAANLIAAGADGLR-ETFPDLEIIAGNVATR-FGFSGFPVTEDGKR-LLIVDDNGNLVSMLSR-NPVTGAQGITLSEGNEILKK-NQNYPLASK-TASAQLEGGVHNLHSYEK		7	0	7
htb1K123R	2-isopropylmalate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LEU4 PE=1 SV=1	sp|P06208,sp|Q12166	68409,3	3%	IPYLPLDPK-TVEALTGAK		2	0	2
htb1K123R	Replication factor A protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RFA2 PE=1 SV=1	sp|P26754	29936,1	9%	DDNDTSSGSSPLQR-VNTLTPVTIK		2	0	2
htb1K123R	Single-strand telomeric DNA-binding protein GBP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GBP2 PE=1 SV=1	sp|P25555	48729,9	7%	GTEPGLAQDAAVHIDETAAK-SDLFDLFGPIGK		2	0	2
htb1K123R	Elongation factor 1-gamma 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TEF4 PE=1 SV=1	sp|P36008	46521,9	21%	ALTYTPPK-IDNLAAVFDAR-IVDLEQSSEFASLFPLK-LLGSDVIEK-NYASEALISYFK-QAPAFLGPK-TPFAEVK-WFNTVAASPIVK		8	0	8
htb1K123R	60S ribosomal protein L6-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL6B PE=1 SV=4	sp|P05739	19986,9	53%	ALLAEIK-ASLVPGTVLILLAGR-EANLFPEQQTK-FNVEYFAK-HLEDNTLLVTGPFK-QYLSASFSLK-VSVEGVNVEK-WYPSEDVAAPK-YVIATSTK		9	0	9
htb1K123R	V-type proton ATPase subunit B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VMA2 PE=1 SV=2	sp|P16140	57751,6	29%	AIVQVFEGTSGIDVK-AVVGEEALSIEDK-GIYPPINVLPSLSR-HVLTILTDMSSYADALR-IPIFSASGLPHNEIAAQIcR-IPVSEDMLGR-LSLEFLEK-TFITQGAYEDR-TSLFLNLANDPTIER-TVFESLDQAWSLLR-YNEIVNLTLPDGTV		11	0	11
htb1K123R	Glucose-6-phosphate 1-dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ZWF1 PE=1 SV=4	sp|P11412	57523,6	4%	sEGPVKFEK-VQPDAAVYLK	n-term: Acetyl (+	2	0	2
htb1K123R	Threonine dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ILV1 PE=1 SV=2	sp|P00927	63831,7	6%	IIGVETYDAATLHNSLQR-IISFEFPERPGALTR		2	0	2
htb1K123R	Transposon Ty1-DR1 Gag polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1A-DR1 PE=1 SV=1	sp|Q03856	49057,2	36%	AHNVSTSNNSPSTDNDSISK-DILSVDYTDIMK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-HDLHLRPGTY-KYVRPPPmLTSPNDFPNWVK-LNNNGIHINNK-mESQQLSNYPHISHGSAcASVTSK-STTEPIQLNNK-VAc		12	11	1
htb1K123R	Keratin, type I cytoskeletal 9 - Homo sapiens	sp|P35527	62131	19%	FSSSSGYGGGSSR-GGSGGSYGGGGSGGGYGGGSGSR-IKFEmEQNLR-LASYLDK-MTLDDFR-QGVDADINGLR-QVLDNLTMEK-SGGGGGGGLGSGGSIR-STMQELNSR-TLLDIDNTR		10	1	9
htb1K123R	Eukaryotic translation initiation factor 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TIF5 PE=1 SV=1	sp|P38431	45262,6	2%	NPETEIIITK		1	0	1
htb1K123R	Transposon Ty1-DR5 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-DR5 PE=1 SV=1	sp|P0C2I2,sp|Q03855	198534,8	9%	AHNVSTSNNSPSTDNDSISK-DILSVDYTDIMK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-KYVRPPPmLTSPNDFPNWVK-LNNNGIHINNK-mESQQLSNYPHISHGSAcASVTSK-SDGTVLAPIVK-STTEPIQLNNK-VAc		12	11	1
htb1K123R	Partitioning protein REP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=REP2 PE=1 SV=1	sp|P03872	33197,1	5%	LVSVVTQLLTLVPPDR		1	0	1
htb1K123R	GTP-binding protein RHO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RHO1 PE=1 SV=3	sp|P06780	23152	5%	NDPQTIEQLR		1	0	1
htb1K123R	60S ribosomal protein L8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL8A PE=1 SV=4	sp|P17076	28125,5	55%	HWGGGILGNK-LGTLVNQK-LKVPPTIAQFQYTLDR-LVSTIDANFADKYDEVK-mGVPYAIVK-NFGIGQAVQPK-NPLTHSTPK-NTAAETFK-SKQDASPKPYAVK-TSAVAALTEVR-VAPAPFGAK-VPPTIAQFQYTLDR-WPEYVR-Y		14	12	2
htb1K123R	Plasma membrane ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PMA1 PE=1 SV=2	sp|P05030	99621,6	14%	ADTGIAVEGATDAAR-DGQLVEIPANEVVPGDILQLEDGTVIPTDGR-GYLVAMTGDGVNDAPSLK-MLTGDAVGIAK-QLGLGTNIYNAER-TLANTAVVIR-VLEFHPFDPVSK-VTAVVESPEGER-VVEILQNR		9	0	9
htb1K123R	Protein SIS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SIS1 PE=1 SV=1	sp|P25294	37591,6	29%	DGDDLIYTLPLSFK-EISEAFEILNDPQKR-EIYDQYGLEAAR-ESLLGFSK-LYDLLGVSPSANEQELKK-TLQFVIQEK-TQIDIQLKPGWK-YKVDYPISLNDAQK		8	0	8
htb1K123R	60S ribosomal protein L17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL17A PE=1 SV=4	sp|P05740	20549,6	30%	FNSSIGR-FVQGLLQNAAANAEAK-LYVSHIQVNQAPK-YGATSTNPAK-YLEQVLDHQR		5	4	1
htb1K123R	ISWI one complex protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IOC2 PE=1 SV=1	sp|Q12072	93448,8	1%	IIELISSTTK		1	0	1
htb1K123R	Mitochondrial DNA replication protein YHM2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YHM2 PE=1 SV=1	sp|Q04013	34185,2	15%	LVEDGIR-NFTFLESVK-PSTTNTAAANVIEK-SASAGGVPQSSWSVFK		4	0	4

htb1K123R	60S acidic ribosomal protein P1-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP1A PE=1 SV=4	sp|P05318	10908,3	8%	ALDGQNLK		1	0	1
htb1K123R	Putative DNA helicase INO80 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=INO80 PE=1 SV=1	sp|A6ZU34,sp|P53115	171461,8	1%	AAENASNALAETR		1	0	1
htb1K123R	60S ribosomal protein L33-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL33B PE=1 SV=2	sp|P41056	12168,2	37%	IAYVYR-IEGVATPQEAQFYLGK-RVNNPNVSLIK-TFGASVR-VNNPNVSLIK		5	0	5
htb1K123R	60S ribosomal protein L23-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL23A PE=1 SV=1	sp|P0CX41,sp|P0CX42	14473,1	37%	ISLGLPVGAIMNcADNSGAR-LPAASLGDMVMATVK-NLYIIAVK-VmPAIVVR	c13: Carbamidon	4	0	4
htb1K123R	Protein transport protein SEC61 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEC61 PE=1 SV=1	sp|P32915	52940,2	2%	GQIGIYPIK		1	0	1
htb1K123R	Pre-mRNA-splicing factor CWC22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CWC22 PE=1 SV=1	sp|P53333	67297,9	2%	LTEEEScPQGR	c7: Carbamidome	1	0	1
htb1K123R	Protein BMH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BMH1 PE=1 SV=4	sp|P29311	30092	27%	ATNASLEAYK-DSTLIMQLLR-EDSVYLAK-ISDDILSVLDSHLIPSATTGESK-IVSSIEQK-TVASSGQELSVEER		6	0	6
htb1K123R	Mitochondrial outer membrane protein porin 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=POR1 PE=1 SV=4	sp|P04840	30429,5	66%	DFYHATPAAFDVQTTTANGIK-DGPLSTNVEAK-GAFDLcLK-lEFANLTPGLK-LPNSNVNIEFATR-lSEPVHK-NELITSLTPGVAK-NINDLLNK-QLLRPGVTLGVGSSFDALK-QTGLGLTQGWSNTNNLQTK-SAVLNTTFTQPFFTAR-S		15	0	15
htb1K123R	U1 small nuclear ribonucleoprotein C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YHC1 PE=1 SV=1	sp|Q05900	27045,8	8%	ELAQTSIDTLK-FDIGDLVK		2	0	2
htb1K123R	Keratin, type II cytoskeletal 5 - Homo sapiens	sp|P13647	62379,6	2%	NLDLDSIIAEVK		1	1	0
htb1K123R	Glucan 1,3-beta-glucosidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BGL2 PE=1 SV=1	sp|P15703	34118,6	24%	AALQTYLPK-HWGVFTSSDNLK-IKESTVAGFLVGSEALYR-NDLTASQLSDK-STSDYETELQALK-SVVADISDSDGK		6	0	6
htb1K123R	DNA topoisomerase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TOP2 PE=1 SV=2	sp|P06786	164223,8	13%	EASADQILK-ELDNDILGVMR-ELILFSLADNIR-ELTVTNKPR-EYLLLGLSGNDK-FIITLSPEEMAK-GIPIEIHNK-GLGTSLAQEVR-IEQIGDNVLEITELPAR-IFDEILVNAADNK-MFEIADANEENALKK-NAIIQELENLGFPR-NVTIV		16	0	16
htb1K123R	40S ribosomal protein S8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS8A PE=1 SV=1	sp|P0CX39,sp|P0CX40	22490,4	31%	IAGVVYHPSNNELVR-IESSVESQFSAGR-IETGNFSWASEGISK-KFELGR-QWFEAHYGQTLGK		5	0	5
htb1K123R	Small nuclear ribonucleoprotein Sm D2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMD2 PE=1 SV=2	sp|Q06217	12853,3	16%	sSQIIDRPK-TPVIISLR	n-term: Acetyl (+	2	0	2
htb1K123R	Cystathionine gamma-lyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CYS3 PE=1 SV=2	sp|P31373	42542,8	12%	IAEFLAADKENVVAVNYPGLK-LVWIETPTNPTLK-QSSPANPIGTYEYSR		3	0	3
htb1K123R	ER-derived vesicles protein ERV14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ERV14 PE=1 SV=3	sp|P53173	15931,3	8%	VQLLDATEIFR		1	0	1
htb1K123R	Ribosome biogenesis protein MAK21 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MAK21 PE=1 SV=1	sp|Q12176	116682	3%	ISAVTLLIQDSPLHNTK-VLEVLEVLSHDPIIHVR		2	0	2
htb1K123R	Protein MMF1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MMF1 PE=1 SV=1	sp|P40185	15908,1	10%	NILAESNSSLDNIVK		1	0	1
htb1K123R	Eukaryotic translation initiation factor 2 subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SUI3 PE=1 SV=2	sp|P09064	31575,7	3%	TGFQATVGK		1	0	1
htb1K123R	Pyruvate decarboxylase isozyme 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDC1 PE=1 SV=7	sp|P06169	61496,9	51%	AQYNEIQGWDHLSLLPTFGAK-EVIDTILALVK-GYKPVAVPAR-IYEVEGmR-KLIDLTQFPAFVTPmGK-LIDLTQFPAFVTPmGK-LLQTPIDmSLKPNDAESEK-LLTTIADAAK-lTAATNAK-mIEIMLPVFDAPQNLVEQAK-MSANISE		21	0	21
htb1K123R	54S ribosomal protein L12, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MNP1 PE=1 SV=1	sp|P53163	20650,8	6%	GLLGLSLVEAK		1	0	1
htb1K123R	Transposon Ty2-LR1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY2B-LR1 PE=3 SV=1	sp|P0C2J3,sp|P25384,sp|Q03494,sp|Q	202130,3	1%	LAcQLILK-SDGTVLAPIVK	c3: Carbamidome	2	1	1
htb1K123R	Transposon Ty1-ML1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-ML1 PE=3 SV=2	sp|Q04711	198533	9%	AHNVSTSNNSPSTDNDSISK-DILSVDYTDIMK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-KYVRPPPmLTSPNDFPNWVK-LNNNGIHINNK-mESQQLSNYPNISHGSAcASVTSK-SDGTVLAPIVK-STTEPIQLNNK-VAc		12	11	1
htb1K123R	Cytochrome b5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CYB5 PE=1 SV=2	sp|P40312	13297,1	8%	GLYIGDVDK		1	0	1
htb1K123R	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TDH1 PE=1 SV=3	sp|P00360	35750,2	65%	DIEVVAVNDPFISNDYAAYmVK-EATYDQIK-EATYDQIKK-eLDTAQK-GTVSHDDKHIIIDGVK-HIIIDGVK-IATYQER-IATYQERDPANLPWGSLK-IDVAVDSTGVFK-IVSNAScTTNcLAPLAK-KDIEVVAVNDPFIS	m20: Oxidation (	20	0	20
htb1K123R	60S ribosomal protein L26-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL26B PE=1 SV=2	sp|P53221	14235,3	46%	DDEVLVVR-ISSVYR-KAYFTAPSSER-QSLDVSSDR-RDDEVLVVR-VLLSAPLSK-VNGASVPINLHPSK		7	0	7
htb1K123R	Chromatin structure-remodeling complex protein RSC6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC6 PE=1 SV=1	sp|P25632	54166,9	5%	IYVYNTTESSPR-TSDIYSNNNNDR		2	0	2
htb1K123R	CDP-diacylglycerol--serine O-phosphatidyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CHO1 PE=1 SV=3	sp|P08456	30805,8	4%	FNVTVAQLPK		1	0	1
htb1K123R	Heat shock protein 78, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP78 PE=1 SV=2	sp|P33416	91340,8	2%	ITDTALVSAAVLSNR		1	0	1
htb1K123R	Vacuolar transporter chaperone 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VTC4 PE=1 SV=2	sp|P47075	83157,5	4%	EVQEQVQHTVR-ISQLYDIAR-TGFILKPVFQVR		3	0	3
htb1K123R	Elongator complex protein 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ELP6 PE=1 SV=1	sp|Q04868	30574,6	14%	DKILSDVLAK-DVTGSLHVcR-FITPLLR-SmINLNLNPLK		4	0	4
htb1K123R	T-complex protein 1 subunit delta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CCT4 PE=1 SV=2	sp|P39078	57605,6	3%	GLIAGGGAPEIEISR		1	0	1
htb1K123R	60S ribosomal protein L13-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL13B PE=1 SV=1	sp|P40212	22525,5	42%	AAGLTAAYAR-APEAEQVLSAAATFPIAQPATDVEAR-AVQDNGESAFR-GFTLAEVK-NQEIFDANVQR-TIGIAVDHR-VHFDQAGK		7	0	7
htb1K123R	Lysyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KRS1 PE=1 SV=2	sp|P15180	67960,5	4%	EVLLFPTLKPDVLR-QLVVGGLDR		2	0	2
htb1K123R	Putative ribosomal RNA methyltransferase Nop2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOP2 PE=1 SV=1	sp|P40991	69814,3	3%	DLAQTLVNR-LVDTGLAIGK		2	0	2
htb1K123R	Eukaryotic translation initiation factor 2 subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SUI2 PE=1 SV=1	sp|P20459	34718,7	9%	FQIPLEELYK-LVAAPLYVLTTQALDK		2	0	2
htb1K123R	Protein TEX1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TEX1 PE=1 SV=1	sp|P53851	47168,8	3%	TITSEVAASVTSK		1	0	1
htb1K123R	RNA-binding protein SRO9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SRO9 PE=1 SV=2	sp|P25567	48059,5	2%	ASITVSGTK		1	0	1
htb1K123R	60S acidic ribosomal protein P2-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP2A PE=1 SV=1	sp|P05319	10746,2	10%	VSSVLSALEGK		1	0	1
htb1K123R	Nucleolar complex protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOC2 PE=1 SV=2	sp|P39744	81605,1	3%	LNQNSTFIQEK-TPLGSYVAVQR		2	0	2
htb1K123R	Proteasome component PRE4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE4 PE=1 SV=1	sp|P30657	29444,1	9%	LIPVGDNTVVGISGDISDMQHIER		1	0	1
htb1K123R	H/ACA ribonucleoprotein complex non-core subunit NAF1 OS=Saccharomyces cerevisiae (strain YJM789) GN=NAF1 PE=3 SV=1	sp|A6ZRW0,sp|P53919	54840,4	2%	TIITPIGVLK		1	0	1
htb1K123R	Transcription initiation factor TFIID subunit 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF6 PE=1 SV=1	sp|P53040	57904	8%	FFLGNLNNWAR-GVSVLEGESIR-ILEIIEQAVK-VISTLTAK		4	0	4
htb1K123R	Flavohemoprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YHB1 PE=1 SV=2	sp|P39676	44647,2	26%	ALQIKPEHYPIVGEYLLK-ATVPVLEQQGTVITR-FGSGIELESLPITPGQYITVNTHPIR-LSAPAGDFAINK-NMLTEHTELLNIFNR-VGAQPNALATTVLAAAK		6	0	6
htb1K123R	Importin subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SRP1 PE=1 SV=1	sp|Q02821	60442,5	13%	DTQQVELR-EHRPPIDVVIQAGVVPR-GLNINENADFIEK-LLEVAEYK-LLLSSPK-LVELLSHESTLVQTPALR		6	0	6
htb1K123R	Eukaryotic translation initiation factor 5B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FUN12 PE=1 SV=2	sp|P39730	112271,5	7%	AVQEEFQSR-GPMIIGVDVLEGTLR-IAANDLEK-IPVMSIGLGPVYK-STPAATPAATPTPSSASPNKK		5	0	5
htb1K123R	Cell division control protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC12 PE=1 SV=1	sp|P32468	46668,9	6%	QVIEAQEIR-SGSNPDSAAVEHAR		2	0	2
htb1K123R	6-phosphogluconate dehydrogenase, decarboxylating 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GND1 PE=1 SV=1	sp|P38720	53545,3	12%	AGAPVDALINQIVPLLEK-GILFVGSGVSGGEEGAR-LPANLLQAQR-SIIGATSIEDFISK		4	0	4
htb1K123R	Acetyl-CoA acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ERG10 PE=1 SV=3	sp|P41338	41728,6	3%	FGQTVLVDGVER		1	0	1
htb1K123R	GMP synthase [glutamine-hydrolyzing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GUA1 PE=1 SV=4	sp|P38625	58483,4	2%	IVNEVDGVAR		1	0	1
htb1K123R	Peroxiredoxin TSA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TSA1 PE=1 SV=3	sp|P34760	21590,1	45%	DYGVLIEEEGVALR-EGGLGPINIPLLADTNHSLSR-GLFIIDPK-HITINDLPVGR-LVEAFQWTDK-NVDEALR-TAVVDGVFDEVSLDKYK		7	0	7
htb1K123R	U1 small nuclear ribonucleoprotein component SNU71 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNU71 PE=1 SV=1	sp|P53207	71385,1	14%	AAAITLPEGTVK-ASEFYSVFK-FQDSLK-LPFTADELNIR-QALLNELR-SAAEDRLPFTADELNIR-SGFIPILK-TGTIPSVKPEK-VFDQIR-YVDELVR		10	0	10
htb1K123R	2-oxoglutarate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KGD1 PE=1 SV=2	sp|P20967	114419,3	5%	IEQLHPFPFAQLR-LNVLSNVVR-SVIDVYTEK-YVNLSLVANPSHLESQDPVVLGR		4	0	4
htb1K123R	Enolase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ENO2 PE=1 SV=2	sp|P00925	46915,1	53%	AADALLLK-AAQDSFAANWGVMVSHR-AVDDFLLSLDGTANK-GNPTVEVELTTEK-GVmNAVNNVNNVIAAAFVK-IATAIEK-IEEELGDK-IGLDcASSEFFK-IGSEVYHNLK-LGANAILGVSmAAAR-LNQLLR-NVPLYQHLADLS		18	0	18
htb1K123R	Heat shock protein 104 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP104 PE=1 SV=2	sp|P31539	102039,6	11%	IEVAEPSVR-LFSLDLAALTAGAK-LIQNEILNK-LPDSALDLVDIScAGVAVAR-QLQLIQVEIK-SNPcLIGEPGIGK-TAIIEGVAQR-VIGATTNNEYR		8	0	8
htb1K123R	40S ribosomal protein S1-B OS=Saccharomyces cerevisiae (strain YJM789) GN=RPS1B PE=3 SV=1	sp|A6ZM02,sp|B3LLJ2,sp|B5VP69,sp	28812,9	64%	APSTFENR-DIFPLQNIHVR-EVQNSTLAQLTSK-FDVGALMALHGEGSGEEK-hSYAQSSHIR-IFAIAFTR-KEWFDIK-KVISEILTR-KVVDPFTR-LIPEVINK-LRVDEVQGK-NLLTNFHGmDFTTDK-TSDDYVLR-VSGFKDEVLETV-V		16	0	16
htb1K123R	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TDH2 PE=1 SV=3	sp|P00358	35846,9	61%	eLDTAQK-ETTYDEIK-ETTYDEIKK-IATFQER-IVSNAScTTNcLAPLAK-KVVITAPSSTAPmFVmGVNEEK-LTGMAFR-LVSWYDNEYGYSTR-NVEVVALNDPFISNDYSAYmFK-TASGNIIPSSTGAAK-VAINGFGR	n-term: Acetyl (+	18	15	3
htb1K123R	60S acidic ribosomal protein P2-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP2B PE=1 SV=2	sp|P02400	11050,3	31%	GSLEEIIAEGQK-YLAAYLLLVQGGNAAPSAADIK		2	0	2
htb1K123R	Citrate synthase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CIT1 PE=1 SV=2	sp|P00890	53362,3	11%	AIGVLPQLIIDR-ALSADLAAR-ANQEVLEWLFK-ITSTDPNADYGK-LPVIASK		5	0	5
htb1K123R	Phosphoglycerate mutase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GPM1 PE=1 SV=3	sp|P00950	27609,7	41%	AIQTANIALEK-HLEGISDADIAK-KVYPDVLYTSK-LWIPVNR-NLFTGWVDVK-SFDVPPPPIDASSPFSQK-TVMIAAHGNSLR-VYPDVLYTSK-YVDPNVLPETESLALVIDR		9	0	9
htb1K123R	Regulatory protein SIR3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SIR3 PE=1 SV=6	sp|P06701	111365,3	1%	FVPIDIFQIIR		1	0	1
htb1K123R	Pyruvate kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC19 PE=1 SV=2	sp|P00549	54545,4	58%	AEVSDVGNAILDGADcVMLSGETAK-AGAGHSNTLQVSTV-AGLNIVR-AIIVLSTSGTTPR-AKEFGILK-EVLGEQGK-FSHLYR-GDLGIEIPAPEVLAVQK-GDTYVSIQGFK-GVFPFVFEK-GVNLPGTDVDLPALSEK	c16: Carbamidon	26	0	26
htb1K123R	Serine/threonine-protein kinase BUR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SGV1 PE=1 SV=1	sp|P23293	74241,6	4%	APELVLGDK-YLPGAELTTTNYKPTLR		2	0	2
htb1K123R	NADP-dependent alcohol dehydrogenase 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADH6 PE=1 SV=1	sp|Q04894	39617,8	5%	IWVETLPVGEAGVHEAFER		1	0	1
htb1K123R	V-type proton ATPase subunit d OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VMA6 PE=1 SV=2	sp|P32366	39792,4	8%	AALANVYEYR-LYPLATFHLAQAQDFEGVR		2	0	2
htb1K123R	Mannose-1-phosphate guanyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PSA1 PE=1 SV=2	sp|P41940	39566,6	11%	ETFPILVEEK-GLILVGGYGTR-IGPDVVIGPNVTIGDGVR		3	0	3
htb1K123R	Peroxiredoxin type-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AHP1 PE=1 SV=4	sp|P38013	19114,4	19%	FASDPGcAFTK-KFPAGDYK-mPQTVEWSK-sDLVNKK	c7: Carbamidome	4	0	4
htb1K123R	Mitochondrial protein import protein MAS5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDJ1 PE=1 SV=1	sp|P25491	44671,7	11%	EASAAYEILSDPEKR-VGIVPGEVIAPGmR-YHPDKNPSEEAAEK		3	0	3
htb1K123R	Eukaryotic translation initiation factor 3 subunit I OS=Saccharomyces cerevisiae (strain YJM789) GN=TIF34 PE=3 SV=1	sp|A6ZMK5,sp|P40217	38756,2	3%	DVTTTSANEGK		1	0	1
htb1K123R	Pyruvate dehydrogenase complex protein X component, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDX1 PE=1	sp|P16451	45363,8	5%	IPQDSVNK-LPQEANTANAK		2	0	2
htb1K123R	THO complex subunit HPR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HPR1 PE=1 SV=2	sp|P17629	87834	16%	ALEEEASFPER-ALPVSFDSIR-INSASQTEGDELK-INSASQTEGDELKSEQTQPK-IPTGLDKIEQEVK-ISSETSGGEAKDEIIR-KVEALDDSFK-LENNDILNTVK-LINNVWK-NLISSDETR-TGVDGLFEEPR		11	0	11
htb1K123R	Chromatin structure-remodeling complex protein RSC8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC8 PE=1 SV=1	sp|P43609	63169,2	15%	IHAFLEK-LSPYEYLTITAVR-NFIINTYR-NVAMDVASIVK-SLEELNVSK-SNPDFFNDSSR-WGLINYQIDPR-YIEESQAIIQELVK		8	0	8
htb1K123R	Protein MET17 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MET17 PE=1 SV=3	sp|P06106	48672,3	11%	FQNPTSNVLEER-LASNLANVGDAK-WIGGHGTTIGGIIVDSGK-YNVPDFEK		4	0	4
htb1K123R	Nucleoporin POM152 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=POM152 PE=1 SV=1	sp|P39685	151659,4	8%	AIFDGNYGESDIHFR-DIPSAAFNFFEPIK-EGLYQLVDIR-EHQSELIIK-ELSVTGSAINHHR-INSIDVPIR-LPNQIPGEYITTIK-NQILVSITDAPK-QTVHPIPDVAFADGGK		9	0	9
htb1K123R	Cell division control protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC3 PE=1 SV=3	sp|P32457	60056,2	10%	ILYENYR-LFSSLPYAVIGSNDIVENYSGNQVR-QLELSINSASPNVNHSPVPTK		3	0	3
htb1K123R	Heat shock protein homolog SSE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSE1 PE=1 SV=4	sp|P32589	77368,6	11%	GIDIVVNEVSNR-IAGLNPVR-IVNDVTAAGVSYGIFK-LVELDDKK-STPSVVGFGPK-YEELASLGNIIR-YNIADAAR		7	0	7
htb1K123R	Nucleoporin NUP84 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP84 PE=1 SV=1	sp|P52891	83639,8	4%	LPASNILR-LYVDAVHSIIALSR-QIETINFLR		3	0	3
htb1K123R	60S ribosomal protein L19-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL19A PE=1 SV=1	sp|P0CX82,sp|P0CX83	21704,6	38%	ALNEEAEAR-ALVEHIIQAK-DALLKEDA-HLYHVLYK-KVWLDPNETSEIAQANSR-LAASVVGVGK-LPSQVVWIR-VWLDPNETSEIAQANSR		8	0	8
htb1K123R	Adenosine kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADO1 PE=1 SV=1	sp|P47143	36372,9	4%	LVAGGAAQNTAR		1	0	1
htb1K123R	Actin-like protein ARP8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARP8 PE=1 SV=1	sp|Q12386	100212,9	1%	IPALDFILTDR		1	0	1
htb1K123R	Transcription-associated protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TRA1 PE=1 SV=1	sp|P38811	433195,7	1%	AIETELGLR-LFDQEHFNNTEITVR-SIQFNLPIAIPLSPQVR		3	0	3
htb1K123R	Partitioning protein REP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=REP1 PE=1 SV=1	sp|P03871	43231,6	2%	VTAFFSYLR		1	0	1
htb1K123R	D-3-phosphoglycerate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SER3 PE=1 SV=1	sp|P40054	51194,1	3%	GTVVDIPSLIQAVK		1	0	1
htb1K123R	Nucleoporin NUP192 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP192 PE=1 SV=1	sp|P47054	191546,8	5%	GEIELSDGSTFK-GGASALIENNLFR-IIAELSFLK-NGALVSNILSAFK-VFSDVLFEFTK-VLSDQVGSEK-VNVTLDNPLLVDK		7	0	7
htb1K123R	Fatty acid synthase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FAS1 PE=1 SV=2	sp|P07149	228696	8%	ALAGSEINWR-ALDTVTNVLNFIK-APSGLDQSR-FLGYVSSLVEPSK-FSAETLSELIR-IDIIELQK-IVDVVGTLSR-LNADFQKPWFATVNGQAR-LVELMFIR-SNYGMIAINPGR-TVVTLSEPVQGELKPTVILK-VIDEPIK-YLGLKPGS		13	0	13
htb1K123R	6-phosphofructokinase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PFK1 PE=1 SV=1	sp|P16861	107972,8	10%	AEVAALAAENK-ASSDASDLLR-LNIGIVHVGAPSAALNAATR-LSDTLVFLK-MPLVESVK-SIITNDEALFK-TAIPGHVQQGGVPSSK-WLATLQGVDAVK		8	0	8
htb1K123R	Malate dehydrogenase, peroxisomal OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MDH3 PE=1 SV=3	sp|P32419	37187,2	33%	AETFLVDYLMLK-EEQLVNTAVK-FKPGNVMGVTNLDLVR-ILVISNPVNSLVPIAVETLK-ILVISNPVNSLVPIAVETLKK-KVTVIGGHSGETIIPIITDK-LSPYVSELALYDIR-VAILGASGGVGQPLSLLLK-VKVAILGASGGVGQPLSLL		9	0	9
htb1K123R	Vacuolar transporter chaperone 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VTC3 PE=1 SV=1	sp|Q02725	96558,3	1%	ISVPDGKTTER		1	0	1
htb1K123R	114 kDa U5 small nuclear ribonucleoprotein component OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNU114 PE=1 SV=1	sp|P36048	114047,2	12%	EGPLAEEPIYGVQYK-GNVFSPIDNNIIFASTK-GQVPVIESAGFETDLR-IINVGVIGPLHSGK-ILDTSQSESR-IVLQPLLPR-NTQSPQTPLVEPVTER-QQTGLVDAITR-VAGTPLLEVR		9	0	9
htb1K123R	Transcription initiation factor TFIID subunit 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF7 PE=1 SV=1	sp|Q05021	67557	2%	ILPDIQLEFVK		1	0	1
htb1K123R	Histone H2A.Z OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HTZ1 PE=1 SV=3	sp|Q12692	14283,6	12%	AGLQFPVGR-HLQLAIR		2	1	1
htb1K123R	Polyamine N-acetyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PAA1 PE=1 SV=1	sp|Q12447	21948,7	8%	IVLIAHEPLIPFYER		1	0	1
htb1K123R	Uncharacterized protein YLR179C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YLR179C PE=1 SV=1	sp|Q06252	22151,8	5%	NNYIGPGPPK		1	0	1
htb1K123R	Cell division control protein 11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC11 PE=1 SV=1	sp|P32458	47650,7	3%	QLGSLVNIIPVISK		1	0	1
htb1K123R	Translation initiation factor RLI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RLI1 PE=1 SV=1	sp|Q03195	68343,3	3%	LNAAQIIR-VIVFEGIPSK		2	0	2
htb1K123R	Protein FMP52, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FMP52 PE=1 SV=1	sp|P40008	25086,7	18%	IDHDLNLQLAQAAK-LLGYPVYGDEVGK-QSGFGGNLTAALGTR		3	0	3
htb1K123R	Eukaryotic translation initiation factor 3 subunit C OS=Saccharomyces cerevisiae (strain YJM789) GN=NIP1 PE=3 SV=1	sp|A6ZN26,sp|P32497	93225,2	9%	AILYNIYYTALNK-ISLNSSNNASADER-LAELFDLPENK-LQTIIDSR-LSFQGPPETLR-SLLNIDPHSSDYLIR		6	0	6
htb1K123R	Protein SPT3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPT3 PE=1 SV=1	sp|P06844	38801,3	4%	SILPEDVIFLIR		1	0	1
htb1K123R	Arginyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDR341C PE=1 SV=1	sp|Q05506	69527,8	1%	LVIPDILTR		1	0	1
htb1K123R	U1 small nuclear ribonucleoprotein 70 kDa homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNP1 PE=1 SV=1	sp|Q00916	34449,2	18%	FASASTSNPAER-GNRPLLSAATPTAAVTSVYK-GYAFIVFKDPISSK-NAQLLDR		4	0	4
htb1K123R	60S ribosomal protein L12-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL12A PE=1 SV=1	sp|P0CX53,sp|P0CX54	17823,2	33%	AVGGEVGASAALAPK-EILGTAQSVGcR-IGPLGLSPK-QAAASVVPSASSLVITALK		4	0	4
htb1K123R	Ubiquitin-40S ribosomal protein S31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS31 PE=1 SV=3	sp|P05759	17216,6	22%	EcSNPTcGAGVFLANHK-LAVLSYYK-TLSDYNIQK	c2: Carbamidome	3	0	3
htb1K123R	Ribosome-associated complex subunit SSZ1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSZ1 PE=1 SV=2	sp|P38788	58239,5	45%	AIPSALSYVGEDEYHGGQALQQLIR-DFIGLPFDK-DVNVVVADFGGIR-EAVLTVPTNFSEEQK-GDFLIGVYEGDHHIEEK-GEFHPVLLAETSFPVQK-KPIGLIGAK-LAAEDYIGSAVK-LISDYDADELAEALQPVIVNTPHLK-LMEL		18	0	18
htb1K123R	Importin subunit beta-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KAP95 PE=1 SV=1	sp|Q06142	94778,6	14%	DVVPNLLNLLTR-ETTAWcIGR-ILAALTLK-ImVDNTGAEQPENVKR-LAALNALADSLIFIK-QFYGQDWVIDYIK-SGQLFSQATK-TNALTALVSIEPR-WITQVSPEAK-YLETFSPYLLK		10	0	10
htb1K123R	Uncharacterized RNA-binding protein YGR250C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YGR250C PE=1 SV=1	sp|P53316	89515,3	15%	AILNTDGYQVSK-DQVLSVSFAQK-FINALMTQNQSQQQVSR-GYGFVSFESPLDAAK-LQVLEQNK-SFGEIISVK-SLSIGELSFLFSK-TSTGLQLEQLANTNLLTIR-VETLITPK-YGPILSMK		10	0	10
htb1K123R	Pre-mRNA-splicing factor 8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP8 PE=1 SV=1	sp|P33334	279514,8	4%	ALNNAIPGGPK-FMAASEVATHSK-IDFTLLNR-ILVLALEDLK-LFVDDTNVYR-LIVDPNIADYITAK-QTDTGITHFR-SAIANTLLYLR-SFSPIPFPPLTYK-TFEGNVATK		10	0	10
htb1K123R	Poly(A) RNA polymerase protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PAP2 PE=1 SV=1	sp|P53632	66033,5	5%	AFAGAFDLLTNR-NNLYSLASHLK-NQTISTIR		3	0	3
htb1K123R	40S ribosomal protein S11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS11A PE=1 SV=1	sp|P0CX47,sp|P0CX48	17748,8	50%	AYLHYIPK-cPFTGLVSIR-ILTGTVVSTK-NVPVHVSPAFR-RAYLHYIPK-sTELTVQSER-TAIEGSYIDK-TAIEGSYIDKK-VQVGDIVTVGQcRPISK		9	0	9
htb1K123R	60S ribosomal protein L11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL11A PE=1 SV=2	sp|P0C0W9,sp|Q3E757	19720	49%	AEEILER-EDTVSWFK-IAVHVTVR-IAVHVTVRGPK-LVLNISVGESGDR-TTKEDTVSWFK-VKEYQLR-VLEQLSGQTPVQSK-YDPSIGIFGmDFYVVmNRPGAR		9	0	9
htb1K123R	60S ribosomal protein L22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL22A PE=1 SV=3	sp|P05749	13693,4	41%	TFTVDVSSPTENGVFDPASYAK-VEGAVGNLGNAVTVTEDGTVVTVVSTAK		2	0	2
htb1K123R	Eukaryotic translation initiation factor 2 subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GCD11 PE=1 SV=1	sp|P32481	57867,2	8%	FAVPGGLIGVGTK-HVIILQNK-LNPLSAEIINR-YNIDAVNEFIVK		4	0	4
htb1K123R	Transposon Ty1-NL2 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-NL2 PE=3 SV=1	sp|Q99337	198206,1	7%	AHNVSTSNNSPSTDNDSISK-DILSVDYTDIMK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-LNNNGIHINNK-SDGTVLAPIVK-STTEPIQLNNK-VAcQLIMR-VTNIIDR		9	9	0
htb1K123R	mRNA export factor MEX67 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MEX67 PE=1 SV=1	sp|Q99257	67353,5	21%	ELLmTNNPITTDK-GVFSSISTQSK-LLNLGALHSDPELIQK-LNPVQLELLNK-LSIGQESINSIFK-LVVLDNVIVR-LVVLDNVIVRDEQK-NLcLANNQIFR-SLIVESVNLADNQLK-VAVYDAHVEGPLVIGYVNSK	m4: Oxidation (+	10	0	10
htb1K123R	FACT complex subunit POB3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=POB3 PE=1 SV=1	sp|Q04636	62995,2	26%	ADDIHHLLVLAIEPPLR-EEQQLLEQFLK-FYIPGVIQTNVDENMTK-GSTTFANISK-INNTNLTSK-ISTSGGSAANQAR-KPFLLPATELSTVQWSR-NQGVIQLDGFSQDDYNLIK-QGQTTYPFLVLQFQK-THIVLSHVLK-VIVPGEYK		11	0	11
htb1K123R	Enolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ENO1 PE=1 SV=3	sp|P00924	46817,4	39%	AADALLLK-AVDDFLISLDGTANK-GNPTVEVELTTEK-IATAIEK-IGLDcASSEFFK-IGSEVYHNLK-LNQLLR-NVNDVIAPAFVK-SGETEDTFIADLVVGLR-SIVPSGASTGVHEALEmR-TAGIQIVADDLTVTNPK-TFAEALR-VNQIG		14	10	4
htb1K123R	Peroxisomal membrane protein PMP27 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PEX11 PE=1 SV=2	sp|Q12462	26876,2	5%	FLAVQNSSLLAR		1	0	1
htb1K123R	Pre-mRNA-splicing factor 19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP19 PE=1 SV=2	sp|P32523	56572,3	17%	FPVDEEAK-LLLLYPGNQITILDSK-LVAAQLLMEK-NLELLQAQNYSR-SDVEYSSGVLHK-SSQQAVAITR-STLDSLTK-TITTITTPNPR		8	0	8
htb1K123R	Elongation factor 1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EFB1 PE=1 SV=4	sp|P32471	22627,5	19%	AIEmEGLTWGAHQFIPIGFGIK-QLNASLADK-WFNHIASK	m4: Oxidation (+	3	0	3
htb1K123R	rRNA 2'-O-methyltransferase fibrillarin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOP1 PE=1 SV=1	sp|P15646	34465,5	14%	GKEDLLVTK-ISVEEPSKEDGVPPTK-MLIGMVDcVFADVAQPDQAR		3	0	3
htb1K123R	40S ribosomal protein S20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS20 PE=1 SV=3	sp|P38701	13906,8	37%	EKVEEQEQQQQIIK-ITLTSTK-QLENVSSNIVK-VEEQEQQQQIIK-YIDLEAPVQIVK		5	0	5

htb1K123R	Protein HSH49 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSH49 PE=1 SV=1	sp|Q99181	24504,9	5%	SLNNQLVANNR		1	0	1
htb1K123R	S-adenosylmethionine synthase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SAM1 PE=1 SV=2	sp|P10659,sp|P19358	41819,4	8%	FVIGGPQGDAGLTGR-IGYDDSAK-YFIQPSGR		3	0	3
htb1K123R	Keratin 6A - Homo sapiens	sp|A4QPC1,sp|A8K2I0,sp|P02538,sp|	60046,4	4%	AQYEEIAQR-NLDLDSIIAEVK		2	2	0
htb1K123R	Probable alpha-1,6-mannosyltransferase MNN11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MNN11 PE=1 SV=2	sp|P46985	47860,9	8%	ALIDYLNDPLLR-SAGASYSPSHGLYINEIPASSR		2	0	2
htb1K123R	Transcription factor CSR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CSR2 PE=1 SV=1	sp|Q12734	124852,9	1%	STTLSDIK		1	0	1
htb1K123R	Regulation of enolase protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=REE1 PE=1 SV=1	sp|P40893	21966,8	7%	VTFSEWSLTAPLGK		1	0	1
htb1K123R	External NADH-ubiquinone oxidoreductase 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NDE1 PE=1 SV=1	sp|P40215	62776,5	2%	AIADLAVGEAK		1	0	1
htb1K123R	40S ribosomal protein S5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS5 PE=1 SV=3	sp|P26783	25038,5	55%	AQcPIIER-DASLVDYVQVR-GSSTSYAIK-HTLDIINVLTDQNPIQVVVDAITNTGPR-LTNSLmmNGR-QAVDVSPLR-QPIFVAHTAGR-TIAETLAEELINAAK-VNQAIALLTIGAR-WSFEEVEVK	c3: Carbamidome	10	0	10
htb1K123R	Keratin, type I cytoskeletal 10 - Homo sapiens	sp|P13645	59512,4	30%	AETEcQNTEYQQLLDIK-ALEESNYELEGK-GSLGGGFSSGGFSGGSFSR-IRLENEIQTYR-LAADDFR-LASYLDK-LENEIQTYR-LKYENEVALR-NQILNLTTDNANILLQIDNAR-QSLEASLAETEGR-QSVEADING	c5: Carbamidome	19	0	19
htb1K123R	Potassium-activated aldehyde dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ALD4 PE=1 SV=2	sp|P46367	56725,2	9%	IAPALVTGNTVVLK-VAFTGSTATGR-YIPQAGIPPGVINIVSGFGK		3	0	3
htb1K123R	THO complex subunit MFT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MFT1 PE=1 SV=1	sp|P33441	44997,2	13%	ELESINASMK-FLDLQSSIDTK-ITSIFKEELLK-SDIENVR-VHYSEVDTPFNK		5	0	5
htb1K123R	cDNA FLJ75925, highly similar to Homo sapiens keratin 16 - Homo sapiens	sp|A8K488,sp|P08779	51269	5%	LAADDFR-LASYLDK-VTMQNLNDR		3	3	0
htb1K123R	Pre-mRNA-processing protein PRP40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP40 PE=1 SV=1	sp|P33203	69068,5	14%	ENQVDSTWSFSR-ETSWTIPAFEK-IISELGTR-IVNTIENDLQNK-LIADEPIYK-VDKEDISLIVDGLIK-VLTHEDVLNEYLK		7	0	7
htb1K123R	40S ribosomal protein S17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS17A PE=1 SV=1	sp|P02407,sp|P14127	15788,9	57%	DQYVPEVSALDLSR-IAGYTTHLmK-KDQYVPEVSALDLSR-LcDEIATIQSK-LPLSVINVSAQR-LTLDFQTNK-SLGLKLPLSVINVSAQR-SNGVLNVDNQTSDLVK		8	0	8
htb1K123R	Aromatic/aminoadipate aminotransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARO8 PE=1 SV=1	sp|P53090	56180,5	7%	GTYAAVSPEK-GVLVVPGSWFK-SANPSNDIPLSR		3	0	3
htb1K123R	Histone H4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HHF1 PE=1 SV=2	sp|P02309	11368,9	42%	DNIQGITKPAIR-ISGLIYEEVR-SFLESVIR-TVTSLDVVYALK-TVTSLDVVYALKR		5	0	5
htb1K123R	5'-3' exoribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KEM1 PE=1 SV=1	sp|P22147	175468	4%	EVQIIFSGHEVPGEGEHK-GPIPIEEEFPLNSK-LIEAMQPYLR-QLENISLEGER-VVYIQDSGK		5	0	5
htb1K123R	Protein BUR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BUR2 PE=1 SV=1	sp|Q05949	45723,3	3%	LLEENFFNLK		1	0	1
htb1K123R	Elongator complex protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ELP4 PE=1 SV=1	sp|Q02884	51157,7	2%	VTVQNLNETQR		1	0	1
htb1K123R	Small nuclear ribonucleoprotein Sm D1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMD1 PE=1 SV=1	sp|Q02260	16275,9	23%	LTLPQPR-NEQVTIELK-QIILPDSLNLDSLLVDQK		3	0	3
htb1K123R	Nucleoporin NUP145 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP145 PE=1 SV=1	sp|P49687	145668,3	2%	LLLSNNPVQNNELK-LSSILFDPVSYPYK		2	0	2
htb1K123R	PAB1-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PBP1 PE=1 SV=1	sp|P53297	78783	4%	SGSNISQGQSSTGHTTR-TVSPTTQISAGK		2	0	2
htb1K123R	Alcohol dehydrogenase 3, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADH3 PE=1 SV=2	sp|P07246	40369,8	6%	LPLVGGHEGAGVVVK-YVVDTSK		2	1	1
htb1K123R	Protein YRO2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YRO2 PE=1 SV=1	sp|P38079,sp|Q12117	38721,3	4%	INPPTGADFHITSR		1	0	1
htb1K123R	Elongation factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EFT1 PE=1 SV=1	sp|P32324	93290,3	46%	ADLMLYVSK-AEPIDEEVSLAIENGIINPR-ALLELQVSK-ATYAGFLLADPK-AVQYLHEIK-AYLPVNESFGFTGELR-DEIPVLLEK-DTDAEGKPLER-EDLYQTFAR-EGPIFGEEMR-ETVESESSQTALSK-FSVSPVVQVAVEVK-FVEP		32	0	32
htb1K123R	Nucleoporin NUP133 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP133 PE=1 SV=1	sp|P36161	133327,5	3%	EVFNILVEELK-FLNALVWR-IFNTNSSVVSLR		3	0	3
htb1K123R	40S ribosomal protein S12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS12 PE=1 SV=1	sp|P48589	15470,9	34%	KVVGASVVVVK-LVEGLANDPENK-LVEGLANDPENKVPLIK-QLGEWAGLGK-TALVHDGLAR-VVGASVVVVK		6	0	6
htb1K123R	Suppressor protein STM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STM1 PE=1 SV=3	sp|P39015	29995,4	34%	DVTDSATTK-GNNTANATNSANTVQK-KADVPPPSADPSK-KVELDAER-sNPFDLLGNDVEDADVVVLPPK-TAQLSLQDYLNQQANNQFNK-TAQLSLQDYLNQQANNQFNKVPEAK		7	0	7
htb1K123R	Endoplasmic reticulum transmembrane protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YET3 PE=1 SV=1	sp|Q07451	22904,2	5%	ASPPVASSDVK		1	0	1
htb1K123R	ATP-dependent RNA helicase DOB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MTR4 PE=1 SV=1	sp|P47047	122058,7	7%	ELVDVANTIGNSSLK-GATFTQIcK-GIGIHHSGLLPILK-ISESQAVIQLDDLR-KIDVLNTK-LSSNPLTNSMR-VIYTSPIK		7	0	7
htb1K123R	Triosephosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TPI1 PE=1 SV=2	sp|P00942	26795,6	22%	ADVDGFLVGGASLKPEFVDIINSR-KPQVTVGAQNAYLK-QLNAVLEEVK-TLDVVER		4	0	4
htb1K123R	Helicase SEN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEN1 PE=1 SV=2	sp|Q00416	252506,4	0%	FPLEPIFK		1	0	1
htb1K123R	ADP-ribosylation factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARF2 PE=1 SV=3	sp|P19146	20658,2	29%	ILMVGLDGAGK-LFSNLFGNK-mLNEDELR-NAVWLVFANK-NISFTVWDVGGQDR		5	0	5
htb1K123R	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDB1 PE=1 SV	sp|P32473	40054,2	30%	EGTDISIVTYTR-ELEDFAFPDTPTIVK-NVQFSLEAAEILQK-RVVDTPITEYGFTGLAVGAALK-SIRPLDTEAIIK-VLVPYSAEDAR-VTGADVPTPYAK-VVDTPITEYGFTGLAVGAALK-YGVSAEVINLR		9	0	9
htb1K123R	Dihydrolipoyl dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LPD1 PE=1 SV=1	sp|P09624	54010,9	17%	AAQLGFNTAcVEK-IGLEVDKR-IVSSTGALSLK-LVIDDQFNSK-QLTGGIELLFK-RPYIAGLGAEK-TNQDTEGFVK-VTPVDGLEGTVK	c10: Carbamidon	8	0	8
htb1K123R	Elongator complex protein 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IKI1 PE=1 SV=1	sp|P38874	35220,9	15%	aSSSHNPVILLK-GLNNDIFQLR-LIQEFVHQSK-QIISYLPAATATQAK	n-term: Acetyl (+	4	0	4
htb1K123R	Transcription initiation factor TFIID subunit 11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF11 PE=1 SV=1	sp|Q04226	40625,1	4%	LLVTNLDKDQTNR		1	0	1
htb1K123R	Fatty acid synthase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FAS2 PE=1 SV=2	sp|P19097	206951,1	2%	AISAQADKQDISSSTR-ATSNTLEEFEHGR-YETSILEHSGIR		3	0	3
htb1K123R	Chromatin structure-remodeling complex subunit RSC7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NPL6 PE=1 SV=1	sp|P32832	49651,9	4%	FILNQTQK-VLLVDQQGLR		2	0	2
htb1K123R	Cell division control protein 48 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC48 PE=1 SV=3	sp|P25694	91998,4	5%	AVATEVSANFISVK-FALGNSNPSALR-GGSLGDAGGASDR		3	0	3
htb1K123R	40S ribosomal protein S18-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS18A PE=1 SV=1	sp|P0CX55,sp|P0CX56	17037,9	67%	AGELTQEELER-DYHTLANNVESK-HFWGLR-IPAWFLNR-IVQImQNPTHYK-IVYALTTIK-LLNTNVDGNIK-LRDDLER-sLVVQEQGSFQHILR-YSNLVcK		10	0	10
htb1K123R	Poly(A) polymerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PAP1 PE=1 SV=1	sp|P29468	64554	1%	VILQEFVR		1	0	1
htb1K123R	DNA-directed RNA polymerase II subunit RPB9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB9 PE=1 SV=1	sp|P27999	14288	21%	HELITNIGETAGVVQDIGSDPTLPR		1	0	1
htb1K123R	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP43 PE=1 SV=	sp|P53131	87564,8	2%	YFNDAPLLAVPGR		1	0	1
htb1K123R	Histone H2B.1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HTB1 PE=1 SV=2	sp|P02293,sp|P02294	14253	31%	EIQTAVR-ETYSSYIYK-KETYSSYIYK-lILPGELAK-SmSILNSFVNDIFER		5	0	5
htb1K123R	Replication factor A protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RFA3 PE=1 SV=1	sp|P26755	13816,1	12%	VDPTEISNVNAPVFR		1	0	1
htb1K123R	Mitochondrial phosphate carrier protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MIR1 PE=1 SV=1	sp|P23641	32813,9	26%	ASEFYYGFAGPK-EEGIGSFYSGFTPILFK-FFIDNLGYDTASR-IQLEPTVYNK-QLGFFGSFAGLPTR-STLGcPPTIEIGGGGH		6	0	6
htb1K123R	Multiprotein-bridging factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MBF1 PE=1 SV=2	sp|O14467	16404	38%	GNNIGSPLGAPK-INEKPTVVNDYEAAR-KLDPNVGR-QGLVVSVDKK-RQGLVVSVDK-sDWDTNTIIGSR		6	0	6
htb1K123R	ADP,ATP carrier protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PET9 PE=1 SV=2	sp|P18239	34428	36%	GFLPSVVGIVVYR-GVAGAGVISmYDQLQmILFGK-IVAAEGVGSLFK-LLIQNQDEMLK-QFNGLIDVYK-SDGVAGLYR-TAASPIER-TPLPPAPAPK-YDGAFDcLR-YFPTQALNFAFK		10	0	10
htb1K123R	13 kDa ribonucleoprotein-associated protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNU13 PE=1 SV=1	sp|P39990	13569,4	25%	AcGVSRPVIAASITTNDASAIK-NVPYVFVPSR	c2: Carbamidome	2	0	2
htb1K123R	Nuclear polyadenylated RNA-binding protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HRP1 PE=1 SV=1	sp|Q99383	59650,6	2%	IFVGGIGPDVRPK		1	0	1
htb1K123R	Pyruvate carboxylase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PYC1 PE=1 SV=2	sp|P11154,sp|P32327	130101,6	1%	VFDALNDLEQLK		1	0	1
htb1K123R	Actin-related protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARP4 PE=1 SV=1	sp|P80428	54833,5	5%	ATLAHNVVLTGGTSSIPGLSDR		1	0	1
htb1K123R	Acetolactate synthase catalytic subunit, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ILV2 PE=1 SV=1	sp|P07342	74937,5	4%	AQIPVTTTLQGLGSFDQEDPK-SVEELPLR		2	0	2
htb1K123R	Elongation factor 3A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YEF3 PE=1 SV=4	sp|P16521	115948,1	33%	AIANGQVDGFPTQEEcR-ALLPHLTNAIVETNK-ATETVDNKDIER-AYEELSNTDLEFK-DKEIQSVASETLISIVNAVNPVAIK-DSLGALSK-EALASGQFRPLTR-EFEGGVIIITHSAEFTK-EIQSVASETLISIVNAVNPVA	c16: Carbamidon	27	0	27
htb1K123R	ISWI chromatin-remodeling complex ATPase ISW2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ISW2 PE=1 SV=1	sp|Q08773	130333,5	8%	FVFLLTTR-FVTENAIEEK-LAWQYIVIDEAHR-LLDILEDYcYFR-QIEGPFLIIVPK-TLQTISFLGYLR-VLIFSQMSR-YLLGVTDLFR		8	4	4
htb1K123R	U3 small nucleolar RNA-associated protein 22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UTP22 PE=1 SV=1	sp|P53254	140492,9	1%	TLENISHSYQFYSPVVR		1	0	1
htb1K123R	E3 ubiquitin-protein ligase BRE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BRE1 PE=1 SV=1	sp|Q07457	80696,7	1%	IIDLNNTSTK		1	0	1
htb1K123R	Inorganic phosphate transporter PHO86 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PHO86 PE=1 SV=1	sp|P46956	34883,2	8%	LLIDVYSFDSTLK-VFGINLNDLVAR		2	0	2
htb1K123R	Nuclear protein STH1/NPS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STH1 PE=1 SV=1	sp|P32597	156750,6	10%	GNSDLLFR-HLVALQLLEK-INSIIDFIK-LGSEEQPEITIPKPR-LIQLDELPK-LITTDSVEEVILER-QSEQWSR-SNDEEAYLK-TALGDPDTEIR-TTVLENNDGK-VIEKPMAIDIILK-VIVPQTVR-WAPSLNTIIYK		13	0	13
htb1K123R	DNA-directed RNA polymerase II subunit RPB11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB11 PE=1 SV=1	sp|P38902	13616,4	30%	APNAVVITFEK-IQTTEGYDPK-LKIDPDTK-VLFAAYK		4	0	4
htb1K123R	Pre-mRNA-processing factor 17 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC40 PE=1 SV=2	sp|P40968	52049,2	2%	FISSSEDK		1	0	1
htb1K123R	Pre-mRNA-splicing factor CWC2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CWC2 PE=1 SV=1	sp|Q12046	38432,2	3%	HLKPAQIESR		1	0	1
htb1K123R	Chromatin structure-remodeling complex protein RSC3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC3 PE=1 SV=1	sp|Q06639	101727	2%	YLSTITETNSILPILKPK		1	0	1
htb1K123R	Histone H2A.1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HTA1 PE=1 SV=2	sp|P04911,sp|P04912	13989,9	12%	AGLTFPVGR-HLQLAIR		2	0	2
htb1K123R	NADPH dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=OYE2 PE=1 SV=3	sp|Q03558	45012	16%	DFKPQALGDTNLFKPIK-FFISNPDLVDR-FTLEVVDAVVDAIGPEK-IGNNELLHR-LAFVHLVEPR		5	0	5
htb1K123R	Bromodomain-containing factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BDF1 PE=1 SV=3	sp|P35817	76980,8	6%	EPMDLGTIAK-FNGPNAGISQMAR-HALLAIK-LDIPFYFNYIK		4	0	4
htb1K123R	Suppressor of mar1-1 protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SUM1 PE=1 SV=2	sp|P46676	118205,7	8%	IKNEIPINSLLPSSK-LPPVSSPAAATAAAAAAVTSEMNR-LSTMLQNTSK-LVSNAASVNLK-VNHSNLLIENSSNNTSSQHNTSSSR		5	0	5
htb1K123R	Eukaryotic translation initiation factor 5A-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HYP2 PE=1 SV=3	sp|P23301	17114,6	24%	IVDMSTSK-KLEDLSPSTHNMEVPVVK-VHLVAIDIFTGK		3	0	3
htb1K123R	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VIP1 PE	sp|Q06685	129761,4	6%	IIDSHSMNNSGK-LDIGLLTSLPLAK-SSEFDPTLVHPR-SSSQFDEPR-VLANALEK-VLFDFIcPK		6	0	6
htb1K123R	Heat shock protein STI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STI1 PE=1 SV=1	sp|P15705	66267,6	2%	IQTLIAAGIIR		1	0	1
htb1K123R	Cofilin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=COF1 PE=1 SV=1	sp|Q03048	15901,2	19%	FILFGLNDAK-SGVAVADESLTAFNDLK		2	0	2
htb1K123R	Inosine-5'-monophosphate dehydrogenase IMD2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IMD2 PE=1 SV=1	sp|P38697	56531	12%	EQAANLIAAGADGLR-NPVTGAQGITLSEGNEILKK-NQNYPLASK-TASAQLEGGVHNLHSYEK		4	4	0
htb1K123R	Keratin, type II cytoskeletal 2 epidermal - Homo sapiens	sp|P35908	65866,4	14%	AQYEEIAQR-FLEQQNQVLQTK-GFSSGSAVVSGGSR-IEISELNR-NLDLDSIIAEVK-SKEEAEALYHSK-VDLLNQEIEFLK-YEELQVTVGR		8	2	6
htb1K123R	Carboxypeptidase S OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CPS1 PE=1 SV=2	sp|P27614	64599,3	6%	HSVDTILHDPAFR-IPTVVQDK-TTQAVDIINGGVK		3	0	3
htb1K123R	Guanine nucleotide exchange factor SRM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SRM1 PE=1 SV=1	sp|P21827	53014,4	7%	LDmFEVGIPK-THASHIINAQEDYK-YNIVQLAPGK	m3: Oxidation (+	3	0	3
htb1K123R	Heat shock protein SSC1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSC1 PE=1 SV=1	sp|P12398	70628,8	8%	DAGQIVGLNVLR-NAVVTVPAYFNDSQR-TTPSVVAFTK-VQGGEEVNAEELK		4	0	4
htb1K123R	RuvB-like protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RVB2 PE=1 SV=1	sp|Q12464	51613,1	16%	AVLVAGPPSTGK-AYLLFLDSAR-NNTVEVEDVKR-SPHGLPLDLLDR-TALAMGVSQSLGK-TQGFLALFTGDTGEIR		6	0	6
htb1K123R	Nuclear localization sequence-binding protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NSR1 PE=1 SV=1	sp|P27476	44536,1	4%	ALDALQGEYIDNRPVR		1	0	1
htb1K123R	Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TDH3 PE=1 SV=3	sp|P00359	35746,6	70%	DPANLPWGSSNVDIAIDSTGVFK-eLDTAQK-ETTYDEIK-ETTYDEIKK-IALSRPNVEVVALNDPFITNDYAAYMFK-IATYQER-IVSNAScTTNcLAPLAK-KVVITAPSSTAPmFVmGVNEEK-LTGMAFR-LVSWYDNEYGYSTR-TASG		19	7	12
htb1K123R	Aspartate aminotransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AAT1 PE=1 SV=2	sp|Q01802	51797	2%	VVNVVLSDFK		1	0	1
htb1K123R	Origin recognition complex subunit 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ORC4 PE=1 SV=1	sp|P54791	60708,3	2%	ILLLLDSTTK		1	0	1
htb1K123R	FK506-binding nuclear protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FPR3 PE=1 SV=2	sp|P38911	46554,2	5%	IIIPAPYAYGK-VLEGGIVIEDR		2	0	2
htb1K123R	Eukaryotic translation initiation factor 3 subunit A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPG1 PE=1 SV=1	sp|P38249	110348,5	6%	DPFDIFASTASK-FQQVDVSVK-FTTVSQSELYK-VFFVSGDPLLHTTAWK-WATPSTVEPVVFK		5	0	5
htb1K123R	mRNA turnover protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRT4 PE=1 SV=1	sp|P33201	27058,8	3%	TPVLQEIR		1	0	1
htb1K123R	H/ACA ribonucleoprotein complex subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NHP2 PE=1 SV=2	sp|P32495	17122,1	6%	QDLGAAGATK		1	0	1
htb1K123R	Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDA1 PE=1 S	sp|P16387	46344,4	35%	ATLLQmYK-AVLAELMGR-DmVIIR-GGSMHLYAPGFYGGNGIVGAQVPLGAGLAFAHQYK-GPLVLEYETYR-KYVDEQVELADAAPPPEAK-LDSIITSYR-lSILFEDVYVK-NDPIAGLK-SSAmTEYFK-TRDEIQHM	m6: Oxidation (+	12	0	12
htb1K123R	DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB5 PE=1 SV=1	sp|P20434	25079,6	9%	ADPVALYLGLK-TFVIHIQEK		2	0	2
htb1K123R	40S ribosomal protein S7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS7A PE=1 SV=4	sp|P26786	21622,7	62%	AELRPLQFK-ALAIFVPVPSLAGFHK-DVQQIDYK-HVIFLAER-ILEDLVFPTEIVGK-ILPKPSR-ILSQAPTELELQVAQAFVELENSSPELK-LESFQAVYNK-QIVFEIPSETH-YLVGGNK		10	0	10
htb1K123R	Eukaryotic translation initiation factor 4E OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC33 PE=1 SV=1	sp|P07260	24254,6	34%	GADIDELWLR-KFEENVSVDDTTATPK-SDYHVFR-SEDKEPLLR-sVEEVSKK-TVLSDSAHFDVK-WTLWYTKPAVDK		7	0	7
htb1K123R	60S ribosomal protein L28 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL28 PE=1 SV=3	sp|P02406	16721,9	38%	ETAPVIDTLAAGYGK-IPNVPVIVK-LWTLIPEDK-LWTLIPEDKR-QQAHFWKPVLNLDK-YHPGYFGK		6	0	6
htb1K123R	U2 small nuclear ribonucleoprotein B'' OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MSL1 PE=1 SV=1	sp|P40567	12830,3	10%	NTLYVSQLNEK		1	0	1
htb1K123R	Putative glycosyltransferase HOC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HOC1 PE=1 SV=3	sp|P47124	46298,8	3%	LLSDVLVFPK		1	0	1
htb1K123R	Single-stranded DNA-binding protein RIM1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RIM1 PE=1 SV=1	sp|P32445	15386,6	17%	IGSEFTEHTSANNNR-YSIASQPR		2	0	2
htb1K123R	ARS-binding factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ABF1 PE=1 SV=4	sp|P14164	81753,2	1%	ILQNDLK		1	0	1
htb1K123R	DNA-directed RNA polymerases I and III subunit RPAC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPC40 PE=1 SV=1	sp|P07703	37687,6	12%	FSPVSTASYR-LLPQINILQPIK-LLPQINILQPIKGESAR-VTNTTSTDFPGFSK		4	0	4
htb1K123R	Polyadenylate-binding protein, cytoplasmic and nuclear OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PAB1 PE=1 SV=4	sp|P04147	64345,4	53%	AHYTNLYVK-AIEQLNYTPIK-ALYDTFSVFGDILSSK-AVEALNDSELNGEK-EASAAYESFK-EASAAYESFKK-FGPIVSASLEK-GFGFVcFSTPEEATK-GFGFVHFEEEGAAK-GFGFVNYEK-GSGNIFIK-GVPFNGPNPQQMNPMGG		26	0	26
htb1K123R	Glucose-6-phosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PGI1 PE=1 SV=3	sp|P12709	61300,4	12%	EANVTGLR-LATELPAWSK-LIPSDFILAAQSHNPIENK-TFTTAETITNANTAK-VVDPETTLFLIASK		5	0	5
htb1K123R	Eukaryotic peptide chain release factor subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SUP45 PE=1 SV=2	sp|P12385	49007,3	5%	LIVFENLETIR-LSVLSAITSTQQK		2	0	2
htb1K123R	Transcription initiation factor TFIID subunit 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF10 PE=1 SV=1	sp|Q12030	23019,3	7%	SSVAVSNANNSQAR		1	0	1
htb1K123R	60S ribosomal protein L8-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL8B PE=1 SV=3	sp|P29453	28112,8	56%	AKNPLTHSTPK-HWGGGILGNK-LGTLVNQK-LKVPPTIAQFQYTLDR-LVSTIDANFADKYDEVK-mGVPYAIIK-NFGIGQAVQPK-NPLTHSTPK-NTAAETFK-SKQDASPKPYAVK-TSAVAALTEVR-VAPAPFGAK-VPPTIAQFQYTL		16	0	16
htb1K123R	Vacuolar protein sorting-associated protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VPS1 PE=1 SV=2	sp|P21576	78740	34%	AEQTYINTAHPDLLK-EAISNQFIQFLK-ELSSQELSGGAR-ENDITIQR-ETDKVTGANSGISSVPINLR-EVDPEGTR-IYSPHVLTLTLVDLPGLTK-LAALESPPPVLK-LLISSYFSIVKR-LQDALAPLGGGSQSPIDLPQITVVGSQSSGK-L		19	0	19
htb1K123R	RuvB-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RVB1 PE=1 SV=1	sp|Q03940	50454	24%	AILLAGGPSTGK-ALESNIAPVVVLASNR-EIVVNDVNEAK-GLGLDESGVAK-GTEDVISPHGVPPDLIDR-LDPTIYESIQR-TALALAISQELGPK-VPFcPLVGSELYSVEVK		8	0	8
htb1K123R	THO complex subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=THO2 PE=1 SV=1	sp|P53552	183940,5	30%	AFEENVLPFVELNNR-AISLVENDDETR-ALSIDTIAK-DcGEDQIK-DDNSVISSR-DILVTGISHQR-DLFTTFWR-ELIITVGGIR-EQTTLLR-FFIALLR-FPEKPFQEGK-FQTQDYR-HLIYDFR-HVTSVFPVVK-IDNGILAHKPR-IFLQNcV		43	0	43
htb1K123R	Ribosome-interacting GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RBG1 PE=1 SV=1	sp|P39729	40702,5	6%	GQIPDFTDPVVLR-NALVYGSSVK		2	0	2
htb1K123R	Chromatin structure-remodeling complex subunit RSC9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC9 PE=1 SV=1	sp|Q03124	65221,5	12%	NLAQDTDSVQILVK-NVSNAFNNAAAIVITDPVTGK-SIHYSLANFNVFQSLPK-TFILPLER-TLPDLLPLFK		5	0	5
htb1K123R	Clathrin heavy chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CHC1 PE=1 SV=1	sp|P22137	187243,2	2%	FIETYVQQVNPSK-SFTLDEPVIFWR		2	0	2
htb1K123R	ATP-dependent RNA helicase DHH1 OS=Saccharomyces cerevisiae (strain YJM789) GN=DHH1 PE=3 SV=1	sp|A6ZXG9,sp|P39517	57545,4	2%	ELALQTSQVVR		1	0	1
htb1K123R	Pre-mRNA-splicing factor CWC23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CWC23 PE=1 SV=2	sp|P52868	33239,2	8%	LEESESSTIPTTTPHPDLLQIQR		1	0	1
htb1K123R	Processing of GAS1 and ALP protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PGA2 PE=1 SV=3	sp|P53903	15053,6	7%	kQLAAQVEK	n-term: Acetyl (+	1	0	1
htb1K123R	60S ribosomal protein L33-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL33A PE=1 SV=3	sp|P05744	12154,2	37%	IAYVYR-IEGVATPQDAQFYLGK-RVNNPNVSLIK-TFGASVR-VNNPNVSLIK		5	4	1
htb1K123R	Transcription initiation factor TFIID subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF1 PE=1 SV=1	sp|P46677	120701,7	1%	NNLLQSNSSASR		1	0	1
htb1K123R	Protein MKT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MKT1 PE=1 SV=2	sp|P40850	94499,4	23%	EINLLTQPINR-ENIQNYQR-EQYLDAIGGFPTSLK-FILGmEFPNK-FLLEISK-LIDENVFK-LNELNIDSK-LNSPFNLLSTNFLR-LSLDNFGWAR-SIGLVTGK-SLESFLFER-SNLSSPSSASSSASPATTVTK-SNTESVLLQR-STPNLDEQF		17	0	17
htb1K123R	Nascent polypeptide-associated complex subunit beta-1 OS=Saccharomyces cerevisiae (strain YJM789) GN=EGD1 PE=3 SV=1	sp|A6ZWL1,sp|Q02642	17020,5	24%	LHAVTIDNVAEANFFK-VGVQVAAQHNTSVFYGLPQEK		2	0	2
htb1K123R	Elongator complex protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IKI3 PE=1 SV=1	sp|Q06706	152994,2	13%	ASGLVGNQLR-EAMSIAVQK-EYLPFLQELQDNEPLR-FPQLVR-GNLETIYPR-GQINSQLR-GSILVSVIPSK-IMVLAEVR-IQLWTSK-MAQGPTLEPFDNGTSLVVDGR-NFVEVLDLLK-QELYASDISYVK-SDFDYNHLVYETR-SSVV		16	0	16
htb1K123R	Uracil phosphoribosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FUR1 PE=1 SV=2	sp|P18562	24595,5	4%	LPEDISER		1	0	1
htb1K123R	Uncharacterized oxidoreductase YKL071W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YKL071W PE=1 SV=1	sp|P36086	28041	3%	VYPLLLLK		1	0	1
htb1K123R	Translation-associated element 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAE2 PE=1 SV=1	sp|Q12532	119075,1	1%	ISALDLLLLAR		1	0	1
htb1K123R	Small COPII coat GTPase SAR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SAR1 PE=1 SV=1	sp|P20606	21451,5	14%	FTTFDLGGHIQAR-SALGLLNTTGSQR		2	0	2
htb1K123R	Pre-mRNA-splicing factor PRP11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP11 PE=1 SV=1	sp|Q07350	29921,2	4%	IVSGLELSDTK		1	0	1

htb1K123R	Zuotin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ZUO1 PE=1 SV=1	sp|P32527	49021,5	13%	ATESQIIK-LPSSLLSYFV-QSAAGGSLDQDGFFK-TADLYAAmGLSK-TPIPSLGNK		5	0	5
htb1K123R	RNA polymerase-associated protein CTR9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CTR9 PE=1 SV=3	sp|P89105	124717,2	3%	SESIYSQVTSLHPAYIAAR-TRPHILNLLGR		2	0	2
htb1K123R	Actin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ACT1 PE=1 SV=1	sp|P60010	41690,4	41%	AGFAGDDAPR-APEALFHPSVLGLESAGIDQTTYNSIMK-DSYVGDEAQSK-EITALAPSSmK-GYSFSTTAER-IIAPPER-QEYDESGPSIVHHK-TTGIVLDSGDGVTHVVPIYAGFSLPHAILR-VAPEEHPVLLTEAPmNPK-YPIEHGIVTN		10	0	10
htb1K123R	Phosphoglycerate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PGK1 PE=1 SV=2	sp|P00560	44739,6	57%	AAGFLLEK-AHSSMVGFDLPQR-ALENPTRPFLAILGGAK-ALLDEVVK-ASAPGSVILLENLR-EGIPAGWQGLDNGPESR-ELPGVAFLSEK-ELQSLLGK-HELSSLADVYINDAFGTAHR-ISHVSTGGGASLELLEGK-IVAALPTIK-KLI		20	0	20
htb1K123R	ER membrane protein complex subunit 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KRE27 PE=1 SV=1	sp|P40540	15908,3	9%	LNSLNNAQGAISK		1	0	1
htb1K123R	Heat shock protein 60, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP60 PE=1 SV=1	sp|P19882	60753	24%	AAVEEGILPGGGTALVK-GFISPYFITDPK-GVETLAEAVAATLGPK-ISSIQDILPALEISNQSR-LLQEVASK-QIIENAGEEGSVIIGK-TNEAAGDGTTSATVLGR-VEFEKPLLLLSEK-VGGASEVEVGEK-YDDALNATR		10	0	10
htb1K123R	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=QCR2 PE=1 SV=1	sp|P07257	40479,7	41%	DGVAHLLNR-DLSPAINYTK-ESELLGGTFK-FFLGEENR-FIGDSVAAIGIPVNK-FTDGGLFTLFVR-FVDESLLSTLPAGK-GLGNPLLYDGVER-LDKFTDGGLFTLFVR-NAVQNESVSSPIELNFDAVK-SAEDQLYAITFR-TAFKPHELTI		13	0	13
htb1K123R	Probable oxidoreductase AIM17 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AIM17 PE=1 SV=2	sp|P23180	53137,1	9%	GLNLFESHINDFNNQFR-LTAPQDIQISEDGK-LVTTGELYHNEK		3	0	3
htb1K123R	Actin-related protein 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARP7 PE=1 SV=1	sp|Q12406	53812,1	3%	FGGDFLDFQVHER		1	0	1
htb1K123R	Fructose-bisphosphate aldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FBA1 PE=1 SV=3	sp|P14540	39621,5	41%	DYImSPVGNPEGPEKPNKK-FAIPAINVTSSSTAVAALEAAR-GAIAAAHYIR-GISNEGQNASIK-GVEQILK-KTGVIVGEDVHNLFTYAK-SIAPAYGIPVVLHSDHcAK-SLETFR-SPIILQTSNGGAAYFAGK-VNLDTDc	m4: Oxidation (+	10	0	10
htb1K123R	DnaJ homolog 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MDJ1 PE=1 SV=1	sp|P35191	55562	5%	GDPIEIVHK-TITVDLPHGLQDGDVVR		2	0	2
htb1K123R	Proteasome component PRE5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE5 PE=1 SV=1	sp|P40302	25605	30%	LFQVEYALEAIK-NADELSSYQK-NNYDGDTVTFSPTGR-QGSVTVGLR-SGAHLLEFQPSGNVTELYGTAIGAR		5	0	5
htb1K123R	Pre-mRNA-processing factor 39 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP39 PE=1 SV=1	sp|P39682	74752,2	25%	ANTFLPLDFK-FATIEYQLFGLK-FIEFEVGQK-FVTDPSK-GLDTQFLQDNTALVQAYR-ILETSITNYINNQIDAK-INDLYTEEFLK-IYEYIIEVPLHQYAR-NLSIVVVELIK-NSVPFWLTYYK-SIAVLATSVK-SNNTLFNNIFNETVSR-VH		13	0	13
htb1K123R	mRNA 3'-end-processing protein RNA14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RNA14 PE=1 SV=2	sp|P25298	79964,2	7%	cAIFEPK-FGNLNNVYSLEK-ILAQcLSGK-NNLITGGQEAR-TLFETSVEK	c1: Carbamidome	5	0	5
htb1K123R	DNA-directed RNA polymerase II subunit RPB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB2 PE=1 SV=2	sp|P08518	138757,2	25%	AGVSQVLNR-EFLPHITQLEGFESR-ETALDFIGR-FISTLQVK-GDINPEVSMIR-HGTYDKLDDDGLIAPGVR-IDIYQIHIPYAAK-IPQIGDK-KYEISFGK-LDLAGPLLAQLFK-LLFQELMAMNITPR-LLLcALDR-LMAQIFFGPTYYQR-		27	0	27
htb1K123R	UPF0674 endoplasmic reticulum membrane protein YNR021W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YNR021W PE=1 S	sp|P53723	47095,1	3%	sSSIFGPLTGFLER	n-term: Acetyl (+	1	0	1
htb1K123R	Elongation factor 1-gamma 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CAM1 PE=1 SV=2	sp|P29547	47089,3	3%	VVTPDAAAEQFAR		1	0	1
htb1K123R	Orotidine 5'-phosphate decarboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=URA3 PE=1 SV=2	sp|P03962	29240,4	7%	LQYSAGVYR-YNFLLFEDR		2	0	2
htb1K123R	26S protease regulatory subunit 8 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPT6 PE=1 SV=4	sp|Q01939	45272,6	3%	GVILYGPPGTGK		1	0	1
htb1K123R	Cerevisin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRB1 PE=1 SV=1	sp|P09232	69623,2	2%	AITVGASTLSDDR		1	0	1
htb1K123R	60S acidic ribosomal protein P1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP1B PE=1 SV=3	sp|P10622	10668,1	15%	AAGANVDNVWADVYAK		1	0	1
htb1K123R	SWI5-dependent HO expression protein 2 OS=Saccharomyces cerevisiae (strain YJM789) GN=SHE2 PE=3 SV=1	sp|A6ZZJ0,sp|B3LQW9,sp|B5VM30,s	28266,8	4%	VILPIASMFVK		1	0	1
htb1K123R	Adenosylhomocysteinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SAH1 PE=1 SV=1	sp|P39954	49125,8	14%	ATDVmLAGK-HVILLANGR-IADISLAAFGR-ILDEAVAK-LKVPAINVNDSVTK-TGPFEVGVHVLPK	m5: Oxidation (+	6	0	6
htb1K123R	Pre-mRNA-splicing helicase BRR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BRR2 PE=1 SV=2	sp|P32639	246193,9	8%	ALVQEQVR-AVYINPSGEK-FENISLAEFILK-IDFLLSDWNK-ILNDIETLEHNPVALEQK-LVDNLNAEVVAGNIK-NSNNLAIVELVR-NSSSVFLPSR-TAMAELALLNHWR-TEAANVLDPSLR-VAELTGDSR-VLESINEGNQIIVFVHSR		14	0	14
htb1K123R	Actin-like protein ARP9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARP9 PE=1 SV=1	sp|Q05123	53076,7	4%	LIFVSILSDR-QDSILIIYPR		2	0	2
htb1K123R	Chromatin structure-remodeling complex subunit RSC2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC2 PE=1 SV=1	sp|Q06488	102303,9	5%	GPSVIVNER-NQNDPQKPIVGQIFR-VGSPGAGGPLTVQGLK		3	0	3
htb1K123R	Aspartate-semialdehyde dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HOM2 PE=1 SV=1	sp|P13663	39544,7	4%	QTIHVLEQPDRPQPR		1	0	1
htb1K123R	Cysteine desulfurase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NFS1 PE=1 SV=2	sp|P25374	54468,2	6%	IYFHTDAAQAYGK-SGTLAPPLVAGFGEAAR		2	0	2
htb1K123R	40S ribosomal protein S19-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS19A PE=1 SV=2	sp|P07280,sp|P07281	15917,4	11%	IGIVEISPK-VLQALEK		2	0	2
htb1K123R	Prohibitin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PHB1 PE=1 SV=2	sp|P40961	31427,9	17%	LEDVSITHMTFGPEFTK-QIAQQDAER-SIVAQFDAAELITQR-VGDGLLLIR		4	0	4
htb1K123R	Glutamyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GUS1 PE=1 SV=3	sp|P46655	80846,2	6%	APIVAYAELIAAR-FDDTNPSK-IGDIIQFER-TLRDPVIYR		4	0	4
htb1K123R	Phosphomannomutase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEC53 PE=1 SV=1	sp|P07283	29064,1	9%	LTVSEEVR-TIGHSVQSPDDTVK		2	0	2
htb1K123R	60S ribosomal protein L6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL6A PE=1 SV=2	sp|Q02326	19962,1	39%	ALIAEIK-ASLVPGTVLILLAGR-EANLFPEQQNK-FNVEYFAK-QYLSASFSLK-VSVEGVNVEK-YVIATSTK		7	6	1
htb1K123R	60S ribosomal protein L25 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL25 PE=1 SV=4	sp|P04456	15758,2	35%	ELYEVDVLK-KVEDGNILVFQVSmK-LTADYDALDIANR-VIEQPITSETAmK-VIEQPITSETAmKK		5	0	5
htb1K123R	NADPH-dependent alpha-keto amide reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDL124W PE=1 SV=1	sp|Q07551	35562	4%	NIGVSNFAVEDLQR		1	0	1
no tap	Trypsin precursor - Sus scrofa	sp|P00761	24409,3	29%	APVLSDSScK-IITHPNFNGNTLDNDImLIK-IITHPNFNGNTLDNDIMLIKLSSPATLNSR-LGEHNIDVLEGNEQFINAAK-LSSPATLNSR-VATVSLPR	c9: Carbamidome	6	0	6
no tap	Imidazoleglycerol-phosphate dehydratase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HIS3 PE=1 SV=2	sp|P06633	23833,2	7%	ALAVAIR-ITLHVDcLR		2	0	2
no tap	40S ribosomal protein S7-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS7B PE=1 SV=1	sp|P48164	21634,7	13%	HVIFLAER-ILPKPSR-LESFQAVYNK		3	3	0
no tap	60S ribosomal protein L3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL3 PE=1 SV=4	sp|P14126	43757,9	24%	AGMTTIVR-AHLAEIQLNGGSISEK-FQTPAEK-GHGFEGVTHR-KALEEVSLK-SKPVALTSFLGYK-SLTTVWAEHLSDEVK-TITPmGGFVHYGEIK		8	0	8
no tap	U1 small nuclear ribonucleoprotein A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MUD1 PE=1 SV=1	sp|P32605	34379,9	8%	LQNNDVTIGFAK-YAINPSLPLPHNK		2	0	2
no tap	Heat shock protein 60, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP60 PE=1 SV=1	sp|P19882	60753	12%	GVETLAEAVAATLGPK-NVLIEQPFGPPK-TNEAAGDGTTSATVLGR-VEFEKPLLLLSEK-VLDEVVVDNFDQK		5	0	5
no tap	26S protease regulatory subunit 8 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPT6 PE=1 SV=4	sp|Q01939	45272,6	3%	GVILYGPPGTGK		1	0	1
no tap	Protein ARG5,6, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARG5,6 PE=1 SV=1	sp|Q01217	94872,2	2%	STVIQLLNNISTK		1	0	1
no tap	ADP-ribosylation factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARF2 PE=1 SV=3	sp|P19146	20658,2	11%	ILmVGLDGAGK-LFSNLFGNK	m3: Oxidation (+	2	0	2
no tap	rRNA 2'-O-methyltransferase fibrillarin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOP1 PE=1 SV=1	sp|P15646	34465,5	6%	GKEDLLVTK-NMAPGESVYGEK		2	0	2
no tap	Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IDH1 PE=1 SV=2	sp|P28834	39325,3	14%	DIGGSSSTTDFTNEIINK-FTVTLIPGDGVGK-IPDIDLIVIR-NIITEIGQK		4	0	4
no tap	60S ribosomal protein L34-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL34B PE=1 SV=1	sp|P40525,sp|P87262	13641,1	14%	cGDcGSALQGISTLRPR	c1: Carbamidome	1	0	1
no tap	Ribosome-associated complex subunit SSZ1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSZ1 PE=1 SV=2	sp|P38788	58239,5	18%	GEFHPVLLAETSFPVQK-LAAEDYIGSAVK-LISDYDADELAEALQPVIVNTPHLK-LTVDEVVSR-NASNNPNELAASGAALQAR-VFAQFSSFVDSVIAK		6	0	6
no tap	Spermidine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPE3 PE=1 SV=1	sp|Q12074	33324,4	4%	VLVIGGGDGGVLR		1	0	1
no tap	Ketol-acid reductoisomerase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ILV5 PE=1 SV=1	sp|P06168	44369,9	9%	EVNSDLYGER-GALDWYPIFK-GINSSYAVWNDVTGK		3	0	3
no tap	Transposon Ty1-PR1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-PR1 PE=3 SV=1	sp|P0C2I9,sp|Q03612	198575,8	8%	AHNVSTSNNSPSTDNDSISK-DILSVDYTDImK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-LNVPLNPK-STTEPIQLNNK-TVDTTNYVILQGK-VAcQLIMR-VTNIIDR-YVRPPPMLTSPNDFPNWVK		10	0	10
no tap	mRNA turnover protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRT4 PE=1 SV=1	sp|P33201	27058,8	8%	QFGIAASEFK-TPVLQEIR		2	0	2
no tap	ATPase synthesis protein 25, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) GN=ATP25 PE=3 SV=1	sp|A6ZMF5,sp|B3LLY9,sp|B5VPM5,s	70410,8	2%	IIQSSSGTETHNIR		1	0	1
no tap	Zuotin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ZUO1 PE=1 SV=1	sp|P32527	49021,5	3%	QSAAGGSLDQDGFFK		1	0	1
no tap	Cytochrome c oxidase subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=COX2 PE=1 SV=1	sp|P00410	28568,3	15%	FVVTAADVIHDFAIPSLGIK-LLDTDTSMVVPVDTHIR		2	0	2
no tap	U3 small nucleolar RNA-associated protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UTP10 PE=1 SV=1	sp|P42945	200093,1	2%	SLGLTGELFEIR-VLSLFTEAIGK-VTISPAAPTALK		3	0	3
no tap	Nuclear localization sequence-binding protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NSR1 PE=1 SV=1	sp|P27476	44536,1	6%	IPTHPETEQPK-KEFEHIGGVIGAR		2	0	2
no tap	ADP-ribosylation factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARF1 PE=1 SV=3	sp|P11076	20530,1	11%	ILmVGLDGAGK-LFSNLFGNK	m3: Oxidation (+	2	2	0
no tap	Heat shock protein SSA4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSA4 PE=1 SV=3	sp|P22202	69652,7	26%	ARFEELcADLFR-ATAGDTHLGGEDFDSR-AVGIDLGTTYScVAHFANDR-DAGTIAGLNVLR-FEELcADLFR-FELSGIPPAPR-IINEPTAAAIAYGLDK-IINEPTAAAIAYGLDKK-ITITNDK-LVNFLAEEFKR-NQLESY	c7: Carbamidome	14	9	5
no tap	Cell division control protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC12 PE=1 SV=1	sp|P32468	46668,9	31%	ADTLTAQELQQFK-ANLIPVIAK-FDNGQGTQVVAR-KFDNGQGTQVVAR-QLIEAmPFAIVGSEK-QVIEAQEIR-QWEQNIVNER-sAATATAAPVPPPVGISNLPNQR-SGSNPDSAAVEHAR-TTFINTLFQTVLK-TTFINTLFQTVLKR-T		12	0	12
no tap	40S ribosomal protein S6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS6A PE=1 SV=1	sp|P0CX37,sp|P0CX38	26997,2	11%	GAIVGPDLAVLALVIVK-QGVLLPTR		2	0	2
no tap	ATP synthase subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ATP1 PE=1 SV=5	sp|P07251	58609,4	3%	AVDALVPIGR-LFLAQYR		2	0	2
no tap	40S ribosomal protein S16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS16A PE=1 SV=1	sp|P0CX51,sp|P0CX52	15847,9	23%	FSNIDIR-VTGGGHVSQVYAIR-VYEPLLLVGLDK		3	0	3
no tap	40S ribosomal protein S0-B OS=Saccharomyces cerevisiae (strain YJM789) GN=RPS0B PE=3 SV=1	sp|A7A0V3,sp|B3LT19,sp|P46654	27962,3	41%	FAAHTGATPIAGR-FTPGSFTNYITR-IIAAIPNPEDVVAISSR-LDAQAIK-LVIVTDPR-LVLAAR-sLPATFDLTPEDAQLLLAANTHLGAR-TQPWSImPDLYFYR		8	0	8
no tap	Protein FAF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FAF1 PE=1 SV=1	sp|P40546	38890,9	3%	ISGGERSGK		1	0	1
no tap	Phosphomannomutase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEC53 PE=1 SV=1	sp|P07283	29064,1	6%	FVEALKK-LTVSEEVR		2	0	2
no tap	40S ribosomal protein S20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS20 PE=1 SV=3	sp|P38701	13906,8	36%	ITLTSTK-QLENVSSNIVK-VEEQEQQQQIIK-YIDLEAPVQIVK		4	0	4
no tap	60S ribosomal protein L28 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL28 PE=1 SV=3	sp|P02406	16721,9	17%	ETAPVIDTLAAGYGK-GRIPNVPVIVK-IPNVPVIVK		3	0	3
no tap	ATP-dependent molecular chaperone HSP82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP82 PE=1 SV=1	sp|P02829	81410,2	24%	AELINNLGTIAK-AILFIPK-APFDLFESK-ELISNASDALDK-GVVDSEDLPLNLSR-KTFEISPK-LGVHEDTQNR-LLDAPAAIR-NIYYITGESLK-NPSDITQEEYNAFYK-QLETEPDLFIR-RAPFDLFESK-SISNDWEDPLYVK-SVDELTS		18	0	18
no tap	40S ribosomal protein S8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS8A PE=1 SV=1	sp|P0CX39,sp|P0CX40	22490,4	34%	AAIVQIDATPFR-IAGVVYHPSNNELVR-IESSVESQFSAGR-IETGNFSWASEGISK-QWFEAHYGQTLGK		5	0	5
no tap	Heat shock protein SSB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSB2 PE=1 SV=2	sp|P40150	66595,7	22%	AADEAFAK-AVITVPAYFNDAQR-DAGAISGLNVLR-ENTLLGEFDLK-IINEPTAAAIAYGLGAGK-LLSDFFDGK-LSSEEIEK-MVNQAEEFK-RFDDESVQK-SQIDEVVLVGGSTR-SSNITISNAVGR-TGLDISDDAR		12	12	0
no tap	Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TDH3 PE=1 SV=3	sp|P00359	35746,6	47%	eLDTAQK-ETTYDEIKK-IATYQER-IVSNAScTTNcLAPLAK-KVVITAPSSTAPmFVMGVNEEK-LTGmAFR-TASGNIIPSSTGAAK-VINDAFGIEEGLMTTVHSLTATQK-VLPELQGK-VPTVDVSVVDLTVK-VVDLVE	n-term: Acetyl (+	13	7	6
no tap	40S ribosomal protein S1-B OS=Saccharomyces cerevisiae (strain YJM789) GN=RPS1B PE=3 SV=1	sp|A6ZM02,sp|B3LLJ2,sp|B5VP69,sp	28812,9	48%	APSTFENR-DIFPLQNIHVR-FDVGALmALHGEGSGEEK-HSYAQSSHIR-IFAIAFTR-LIPEVINK-LRVDEVQGK-NLLTNFHGmDFTTDK-TSDDYVLR-VISEILTR-VVEVcLADLQGSEDHSFR		11	0	11
no tap	Protein BMH2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BMH2 PE=1 SV=3	sp|P34730	31061,7	18%	ISDDILSVLDSHLIPSATTGESK-NLLSVAYK-TASEIATTELPPTHPIR		3	3	0
no tap	ATP-dependent RNA helicase eIF4A OS=Saccharomyces cerevisiae (strain YJM789) GN=TIF1 PE=3 SV=1	sp|A6ZQJ1,sp|P10081	44698,3	16%	AImPIIEGHDVLAQAQSGTGK-APQALmLAPTR-DAQIVVGTPGR-ILISTDLLAR-TGTFSIAALQR	m3: Oxidation (+	5	0	5
no tap	60S ribosomal protein L8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL8A PE=1 SV=4	sp|P17076	28125,5	33%	LGTLVNQK-LVSTIDANFADK-LVSTIDANFADKYDEVK-NFGIGQAVQPK-NTAAETFK-TSAVAALTEVR-VAPAPFGAK-VPPTIAQFQYTLDR-WPEYVR		9	9	0
no tap	V-type proton ATPase subunit d OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VMA6 PE=1 SV=2	sp|P32366	39792,4	3%	AALANVYEYR		1	0	1
no tap	Protein MKT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MKT1 PE=1 SV=2	sp|P40850	94499,4	16%	EINLLTQPINR-EQYLDAIGGFPTSLK-FILGMEFPNK-LDEEVQPPAPSALSQATLR-LIDENVFK-LSLDNFGWAR-SLESFLFER-SNTESVLLQR-VIFPNSVPIESK-VMQELNAAK-WGEVFLK-WYAANEPTTLTNR		12	0	12
no tap	Dihydrolipoyl dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LPD1 PE=1 SV=1	sp|P09624	54010,9	25%	AAQLGFNTAcVEK-GIDVNGDIK-IGLEVDKR-INVANFQK-IVSSTGALSLK-LVIDDQFNSK-QLTGGIELLFK-RPYIAGLGAEK-SHDVVIIGGGPAGYVAAIK-TNQDTEGFVK-VVGDVTFGPmLAHK	c10: Carbamidon	11	0	11
no tap	60S ribosomal protein L20-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL20A PE=1 SV=1	sp|P0CX23,sp|P0CX24	20437,1	39%	ASGEIVSINQINEAHPTK-EYQVIGR-IFASNEVIAK-KASGEIVSINQINEAHPTK-LPTESVPEPK-NFGVWVR-VAAVETLYQDMAAR		7	0	7
no tap	Sphingolipid long chain base-responsive protein LSP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LSP1 PE=1 SV=1	sp|Q12230	38071,6	5%	APTAAELQAPPPPPSSTK		1	0	1
no tap	60S ribosomal protein L10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL10 PE=1 SV=1	sp|P41805	25362,1	28%	DAFHLR-GAWGKPHGLAAR-GSLENNIR-IYDLGK-KGSLENNIR-mLScAGADR-VDIGQIIFSVR-YmTTVSGR		8	0	8
no tap	ATP-dependent RNA helicase DHH1 OS=Saccharomyces cerevisiae (strain YJM789) GN=DHH1 PE=3 SV=1	sp|A6ZXG9,sp|P39517	57545,4	3%	LNETVHILVGTPGR		1	0	1
no tap	Citrate synthase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CIT1 PE=1 SV=2	sp|P00890	53362,3	6%	AIGVLPQLIIDR-ALSADLAAR-LPVIASK		3	0	3
no tap	60S ribosomal protein L4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL4A PE=1 SV=4	sp|P10664	39092	49%	AGHQTSAESWGTGR-AVGAHSDLLK-FVIWTEAAFTK-GPLVVYAEDNGIVK-IINSSEIQSAIRPAGQATQK-IPEIPLVVSTDLESIQK-LDQVWGSETVASSK-NVPGVETANVASLNLLQLAPGAHLGR-TGTKPAAVFTETLK-VGYTLPS		11	0	11
no tap	High mobility group protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HMO1 PE=1 SV=1	sp|Q03973	27545,1	5%	QAYNVELENYQR		1	0	1
no tap	Phosphoglycerate mutase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GPM1 PE=1 SV=3	sp|P00950	27609,7	38%	AIQTANIALEK-HLEGISDADIAK-KVYPDVLYTSK-LLPYWQDVIAK-LWIPVNR-NLFTGWVDVK-TVMIAAHGNSLR-VYPDVLYTSK-YVDPNVLPETESLALVIDR		9	0	9
no tap	Single-stranded DNA-binding protein RIM1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RIM1 PE=1 SV=1	sp|P32445	15386,6	24%	GTTLSLVQK-IGSEFTEHTSANNNR-YSIASQPR		3	0	3
no tap	60S ribosomal protein L25 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL25 PE=1 SV=4	sp|P04456	15758,2	9%	LTADYDALDIANR		1	0	1
no tap	V-type proton ATPase subunit B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VMA2 PE=1 SV=2	sp|P16140	57751,6	8%	AIVQVFEGTSGIDVK-TTVEFTGESLR-YNEIVNLTLPDGTVR		3	0	3
no tap	60S ribosomal protein L6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL6A PE=1 SV=2	sp|Q02326	19962,1	39%	ALIAEIK-ASLVPGTVLILLAGR-EANLFPEQQNK-FNVEYFAK-QYLSASFSLK-VSVEGVNVEK-YVIATSTK		7	6	1
no tap	60S ribosomal protein L9-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL9B PE=1 SV=1	sp|P51401	21657	11%	HIDVTFTK-SLVDNmITGVTK		2	2	0
no tap	Prohibitin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PHB1 PE=1 SV=2	sp|P40961	31427,9	29%	DLQMVSLTLR-LEDVSITHMTFGPEFTK-LIDVITK-QIAQQDAER-QQVVGEGTHFLVPWLQK-SIVAQFDAAELITQR-VGDGLLLIR		7	0	7
no tap	C-1-tetrahydrofolate synthase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MIS1 PE=1 SV=1	sp|P09440	106220,5	5%	IIQVGARPDSSTYVR-LNINPDTITIR-QPSLGPTLGVK-SSIVGNPIASLLK		4	1	3
no tap	U3 small nucleolar RNA-associated protein 15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UTP15 PE=1 SV=1	sp|Q04305	57687,1	2%	VFDPLDNFQVK		1	0	1
no tap	Histone H3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HHT1 PE=1 SV=2	sp|P61830	15356,8	5%	STELLIR		1	0	1
no tap	Histone H2A.1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HTA1 PE=1 SV=2	sp|P04911,sp|P04912	13989,9	23%	HLQLAIR-LLGNVTIAQGGVLPNIHQNLLPK		2	0	2
no tap	Enolase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ENO2 PE=1 SV=2	sp|P00925	46915,1	46%	AADALLLK-AAQDSFAANWGVMVSHR-AVDDFLLSLDGTANK-GNPTVEVELTTEK-GVmNAVNNVNNVIAAAFVK-IATAIEK-IGLDcASSEFFK-IGSEVYHNLK-LGANAILGVSmAAAR-LNQLLR-NVPLYQHLADLSK-SIVPSGAS		15	0	15
no tap	60S ribosomal protein L33-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL33B PE=1 SV=2	sp|P41056	12168,2	37%	IAYVYR-IEGVATPQEAQFYLGK-IFLYPSNI-VNNPNVSLIK		4	0	4
no tap	Triosephosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TPI1 PE=1 SV=2	sp|P00942	26795,6	15%	ASGAFTGENSVDQIK-KPQVTVGAQNAYLK-TLDVVER		3	0	3
no tap	Ubiquitin carboxyl-terminal hydrolase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UBP3 PE=1 SV=1	sp|Q01477	101920,1	1%	TVEIVPSPISK		1	0	1
no tap	Vesicle-associated membrane protein-associated protein SCS2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SCS2 PE=1 SV=3	sp|P40075	26924,8	5%	sAVEISPDVLVYK	n-term: Acetyl (+	1	0	1
no tap	C-1-tetrahydrofolate synthase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADE3 PE=1 SV=1	sp|P07245	102207,3	11%	GVPTGFTFPIR-LLTPVPSDIDISR-QPSLGPTLGVK-SDIVGSPVAELLK-SLNSTVTITHSK-SSGLTPNAVVLVATVR-VVVAADVNR-YILVSGITPTPLGEGK		8	0	8
no tap	Threonine dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ILV1 PE=1 SV=2	sp|P00927	63831,7	5%	IISFEFPERPGALTR-TPLPVVGTFADGTSVR		2	0	2
no tap	Guanine nucleotide-binding protein subunit beta-like protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ASC1 PE=1 SV=4	sp|P38011	34805,9	53%	AmYTLSAQDEVFSLAFSPNR-ASMIISGSR-aSNEVLVLR-DGEImLWNLAAK-DKTLISWK-FGVPVR-GQcLATLLGHNDWVSQVR-GTLEGHNGWVTSLATSAGQPNLLLSASR-KAMYTLSAQDEVFSLAFSPNR-LW	m2: Oxidation (+	14	0	14
no tap	Acetyl-coenzyme A synthetase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ACS2 PE=1 SV=1	sp|P52910	75492,2	1%	IITFGELLR		1	0	1
no tap	Heat shock protein 104 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP104 PE=1 SV=2	sp|P31539	102039,6	17%	ALTILTLAQK-EAQVDIEAIK-GADTNTPLEYLSK-IEVAEPSVR-ILDSALVTAAQLAK-IPQQQPAPAEITPSYALGK-ISSIVIFNK-LFSLDLAALTAGAK-LIQNEILNK-LNLTQEAK-QPASFLFLGLSGSGK-QQALELR-QTVAILR-VIGAT		14	0	14
no tap	Nicotinamidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PNC1 PE=1 SV=1	sp|P53184	24993,4	4%	AHNINVVDK		1	0	1
no tap	Suppressor protein STM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STM1 PE=1 SV=3	sp|P39015	29995,4	19%	EAYVPATK-GNNTANATNSANTVQK-KVELDAER-TAQLSLQDYLNQQANNQFNK		4	0	4
no tap	Elongation factor 1-gamma 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TEF4 PE=1 SV=1	sp|P36008	46521,9	7%	IDNLAAVFDAR-TPFAEVK-WFNTVAASPIVK		3	0	3
no tap	Inosine-5'-monophosphate dehydrogenase IMD2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IMD2 PE=1 SV=1	sp|P38697	56531	8%	EQAANLIAAGADGLR-NPVTGAQGITLSEGNEILKK-NQNYPLASK		3	3	0
no tap	60S ribosomal protein L26-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL26B PE=1 SV=2	sp|P53221	14235,3	13%	FAVQVDK-VLLSAPLSK		2	0	2
no tap	54S ribosomal protein L12, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MNP1 PE=1 SV=1	sp|P53163	20650,8	6%	GLLGLSLVEAK		1	0	1
no tap	Mitochondrial genome maintenance protein MGM101 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MGM101 PE=1 SV=1	sp|P32787	30091,1	17%	AFGAGGWGLVPR-FVEHVTTK-SFNSTETKPVFATK-STADDSLNNSYK		4	0	4
no tap	60S ribosomal protein L18-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL18A PE=1 SV=1	sp|P0CX49,sp|P0CX50	20563,7	24%	AGGEcITLDQLAVR-GQNTLILR-INRPPVSVSR-TVVVVGTVTDDAR	c5: Carbamidome	4	0	4
no tap	Uncharacterized protein YNL134C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YNL134C PE=1 SV=1	sp|P53912	41165,7	2%	LGPNVDAAR		1	0	1
no tap	Heat shock protein STI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STI1 PE=1 SV=1	sp|P15705	66267,6	3%	AIEVSETPNHVLYSNR		1	0	1
no tap	Transcription initiation factor TFIID subunit 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF10 PE=1 SV=1	sp|Q12030	23019,3	7%	SSVAVSNANNSQAR		1	0	1
no tap	Eukaryotic translation initiation factor 5A-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HYP2 PE=1 SV=3	sp|P23301	17114,6	13%	IVDMSTSK-VHLVAIDIFTGK		2	0	2
no tap	Nucleolar protein NET1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NET1 PE=1 SV=1	sp|P47035	128535,1	1%	SAVSESSVTNSK		1	0	1

no tap	60S ribosomal protein L6-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL6B PE=1 SV=4	sp|P05739	19986,9	41%	ALLAEIK-ASLVPGTVLILLAGR-FNVEYFAK-HLEDNTLLVTGPFK-QYLSASFSLK-VSVEGVNVEK-YVIATSTK		7	0	7
no tap	Transposon Ty1-DR5 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-DR5 PE=1 SV=1	sp|P0C2I2,sp|Q03855	198534,8	9%	AHNVSTSNNSPSTDNDSISK-DILSVDYTDImK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-LNVPLNPK-mESQQLSNYPHISHGSAcASVTSK-STTEPIQLNNK-TVDTTNYVILQGK-VAcQLIMR-VTNIIDR-YVRPPPMLT		11	10	1
no tap	Heat shock protein SSB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSB1 PE=1 SV=3	sp|P11484	66602,8	22%	AADEAFAK-AVITVPAYFNDAQR-DAGAISGLNVLR-ENTLLGEFDLK-IINEPTAAAIAYGLGAGK-LLSDFFDGK-LSSEEIEK-MVNQAEEFK-RFDDESVQK-SQIDEVVLVGGSTR-SSNITISNAVGR-TGLDISDDAR		12	0	12
no tap	Orotidine 5'-phosphate decarboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=URA3 PE=1 SV=2	sp|P03962	29240,4	4%	ELLELVEALGPK		1	0	1
no tap	Nuclear migration protein NUM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUM1 PE=1 SV=2	sp|Q00402	313042,2	0%	LTNLSMEcR	c8: Propionamide	1	0	1
no tap	Cell division control protein 48 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC48 PE=1 SV=3	sp|P25694	91998,4	2%	GGSLGDAGGASDR		1	0	1
no tap	Elongation factor 1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EFB1 PE=1 SV=4	sp|P32471	22627,5	20%	AFQSAYPEFSR-AIEMEGLTWGAHQFIPIGFGIK-QLNASLADK		3	0	3
no tap	Vacuolar transporter chaperone 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VTC4 PE=1 SV=2	sp|P47075	83157,5	2%	VKEVQEQVQHTVR		1	0	1
no tap	54S ribosomal protein L35, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRPL35 PE=1 SV=1	sp|Q06678	42827	2%	FYELANK		1	0	1
no tap	Histone H2B.1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HTB1 PE=1 SV=2	sp|P02293,sp|P02294	14253	24%	EIQTAVR-LILPGELAK-SmSILNSFVNDIFER		3	0	3
no tap	Nucleolar protein 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOP6 PE=1 SV=1	sp|Q07623	25217,1	15%	FIVFVGSLPR-TTATAAQTSGTDNKPVPAGIHPDR		2	0	2
no tap	Eukaryotic translation initiation factor 4E OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC33 PE=1 SV=1	sp|P07260	24254,6	16%	GADIDELWLR-KFEENVSVDDTTATPK-SDYHVFR		3	0	3
no tap	Peroxiredoxin type-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AHP1 PE=1 SV=4	sp|P38013	19114,4	25%	FASDPGcAFTK-FQYIAISQSDADSEScK-mPQTVEWSK-sDLVNKK	c7: Carbamidome	4	0	4
no tap	FK506-binding protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FPR4 PE=1 SV=1	sp|Q06205	43904,6	3%	LLEGGIIIEDR		1	0	1
no tap	Sphingolipid long chain base-responsive protein PIL1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PIL1 PE=1 SV=1	sp|P53252	38350,3	9%	APTASQLQNPPPPPSTTK-SAAGAFGPELSR		2	0	2
no tap	60S ribosomal protein L36-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL36B PE=1 SV=3	sp|O14455	11135,9	31%	EIAGLSPYER-TGIAIGLNK-VEEmNNIIAASR		3	0	3
no tap	Mitochondrial protein import protein MAS5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDJ1 PE=1 SV=1	sp|P25491	44671,7	6%	VGIVPGEVIAPGmR-YGGYGNLIIK	m13: Oxidation (	2	0	2
no tap	Pyruvate decarboxylase isozyme 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDC1 PE=1 SV=7	sp|P06169	61496,9	46%	AQYNEIQGWDHLSLLPTFGAK-EVIDTILALVK-GYKPVAVPAR-IYEVEGmR-KLIDLTQFPAFVTPmGK-LIDLTQFPAFVTPmGK-LLTTIADAAK-mIEIMLPVFDAPQNLVEQAK-NATFPGVQMK-NIVEFHSDHMK-NPVILADAccSR-		19	0	19
no tap	DNA-directed RNA polymerases I and III subunit RPAC2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPC19 PE=1 SV=1	sp|P28000	16150,9	18%	IQTYGETTAVDALQK-TATEVTPQEPK		2	0	2
no tap	Putative COX1/OXI3 intron 1 protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=aI1 PE=1 SV=2	sp|P03875	96085	1%	TIINNYK		1	0	1
no tap	Histone H2A.Z OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HTZ1 PE=1 SV=3	sp|Q12692	14283,6	5%	HLQLAIR		1	1	0
no tap	60S ribosomal protein L33-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL33A PE=1 SV=3	sp|P05744	12154,2	22%	IAYVYR-IFLYPSNI-VNNPNVSLIK		3	3	0
no tap	Transposon Ty1-ML1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-ML1 PE=3 SV=2	sp|Q04711	198533	8%	AHNVSTSNNSPSTDNDSISK-DILSVDYTDImK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-LNVPLNPK-STTEPIQLNNK-TVDTTNYVILQGK-VAcQLIMR-VTNIIDR-YVRPPPMLTSPNDFPNWVK		10	10	0
no tap	60S ribosomal protein L27-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL27A PE=1 SV=1	sp|P0C2H6,sp|P0C2H7	15531,2	50%	KVVIVKPHDEGSK-NQWFFSK-SHPFGHALVAGIER-SVVSTETFEQPSQR-VVNYNHLLPTR-YTLDVEAFK		6	0	6
no tap	40S ribosomal protein S5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS5 PE=1 SV=3	sp|P26783	25038,5	38%	AQcPIIER-DASLVDYVQVR-GSSTSYAIK-QAVDVSPLR-QPIFVAHTAGR-TIAETLAEELINAAK-vNQAIALLTIGAR-WSFEEVEVK	c3: Carbamidome	8	0	8
no tap	60S ribosomal protein L5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL5 PE=1 SV=4	sp|P26321	33716,1	8%	IAALAGQQ-LGLDETYK-VFLDIGLQR		3	0	3
no tap	40S ribosomal protein S18-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS18A PE=1 SV=1	sp|P0CX55,sp|P0CX56	17037,9	50%	AGELTQEELER-IPAWFLNR-IVQImQNPTHYK-IVYALTTIK-LLNTNVDGNIK-sLVVQEQGSFQHILR-YSNLVcK		7	0	7
no tap	Peroxiredoxin TSA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TSA1 PE=1 SV=3	sp|P34760	21590,1	29%	EGGLGPINIPLLADTNHSLSR-GLFIIDPK-HITINDLPVGR-LVEAFQWTDK-NVDEALR		5	0	5
no tap	Replication factor A protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RFA3 PE=1 SV=1	sp|P26755	13816,1	27%	SQPTESQLILQSPTISSK-VDPTEISNVNAPVFR		2	0	2
no tap	DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB5 PE=1 SV=1	sp|P20434	25079,6	5%	ADPVALYLGLK		1	0	1
no tap	Nuclear cap-binding protein complex subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STO1 PE=1 SV=2	sp|P34160	100023,3	4%	FIANIDNAIPHESTR-TTDINLLR-YAGLLTSR		3	0	3
no tap	PAB1-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PBP1 PE=1 SV=1	sp|P53297	78783	2%	TVSPTTQISAGK		1	0	1
no tap	Heat shock protein SSA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSA1 PE=1 SV=4	sp|P10591	69659,4	45%	ARFEELcADLFR-AVGIDLGTTYScVAHFANDR-DAGTIAGLNVLR-ELQDIANPImSK-ETAESYLGAK-FEELcADLFR-FELSGIPPAPR-IINEPTAAAIAYGLDK-IINEPTAAAIAYGLDKK-ITITNDK-LIDVDGKPQIQV	c7: Carbamidome	23	0	23
no tap	40S ribosomal protein S7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS7A PE=1 SV=4	sp|P26786	21622,7	35%	ALAIFVPVPSLAGFHK-HVIFLAER-ILEDLVFPTEIVGK-ILPKPSR-LESFQAVYNK-QIVFEIPSETH		6	0	6
no tap	Vacuolar protein sorting-associated protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VPS1 PE=1 SV=2	sp|P21576	78740	20%	AEQTYINTAHPDLLK-DATIPTNEFVVDIIK-EAISNQFIQFLK-ELSSQELSGGAR-ISYVFHETFK-IYSPHVLTLTLVDLPGLTK-LAALESPPPVLK-LVTLVFDELVR-SGFFGGFFSTK-SSVLENIVGR-VPVGDQPPDIER		11	0	11
no tap	ATP-dependent DNA helicase MPH1 OS=Saccharomyces cerevisiae (strain YJM789) GN=MPH1 PE=3 SV=1	sp|A6ZVS0,sp|P40562	114209,5	1%	IIANPTIPEGIK		1	0	1
no tap	60S ribosomal protein L8-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL8B PE=1 SV=3	sp|P29453	28112,8	41%	EAAAIAEGK-LGTLVNQK-LVSTIDANFADK-LVSTIDANFADKYDEVK-NFGIGQAVQPK-NTAAETFK-TSAVAALTEVR-VAPAPFGAK-VPPTIAQFQYTLDR-WPEYVR-YGLNHVVSLIENK		11	0	11
no tap	Cell division control protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC10 PE=1 SV=1	sp|P25342	37026,3	39%	ELIQNEFEK-FITDTR-ISTHTLVEDR-LDVEALKR-LNINVIDTPGFGDFIDNSK-LTEIANVIPVIGK-mDPLSSVQPASYVGFDTITNQIEHR-SDTLTLDER-STLINTLFASHLIDSATGDDISALPVTK		9	0	9
no tap	mRNA-decapping enzyme subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DCP1 PE=1 SV=1	sp|Q12517	26267,3	4%	ALNFNVIGR		1	0	1
no tap	Protoplast secreted protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PST2 PE=1 SV=1	sp|Q12335	20966	8%	SPSALELQVHEIQGK		1	0	1
no tap	Enolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ENO1 PE=1 SV=3	sp|P00924	46817,4	29%	AADALLLK-AVDDFLISLDGTANK-GNPTVEVELTTEK-IATAIEK-IGLDcASSEFFK-IGSEVYHNLK-LNQLLR-SIVPSGASTGVHEALEmR-TAGIQIVADDLTVTNPK-TFAEALR-vNQIGTLSESIK		11	10	1
no tap	UPF0202 protein KRE33 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KRE33 PE=1 SV=1	sp|P53914	119353,8	1%	ESTQTAVVSR		1	0	1
no tap	Mitochondrial DNA replication protein YHM2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YHM2 PE=1 SV=1	sp|Q04013	34185,2	7%	IGASALGGGLSAWNQPIEVIR		1	0	1
no tap	Transcription initiation factor TFIID subunit 14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF14 PE=1 SV=1	sp|P35189	27440,7	14%	SGSTEETTANTGTIGK-TQQHILPEVPPVENFPVR		2	0	2
no tap	40S ribosomal protein S22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS22A PE=1 SV=2	sp|P0C0W1,sp|Q3E7Y3	14626,5	5%	FLQVmQK	m5: Oxidation (+	1	0	1
no tap	60S ribosomal protein L17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL17A PE=1 SV=4	sp|P05740	20549,6	39%	FNSSIGR-FVQGLLQNAAANAEAK-LYVSHIQVNQAPK-YESSPSHIELVVTEK-YGATSTNPAK-YLEQVLDHQR		6	5	1
no tap	DNA-directed RNA polymerase I subunit RPA49 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA49 PE=1 SV=2	sp|Q01080	46653,2	3%	GATVAQAEAFGIPK		1	0	1
no tap	40S ribosomal protein S9-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS9A PE=1 SV=3	sp|O13516,sp|P05755	22443,9	29%	ISFQLSK-LAGEFGLK-LFEGNALIR-LQTQVYK-QIVNIPSFMVR-VGVLSEDKK-VLITQR		7	0	7
no tap	Protein MET17 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MET17 PE=1 SV=3	sp|P06106	48672,3	2%	LSGAQVVDNLK		1	0	1
no tap	Single-stranded nucleic acid-binding protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SBP1 PE=1 SV=2	sp|P10080	32989,9	3%	IFTSDSANR		1	0	1
no tap	ATP synthase subunit beta, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ATP2 PE=1 SV=2	sp|P00830	54794,7	19%	FTQAGSEVSALLGR-GISELGIYPAVDPLDSK-IINVIGEPIDER-TIAMDGTEGLVR-TVFIQELINNIAK-VALTGLTIAEYFR-VLDTGGPISVPVGR		7	0	7
no tap	Keratin, type I cytoskeletal 9 - Homo sapiens	sp|P35527	62131	34%	FSSSSGYGGGSSR-GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR-GGSGGSYGGGGSGGGYGGGSGSR-HGVQELEIELQSQLSK-IKFEMEQNLR-LASYLDK-MTLDDFR-NYSPYYNTIDDLKDQIVDLTVGNNK-QEYEQLIAK-Q		15	1	14
no tap	Keratin, type II cytoskeletal 2 epidermal - Homo sapiens	sp|P35908	65866,4	22%	AQYEEIAQR-FASFIDK-FLEQQNQVLQTK-GFSSGSAVVSGGSR-IEISELNR-LNDLEEALQQAK-NLDLDSIIAEVK-NVQDAIADAEQR-SKEEAEALYHSK-STSSFScLSR-TAAENDFVTLKK-VDLLNQEIEFLK-YEELQVTVGR		13	2	11
no tap	Eukaryotic translation initiation factor 3 subunit G OS=Saccharomyces cerevisiae (strain YJM789) GN=TIF35 PE=3 SV=1	sp|A6ZZ25,sp|Q04067	30474,6	4%	GSPAGPSAVTAR		1	0	1
no tap	Heat shock protein homolog SSE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSE1 PE=1 SV=4	sp|P32589	77368,6	7%	GIDIVVNEVSNR-sTPFGLDLGNNNSVLAVAR-YEELASLGNIIR-YNIADAAR		4	0	4
no tap	DNA-directed RNA polymerase I subunit RPA190 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA190 PE=1 SV=2	sp|P10964	186435,3	14%	ALANQLLTPSSNVSTHTLNK-DISSTLLNELK-GSFTATVNDER-GSLENEVLFK-LNNVGTGSFDVLAK-LQTDVANSSSNSK-LTYPEPVTAYNIAELR-QAVINGPDK-QGTYLAFNR-SGILDAVTSSK-TGSTYILSTEVK-TLPSFKPYETD		18	0	18
no tap	Probable oxidoreductase AIM17 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AIM17 PE=1 SV=2	sp|P23180	53137,1	3%	LTAPQDIQISEDGK		1	0	1
no tap	60S ribosomal protein L13-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL13B PE=1 SV=1	sp|P40212	22525,5	15%	AAGLTAAYAR-NQEIFDANVQR-TIGIAVDHR		3	0	3
no tap	NAD-dependent malic enzyme, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MAE1 PE=1 SV=1	sp|P36013	74377,4	2%	LATAVILQALEEGTAR		1	0	1
no tap	Probable inosine-5'-monophosphate dehydrogenase IMD3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IMD3 PE=1 SV=1	sp|P50095	56586,2	8%	EQAANLIAAGADGLR-NPVTGAQGITLSEGNEILKK-NQNYPLASK		3	0	3
no tap	60S acidic ribosomal protein P0 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP0 PE=1 SV=2	sp|P05317	33717,4	38%	AGAVAPEDIWVR-AVNTGMEPGK-AVVLMGK-EYLEEYK-GFLSDLPDFEK-GNVGFVFTNEPLTEIK-GTIEIVSDVK-LLPFVK-LREYLEEYK-NVIVSNR-SLFVVGVDNVSSQQmHEVR-TSFFQALGVPTK		12	0	12
no tap	rRNA biogenesis protein RRP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RRP5 PE=1 SV=1	sp|Q05022	193141,4	4%	APESVADFER-DTIENIVPGR-INNVIPTTVLSVDEQNKK-LLPGAVFLGNITK-SLFEGLVADAPK-VLILSNLPHILK		6	0	6
no tap	S-adenosylmethionine synthase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SAM1 PE=1 SV=2	sp|P10659,sp|P19358	41819,4	6%	FVIGGPQGDAGLTGR-YFIQPSGR		2	0	2
no tap	60S ribosomal protein L21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL21A PE=1 SV=1	sp|Q02753	18242	40%	HGAVHLSTYLK-IVSTEGNVPQTLAPVPYETFI-QEFLER-SSVGVIINK-TGVVYNVTK-VGDIVDIK		6	0	6
no tap	60S ribosomal protein L32 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL32 PE=1 SV=1	sp|P38061	14771,8	21%	TFLVANVK-TYAAEIAHNISAK-VVILAR		3	0	3
no tap	Mitochondrial phosphate carrier protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MIR1 PE=1 SV=1	sp|P23641	32813,9	3%	IQLEPTVYNK		1	0	1
no tap	U3 small nucleolar RNA-associated protein 13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UTP13 PE=1 SV=1	sp|Q05946	91036,1	3%	IVDAIIPYTQR-LALATNSPSLR		2	0	2
no tap	60S ribosomal protein L11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL11A PE=1 SV=2	sp|P0C0W9,sp|Q3E757	19720	31%	AEEILER-EDTVSWFK-IAVHVTVRGPK-LVLNISVGESGDR-VLEQLSGQTPVQSK		5	0	5
no tap	Clustered mitochondria protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CLU1 PE=1 SV=1	sp|Q03690	145171,1	7%	ALTNLAILEFSNESPYNATVVVYNR-DLTTSTLQDR-ISELEIVSR-LALYPEAIAFcR-LLTSESNIITPcVR-SLSFAPYNPVPPFYR-VSGIDSFEMMR		7	0	7
no tap	Alcohol dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADH1 PE=1 SV=5	sp|P00330	36848,7	47%	aNELLINVK-ANGTTVLVGMPAGAK-ATDGGAHGVINVSVSEAAIEASTR-EALDFFAR-EKDIVGAVLK-GVIFYESHGK-IGDYAGIK-LPLVGGHEGAGVVVGMGENVK-SIGGEVFIDFTK-SISIVGSYVGNR-VLGID	n-term: Acetyl (+	13	0	13
no tap	Fructose-bisphosphate aldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FBA1 PE=1 SV=3	sp|P14540	39621,5	18%	DYIMSPVGNPEGPEKPNKK-GISNEGQNASIK-SPIILQTSNGGAAYFAGK-VNLDTDcQYAYLTGIR		4	0	4
no tap	60S ribosomal protein L16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL16A PE=1 SV=3	sp|P26784	22201,6	37%	AEELNISGEFFR-GPFHFR-LSTSVGWK-SVEPVVVIDGK-VASANATAAESDVAK-VVVPQALR-YEDVVAK-YTTLGK		8	5	3
no tap	Heat shock protein SSA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSA2 PE=1 SV=3	sp|P10592	69471,8	42%	ARFEELcADLFR-DAGTIAGLNVLR-ELQEVANPIMSK-ETAESYLGAK-FEELcADLFR-FELSGIPPAPR-IINEPTAAAIAYGLDK-IINEPTAAAIAYGLDKK-ITITNDK-LIDVDGKPQIQVEFK-LVNHFIQEFK-LVTDYF	c7: Carbamidome	22	17	5
no tap	Replication factor A protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RFA1 PE=1 SV=1	sp|P22336	70350,2	11%	ATAFNDFATK-FANENPNSQK-FNEILQEGK-LFNVNFLDTSGEIR-QEPGmGGQSAASLTK-VIIAEPAIVR		6	0	6
no tap	40S ribosomal protein S3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS3 PE=1 SV=5	sp|P05750	26503	44%	ALPDAVTIIEPK-EEEPILAPSVK-FADGFLIHSGQPVNDFIDTATR-GcEVVVSGK-GLSAVAQAESmK-INELTLLVQK-RINELTLLVQK-TEVIIR-TQDVLGENGR-YAPGTIVLYAER		10	0	10
no tap	60S ribosomal protein L35-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL35A PE=1 SV=1	sp|P0CX84,sp|P0CX85	13910,2	8%	FEASQVTEK		1	0	1
no tap	5'-3' exoribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KEM1 PE=1 SV=1	sp|P22147	175468	4%	FIAVSLESDSLTK-GAFPVLLQTFK-GPIPIEEEFPLNSK-QLENISLEGER-QTFPDFFFR-VVYIQDSGK		6	0	6
no tap	60S ribosomal protein L2-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL2A PE=1 SV=1	sp|P0CX45,sp|P0CX46	27408,9	31%	ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR-GAGSIFTSHTR-KGAGSIFTSHTR-LREEIFIANEGVHTGQFIYAGK-TLDYAER-VDKPLLK		6	0	6
no tap	2-oxoglutarate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KGD1 PE=1 SV=2	sp|P20967	114419,3	1%	LNVLSNVVR		1	0	1
no tap	Something about silencing protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SAS10 PE=1 SV=1	sp|Q12136	70261,9	2%	TMFPEFAPLSK		1	0	1
no tap	Superoxide dismutase [Mn], mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SOD2 PE=1 SV=1	sp|P00447	25774,9	6%	LAGVQGSGWAFIVK		1	0	1
no tap	UTP--glucose-1-phosphate uridylyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UGP1 PE=1 SV=1	sp|P32861	55989,9	26%	DGHEINVLQLETAcGAAIR-EGNTFLDLSVR-FGPNPLIK-GGTLISYDGQVR-HFDGAHGVVVPR-LLEVAQVPK-QIEYLNR-SPNPDEVVK-THSTYAFESNTNSVAASQmR-TTLEWDK-YEIISQQPENVSNLSK	c14: Carbamidon	11	0	11
no tap	Isocitrate dehydrogenase [NAD] subunit 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IDH2 PE=1 SV=1	sp|P28241	39740,6	2%	GPLATPIGK		1	0	1
no tap	Mitochondrial peculiar membrane protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MPM1 PE=1 SV=1	sp|P40364	28471,4	5%	FATAPFWNLFPK		1	0	1
no tap	40S ribosomal protein S15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS15 PE=1 SV=1	sp|Q01855	16002,2	30%	LAAPENEKPAPVR-LLEmSTEDFVK-NmIIVPEmIGSVVGIYNGK		3	0	3
no tap	Ubiquitin-40S ribosomal protein S31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS31 PE=1 SV=3	sp|P05759	17216,6	11%	ESTLHLVLR-LAVLSYYK		2	0	2
no tap	Keratin, type II cytoskeletal 1 - Homo sapiens	sp|P04264	66019,2	39%	AEAESLYQSK-DVDGAYMTK-FLEQQNQVLQTK-GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR-IEISELNR-LALDLEIATYR-LDSELK-LNDLEDALQQAK-LRSEIDNVK-MSGEcAPNVSVSVSTSHTTISGGGSR-NMQDMVED		22	0	22
no tap	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=COR1 PE=1 SV=1	sp|P07256	50229	12%	HEDLVNSIESK-LTISVTDTEVER-SLDFLNQSFIQQK-VLEHLHSTAFQNTPLSLPTR		4	0	4
no tap	Nuclear segregation protein BFR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BFR1 PE=1 SV=1	sp|P38934	54641,7	32%	DLVNIEPIR-DLVNIEPIRK-EELNGLNPK-FKRPDVSVR-IDTEIGLIR-INQLKEELNGLNPK-ITVEQLK-KDDFVNVAPSK-KIDTEIGLIR-KLDTLNVQLK-KNILPDLSSNALETKPAR-LNLDYSNK-NILPDLSSNALETKPAR-NTENEQP		18	0	18
no tap	Prohibitin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PHB2 PE=1 SV=2	sp|P50085	34407,2	30%	AVVAQFNASQLITQR-ILASSPNR-NVASLTGTK-SAELIGEAIKK-SPGEFQR-VILDNEALLLNTVVDAR-VLPSIVNEVLK-VLSRPDVVQLPTIYR		8	0	8
no tap	Pyruvate dehydrogenase complex protein X component, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDX1 PE=1	sp|P16451	45363,8	5%	IPQDSVNK-LPQEANTANAK		2	0	2
no tap	Glucan 1,3-beta-glucosidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BGL2 PE=1 SV=1	sp|P15703	34118,6	3%	AALQTYLPK		1	0	1
no tap	NET1-associated nuclear protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAN1 PE=1 SV=1	sp|Q02931	101241,4	5%	LANVFHSEGNYR-LINDTNLIVATR-TTLNAINLLR-VINPHGISVPITK		4	0	4
no tap	60S ribosomal protein L12-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL12A PE=1 SV=1	sp|P0CX53,sp|P0CX54	17823,2	33%	AVGGEVGASAALAPK-EILGTAQSVGcR-IGPLGLSPK-QAAASVVPSASSLVITALK		4	0	4
no tap	Heat shock protein 78, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP78 PE=1 SV=2	sp|P33416	91340,8	2%	FQPILLNEPSVSDTISILR		1	0	1
no tap	Inorganic phosphate transporter PHO86 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PHO86 PE=1 SV=1	sp|P46956	34883,2	4%	LLIDVYSFDSTLK		1	0	1
no tap	Multiprotein-bridging factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MBF1 PE=1 SV=2	sp|O14467	16404	39%	AIPNQQVLSK-GNNIGSPLGAPK-INEKPTVVNDYEAAR-QGLVVSVDKK-sDWDTNTIIGSR		5	0	5
no tap	60S ribosomal protein L4-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL4B PE=1 SV=2	sp|P49626	39062	45%	AGHQTSAESWGTGR-AVGAHSDLLK-FVIWTEAAFTK-GPLVVYAEDNGIVK-IINSSEIQSAIRPAGQATQK-IPEIPLVVSTDLESIQK-LDQVWGSETVASSK-NVPGVETANVASLNLLQLAPGAHLGR-VGYTLPSHIISTSDVTR-YATAS		10	10	0
no tap	40S ribosomal protein S14-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS14B PE=1 SV=2	sp|P39516	14649,8	25%	DNSQVFGVAR-IEDVTPVPSDSTR-TPGPGGQAALR		3	0	3
no tap	60S ribosomal protein L7-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL7B PE=1 SV=3	sp|Q12213	27697,8	46%	AAGSYYVEAQHK-AIILER-ATLELLK-HFIQGGSFGNR-INSGTFVK-LIEPYVAYGYPSYSTIR-LSNPSGGWGVPR-LVFVVR-QANNFLWPFK-TAEQIAAER-VPLSDNAIIEANLGK		11	10	1
no tap	Keratin, type II cytoskeletal 5 - Homo sapiens	sp|P13647	62379,6	5%	FASFIDK-NLDLDSIIAEVK-YEELQQTAGR		3	2	1
no tap	Threonyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=THS1 PE=1 SV=2	sp|P04801	84522,6	1%	IYNTLVDLLR		1	0	1
no tap	Serine/threonine-protein phosphatase PP1-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GLC7 PE=1 SV=1	sp|P32598	35909	4%	GVSFTFGPDVVNR		1	0	1
no tap	Plasma membrane ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PMA1 PE=1 SV=2	sp|P05030	99621,6	5%	MLTGDAVGIAK-QLGLGTNIYNAER-TLANTAVVIR-VVEILQNR		4	0	4
no tap	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=QCR2 PE=1 SV=1	sp|P07257	40479,7	23%	DQDSAVVSSNIK-ESELLGGTFK-FVDESLLSTLPAGK-GLGNPLLYDGVER-SAEDQLYAITFR-TAFKPHELTESVLPAAR-VSLQDIK		7	0	7
no tap	cDNA FLJ75925, highly similar to Homo sapiens keratin 16 - Homo sapiens	sp|A8K488,sp|P08779	51269	7%	LAADDFR-LASYLDK-VLDELTLAR-VTMQNLNDR		4	3	1
no tap	Cytochrome c1, heme protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CYT1 PE=1 SV=1	sp|P07143	34055,4	4%	TLVGVSHTNEEVR		1	0	1
no tap	ATP-dependent helicase NAM7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAM7 PE=1 SV=1	sp|P30771	109432,6	7%	ANEQQAIGFLR-DGVKPEQIGVITPYEGQR-LITPSQISK-QVILVGDHQQLGPVILER-YGLVILGNPR		5	0	5
no tap	Phosphoglycerate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PGK1 PE=1 SV=2	sp|P00560	44739,6	55%	AGAEIVPK-ALENPTRPFLAILGGAK-ALLDEVVK-ASAPGSVILLENLR-DVTFLNDcVGPEVEAAVK-ELPGVAFLSEK-ELQSLLGK-HELSSLADVYINDAFGTAHR-ISHVSTGGGASLELLEGK-IVAALPTIK-KLFAATVAK-LSVQDL		19	0	19
no tap	Keratin, type I cytoskeletal 14 - Homo sapiens	sp|P02533	51622,6	10%	EVATNSELVQSGK-LAADDFR-LASYLDK-VLDELTLAR-VTMQNLNDR		5	4	1
no tap	60S ribosomal protein L17-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL17B PE=1 SV=2	sp|P46990	20551,6	39%	FNSSIGR-FVQGLLQNAAANAEAK-LYVSHIQVNQAPK-YESSPSHIELVVTEK-YGATSTNPAK-YLDQVLDHQR		6	0	6
no tap	Elongation factor 3B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HEF3 PE=1 SV=2	sp|P53978	115871,6	3%	IAVIGPNGAGK-QINENDAEAMNK-TPSEYIQWR		3	3	0
no tap	6-phosphofructokinase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PFK1 PE=1 SV=1	sp|P16861	107972,8	4%	LNIGIVHVGAPSAALNAATR-TAIPGHVQQGGVPSSK		2	0	2
no tap	Elongation factor 1-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TEF1 PE=1 SV=1	sp|P02994	50032,6	49%	EHALLAFTLGVR-ETSNFIK-fDELLEK-FQEIVK-FVPSKPMcVEAFSEYPPLGR-IGGIGTVPVGR-LPLQDVYK-QLIVAVNK-QTVAVGVIK-SHINVVVIGHVDSGK-SVEMHHEQLEQGVPGDNVGFNVK-TIEKFEK-TLLEAIDAIEQPS		17	0	17
no tap	DNA-directed RNA polymerase I subunit RPA12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA12 PE=1 SV=1	sp|P32529	13660,6	12%	VVTTTADDAFPSSLR		1	0	1
no tap	Cell division control protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC3 PE=1 SV=3	sp|P32457	60056,2	11%	GQVLPDQPEIK-ILYENYR-LFSSLPYAVIGSNDIVENYSGNQVR-VEPGLGmGITSSQSEK		4	0	4
no tap	Malate dehydrogenase, peroxisomal OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MDH3 PE=1 SV=3	sp|P32419	37187,2	13%	AETFLVDYLMLK-ILVISNPVNSLVPIAVETLK-LSPYVSELALYDIR		3	0	3
no tap	T-complex protein 1 subunit delta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CCT4 PE=1 SV=2	sp|P39078	57605,6	3%	GLIAGGGAPEIEISR		1	0	1
no tap	60S acidic ribosomal protein P2-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP2A PE=1 SV=1	sp|P05319	10746,2	28%	VSSVLSALEGK-YLAAYLLLNAAGNTPDATK		2	0	2
no tap	Transposon Ty1-DR1 Gag polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1A-DR1 PE=1 SV=1	sp|Q03856	49057,2	31%	AHNVSTSNNSPSTDNDSISK-DILSVDYTDImK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-mESQQLSNYPHISHGSAcASVTSK-STTEPIQLNNK-VAcQLIMR-VTNIIDR-YVRPPPMLTSPNDFPNWVK		9	9	0

no tap	78 kDa glucose-regulated protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KAR2 PE=1 SV=1	sp|P16474	74470,2	24%	DAGTIAGLNVLR-FASEDASIK-HLPFNVVNK-ITPSYVAFTDDER-IVNEPTAAAIAYGLDK-LTQEEIDR-NQVAANPQNTIFDIK-QIAEDYLGTK-TEILANEQGNR-VAYPITSK-VFTPEEISGMILGK-VLQDSGLEK-VQQLLESYFDGK		14	1	13
no tap	40S ribosomal protein S10-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS10B PE=1 SV=1	sp|P46784,sp|Q08745	12738,7	19%	IHQYLFQEGVVVAK-NLYVIK		2	0	2
no tap	Flavohemoprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YHB1 PE=1 SV=2	sp|P39676	44647,2	12%	ATVPVLEQQGTVITR-IIVHTDTEPLINAAFLK-VGAQPNALATTVLAAAK		3	0	3
no tap	Protein BMH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BMH1 PE=1 SV=4	sp|P29311	30092	23%	ISDDILSVLDSHLIPSATTGESK-NLLSVAYK-TASEIATTELPPTHPIR-TVASSGQELSVEER		4	0	4
no tap	RNA annealing protein YRA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YRA1 PE=1 SV=2	sp|Q12159	24956,3	18%	EFFASQVGGVQR-LNLIVDPNQRPVK-VLLSYNER-VNVEGLPR		4	0	4
no tap	Vacuolar transporter chaperone 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VTC3 PE=1 SV=1	sp|Q02725	96558,3	1%	ISVPDGKTTER		1	0	1
no tap	FACT complex subunit POB3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=POB3 PE=1 SV=1	sp|Q04636	62995,2	2%	ISTSGGSAANQAR		1	0	1
no tap	Polyadenylate-binding protein, cytoplasmic and nuclear OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PAB1 PE=1 SV=4	sp|P04147	64345,4	17%	AVEALNDSELNGEK-EAIDALNGMLLNGQEIYVAPHLSR-FGPIVSASLEK-GSGNIFIK-NQQIVAGKPLYVAIAQR-SQLAQQIQAR-TAEQLENLNIQDDQK		7	0	7
no tap	Histone H4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HHF1 PE=1 SV=2	sp|P02309	11368,9	41%	DNIQGITKPAIR-ISGLIYEEVR-SFLESVIR-TVTSLDVVYALK		4	0	4
no tap	40S ribosomal protein S25-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS25B PE=1 SV=1	sp|P0C0T4,sp|Q3E792	12009,9	34%	AQHAVILDQEK-EGIIKPISK-IGGSLAR-YVSVSVLVDR		4	0	4
no tap	Glucose-6-phosphate 1-epimerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YMR099C PE=1 SV=1	sp|Q03161	33956,4	4%	GGIPLVFPVFGK		1	0	1
no tap	ADP,ATP carrier protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PET9 PE=1 SV=2	sp|P18239	34428	28%	GFLPSVVGIVVYR-IVAAEGVGSLFK-LLIQNQDEMLK-SDGVAGLYR-TATQEGVISFWR-TPLPPAPAPK-YDGAFDcLR-YFPTQALNFAFK		8	0	8
no tap	Mitochondrial acidic protein MAM33 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MAM33 PE=1 SV=1	sp|P40513	30132,7	6%	FSLVETPGKNEAEIVR		1	0	1
no tap	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDB1 PE=1 SV	sp|P32473	40054,2	22%	NVQFSLEAAEILQK-SIRPLDTEAIIK-VLVPYSAEDAR-VTGADVPTPYAK-VVDTPITEYGFTGLAVGAALK-YGVSAEVINLR		6	0	6
no tap	Protein transport protein SEC13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEC13 PE=1 SV=1	sp|Q04491	33042,6	7%	FPDVLWR-LIDTLTGHEGPVWR		2	0	2
no tap	Peroxisomal-coenzyme A synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PCS60 PE=1 SV=1	sp|P38137	60489,9	20%	FVNTNPVK-GENVTLGYANNPK-ISPIELDGImLSHPK-LQSSEILK-MTYEELVNFLK-QDTVAISMR-SSDVALILHTSGTTSTPK-STLNIANTYK-VGEVSIR-VIAETFAK		10	0	10
no tap	Alcohol dehydrogenase 3, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADH3 PE=1 SV=2	sp|P07246	40369,8	2%	YVVDTSK		1	1	0
no tap	NADPH-dependent aldose reductase GRE3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GRE3 PE=1 SV=1	sp|P38715	37120,2	3%	DISALNANIR		1	0	1
no tap	60S ribosomal protein L30 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL30 PE=1 SV=3	sp|P14120	11416	11%	LIIIAANTPVLR		1	0	1
no tap	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MET6 PE=	sp|P05694	85862,4	2%	LDEVVVITK-VIQVDEPALR		2	0	2
no tap	DNA-directed RNA polymerase I subunit RPA135 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA135 PE=1 SV=1	sp|P22138	135745,4	3%	FVGGNETTTVAIPFVLK-IIADTLR-TQVLQYLGDK		3	0	3
no tap	Eukaryotic translation initiation factor 2 subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GCD11 PE=1 SV=1	sp|P32481	57867,2	2%	FAVPGGLIGVGTK		1	0	1
no tap	60S ribosomal protein L24-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL24A PE=1 SV=1	sp|P04449	17614,4	27%	AQRPITGASLDLIK-GITEEVAK-GTLFVR-IAWTVLFR-SASLFK		5	0	5
no tap	Myosin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MYO2 PE=1 SV=1	sp|P19524	180687	2%	ILATNPIMEAFGNAK-IVSNLNYSQALVAK		2	0	2
no tap	60S acidic ribosomal protein P1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP1B PE=1 SV=3	sp|P10622	10668,1	15%	AAGANVDNVWADVYAK		1	0	1
no tap	Elongation factor 3A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YEF3 PE=1 SV=4	sp|P16521	115948,1	13%	ALLPHLTNAIVETNK-EALASGQFRPLTR-IAVIGPNGAGK-LSVATADNR-LVEDPQVIAPFLGK-MTPSGHNWVSGQGAGPR-NLTEEVWAVK-QINENDAEAMNK-SNFATIADPEAR-TPSEYIQWR-VLEELFQK		11	0	11
no tap	40S ribosomal protein S2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS2 PE=1 SV=3	sp|P25443	27450,2	26%	GSGIVASPAVK-GYWGTNLGQPHSLATK-ITTIEEIFLHSLPVK-LSVIPIR-sAPEAQQQK-TLENTLK		6	0	6
no tap	Cytochrome b-c1 complex subunit 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=QCR7 PE=1 SV=2	sp|P00128	14565,7	10%	AHQTELTHHLLPR		1	0	1
no tap	Potassium-activated aldehyde dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ALD4 PE=1 SV=2	sp|P46367	56725,2	11%	IAPALVTGNTVVLK-SPNIVFADAELKK-VAFTGSTATGR-YIPQAGIPPGVINIVSGFGK		4	0	4
no tap	40S ribosomal protein S23-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS23A PE=1 SV=1	sp|P0CX29,sp|P0CX30	16038,3	14%	AKGDIPGVR-VSGVSLLALWK		2	0	2
no tap	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TDH2 PE=1 SV=3	sp|P00358	35846,9	49%	eLDTAQK-ETTYDEIKK-IATFQER-IVSNAScTTNcLAPLAK-KVVITAPSSTAPmFVMGVNEEK-LTGmAFR-NVEVVALNDPFISNDYSAYmFK-TASGNIIPSSTGAAK-VINDAFGIEEGLMTTVHSmTATQK-VLPELQG	n-term: Acetyl (+	13	11	2
no tap	37S ribosomal protein MRP4, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRP4 PE=1 SV=1	sp|P32902	44153,9	3%	SVNFLLGVLAR		1	0	1
no tap	Replication factor A protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RFA2 PE=1 SV=1	sp|P26754	29936,1	10%	GYGSQVAQQFEIGGYVK-VNTLTPVTIK		2	0	2
no tap	Actin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ACT1 PE=1 SV=1	sp|P60010	41690,4	7%	GYSFSTTAER-VAPEEHPVLLTEAPmNPK		2	0	2
no tap	NADPH-dependent alpha-keto amide reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDL124W PE=1 SV=1	sp|Q07551	35562	4%	LPGIIHIDAAEIYR		1	0	1
no tap	DNA-directed RNA polymerases I and III subunit RPAC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPC40 PE=1 SV=1	sp|P07703	37687,6	12%	FSPVSTASYR-LLPQINILQPIKGESAR-VTNTTSTDFPGFSK		3	0	3
no tap	60S ribosomal protein L7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL7A PE=1 SV=3	sp|P05737	27639,6	46%	AAGSYYVEAQHK-AIILER-ATLELLK-HFIQGGSFGNR-INSGTFVK-LIEPYVAYGYPSYSTIR-LSNPSGGWGVPR-LVFVVR-QANNFLWPFK-TAEQVAAER-VPLSDNAIIEANLGK		11	0	11
no tap	60S ribosomal protein L19-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL19A PE=1 SV=1	sp|P0CX82,sp|P0CX83	21704,6	14%	HLYHVLYK-LAASVVGVGK-LPSQVVWIR		3	0	3
no tap	Transcriptional modulator WTM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=WTM1 PE=1 SV=1	sp|Q12363	48383,6	3%	TVHVPGTTVTHTVR		1	0	1
no tap	[PIN+] prion protein RNQ1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RNQ1 PE=1 SV=2	sp|P25367	42578,3	2%	IAGYVMDNR		1	0	1
no tap	Transposon Ty2-LR1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY2B-LR1 PE=3 SV=1	sp|P0C2J3,sp|P25384,sp|Q03494,sp|Q	202130,3	0%	LNVPLNPK		1	1	0
no tap	60S ribosomal protein L14-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL14B PE=1 SV=1	sp|P38754	15153,2	8%	LAAIVEIIDQK		1	0	1
no tap	Cell wall protein ECM33 OS=Saccharomyces cerevisiae (strain YJM789) GN=ECM33 PE=3 SV=2	sp|A6ZL22,sp|B5VE42,sp|C7GQJ1,sp	43756,8	4%	VGQSLSIVSNDELSK		1	0	1
no tap	60S ribosomal protein L22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL22A PE=1 SV=3	sp|P05749	13693,4	18%	TFTVDVSSPTENGVFDPASYAK		1	0	1
no tap	Translationally-controlled tumor protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TMA19 PE=1 SV=1	sp|P35691	18741,3	5%	LQQTAFDKK		1	0	1
no tap	60S ribosomal protein L23-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL23A PE=1 SV=1	sp|P0CX41,sp|P0CX42	14473,1	6%	NLYIIAVK		1	0	1
no tap	Serine hydroxymethyltransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SHM1 PE=1 SV=2	sp|P37292	53688	5%	VETILSALNIAANK-VIVAGTSAYSR		2	0	2
no tap	Heat shock protein SSC1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSC1 PE=1 SV=1	sp|P12398	70628,8	11%	AQFETLTAPLVK-DAGQIVGLNVLR-IIENAEGSR-NAVVTVPAYFNDSQR-QAVVNPENTLFATK-TTPSVVAFTK		6	0	6
no tap	Adenosylhomocysteinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SAH1 PE=1 SV=1	sp|P39954	49125,8	3%	TGPFEVGVHVLPK		1	0	1
no tap	3-methyl-2-oxobutanoate hydroxymethyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ECM31 PE=1 SV=1	sp|P38122	34465,5	4%	QAVNMTDIATQGLK		1	0	1
no tap	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RIP1 PE=1 SV=1	sp|P08067	23365,4	6%	VEVNLAAIPLGK		1	0	1
no tap	Enoyl-[acyl-carrier protein] reductase [NADPH, B-specific], mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ETR1 P	sp|P38071	42068	3%	QDLSQSIVLK		1	0	1
no tap	Uncharacterized protein YDR179W-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDR179W-A PE=1 SV=2	sp|Q03983,sp|Q3E765	53733,7	1%	LLIYR		1	0	1
no tap	Protein SIS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SIS1 PE=1 SV=1	sp|P25294	37591,6	32%	EIYDQYGLEAAR-ESLLGFSK-LYDLLGVSPSANEQELKK-NQGDYNPQTGR-TIQTIDGR-TLQFVIQEK-TQIDIQLKPGWK-VQPVQPSQTSTYPGQGmPTPK-YKVDYPISLNDAQK		9	0	9
no tap	Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDA1 PE=1 S	sp|P16387	46344,4	22%	ATLLQMYK-AVLAELmGR-DmVIIR-GTETPTLR-LDSIITSYR-LSILFEDVYVK-RGQYIPGLK-SSAMTEYFK-VNGmDILAVYQASK-YGMGTAASR		10	0	10
no tap	Keratin, type I cytoskeletal 10 - Homo sapiens	sp|P13645	59512,4	32%	ALEESNYELEGK-GSLGGGFSSGGFSGGSFSR-IRLENEIQTYR-LAADDFR-LASYLDK-LENEIQTYR-LKYENEVALR-NQILNLTTDNANILLQIDNAR-NVSTGDVNVEmNAAPGVDLTQLLNNMR-QSLEASLAETEGR-QSVEADIN		19	0	19
no tap	40S ribosomal protein S4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS4A PE=1 SV=1	sp|P0CX35,sp|P0CX36	29411,2	43%	AILmQR-DSLDNTFVTR-ESLPLIVFLR-GVPYVVTHDGR-HDGGFDLVHIK-IDLASGK-ITDEEASYK-LNNVFVIGEQGKPYISLPK-LSIAEER-TDTTYPAGFMDVITLDATNENFR	m4: Oxidation (+	10	0	10
no tap	40S ribosomal protein S11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS11A PE=1 SV=1	sp|P0CX47,sp|P0CX48	17748,8	44%	cPFTGLVSIR-ILTGTVVSTK-NVPVHVSPAFR-sTELTVQSER-TAIEGSYIDKK-VQVGDIVTVGQcRPISK	c1: Carbamidome	6	0	6
no tap	Pyruvate kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC19 PE=1 SV=2	sp|P00549	54545,4	42%	AGAGHSNTLQVSTV-AGLNIVR-AIIVLSTSGTTPR-GDLGIEIPAPEVLAVQK-GDTYVSIQGFK-GVNLPGTDVDLPALSEK-IENQQGVNNFDEILK-INFGIEK-KGDTYVSIQGFK-KSEELYPGRPLAIALDTK-LTSLNVVAGSDLR-NcT		17	0	17
no tap	60S acidic ribosomal protein P2-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP2B PE=1 SV=2	sp|P02400	11050,3	20%	YLAAYLLLVQGGNAAPSAADIK		1	0	1
no tap	Protein HUA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HUA2 PE=1 SV=1	sp|Q12134	28414,8	6%	VLNIEGIIHNNSIR		1	0	1
no tap	Magnesium-activated aldehyde dehydrogenase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ALD6 PE=1 SV=4	sp|P54115	54415,5	5%	TVGAALTNDPR-VGIPAGVVNIVPGPGR		2	0	2
no tap	40S ribosomal protein S17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS17A PE=1 SV=1	sp|P02407,sp|P14127	15788,9	9%	LPLSVINVSAQR		1	0	1
no tap	60S ribosomal protein L15-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL15A PE=1 SV=3	sp|P05748	24422,6	24%	QGFVIYR-QNTLSLWR-VLNSYWVNQDSTYK-YFEVILVDPQHK-YLEELQR		5	0	5
no tap	Nascent polypeptide-associated complex subunit alpha OS=Saccharomyces cerevisiae (strain YJM789) GN=EGD2 PE=3 SV=1	sp|A6ZT99,sp|P38879	18709,1	7%	SAGGNYVVFGEAK		1	0	1
no tap	60S ribosomal protein L1-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL1A PE=1 SV=1	sp|P0CX43,sp|P0CX44	24486,3	6%	FPTPVSHNDDLYGK		1	0	1
no tap	Protein SCP160 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SCP160 PE=1 SV=3	sp|P06105	134813,7	6%	APIEIPLEK-EAADVIINVPR-IFESILNSPSSK-SGDIVILGPR-SYVVESLDISK-TFLVSGVAANVHEAK		6	0	6
no tap	37S ribosomal protein S17, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRPS17 PE=1 SV=1	sp|Q03246	27636	5%	QNFLGLVVSQGK		1	0	1
no tap	Transcription factor CSR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CSR2 PE=1 SV=1	sp|Q12734	124852,9	1%	STTLSDIK		1	0	1
no tap	60S ribosomal protein L31-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL31A PE=1 SV=1	sp|P0C2H8	12953,2	39%	EYTINLHK-LAPELNQAIWK-LHMGTDDVR-NPLFSYVEPVLVASAK		4	0	4
no tap	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TDH1 PE=1 SV=3	sp|P00360	35750,2	59%	DIEVVAVNDPFISNDYAAYMVK-eLDTAQK-HIIIDGVK-IATYQER-IATYQERDPANLPWGSLK-IDVAVDSTGVFK-IVSNAScTTNcLAPLAK-LISWYDNEYGYSAR-LTGmAFR-TASGNIIPSSTGAAK-VINDAFGIEEGLMTTVHSmTA		15	0	15
no tap	Seventh homolog of septin 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SHS1 PE=1 SV=1	sp|Q07657	62632,3	9%	LEELEAQSAK-LSSVANAEEIGPNSTK-TAFANNLLETK-YTNVLPIITR		4	0	4
no tap	External NADH-ubiquinone oxidoreductase 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NDE1 PE=1 SV=1	sp|P40215	62776,5	4%	AIADLAVGEAK-KVDATTITAK		2	0	2
no tap	Nascent polypeptide-associated complex subunit beta-1 OS=Saccharomyces cerevisiae (strain YJM789) GN=EGD1 PE=3 SV=1	sp|A6ZWL1,sp|Q02642	17020,5	13%	VGVQVAAQHNTSVFYGLPQEK		1	0	1
no tap	Ribosome-interacting GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RBG1 PE=1 SV=1	sp|P39729	40702,5	4%	GQIPDFTDPVVLR		1	0	1
no tap	40S ribosomal protein S12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS12 PE=1 SV=1	sp|P48589	15470,9	47%	GEALLVVLVSSVTEANIIK-KVVGASVVVVK-LVEGLANDPENK-LVEGLANDPENKVPLIK-QLGEWAGLGK-TALVHDGLAR		6	0	6
no tap	(DL)-glycerol-3-phosphatase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RHR2 PE=1 SV=3	sp|P41277	27948,2	6%	VVVFEDAPAGIAAGK		1	0	1
no tap	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Saccharomyces cerevisiae (strain AT	sp|P12695	51819,7	22%	ADIESYLEK-ADVPAFK-DIPVNKPIAVYVEDK-GLSQISNEIK-IFASPLAK-ILVPEGTK-LLQSTQGIPSYIVSSK-LSINDLLVK-TIALEK-VPDANAYWLPNENVIR		10	0	10
no tap	Glucose-6-phosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PGI1 PE=1 SV=3	sp|P12709	61300,4	6%	LIPSDFILAAQSHNPIENK-TFTTAETITNANTAK		2	0	2
no tap	40S ribosomal protein S13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS13 PE=1 SV=3	sp|P05756	17029,8	51%	GISSSAIPYSR-GLTPSQIGVLLR-KGLTPSQIGVLLR-LILIESR-lSSESVIEQIVK-NAPAWFK-SNGLAPEIPEDLYYLIK-TVAVLPPNWK		8	0	8
no tap	Ribosomal RNA small subunit methyltransferase NEP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EMG1 PE=1 SV=1	sp|Q06287	27896,2	4%	GILIEVNPTVR		1	0	1
no tap	40S ribosomal protein S1-A OS=Saccharomyces cerevisiae (strain YJM789) GN=RPS1A PE=3 SV=1	sp|A7A1W1,sp|B3RHV0,sp|B5VNY0	28743,8	57%	APSTFENR-DIFPLQNIHVR-EVQGSTLAQLTSK-FDVGALmALHGEGSGEEK-HSYAQSSHIR-IFAIAFTR-LIPEVINK-LRVDEVQGK-NLLTNFHGmDFTTDK-TSDDYVLR-VISEILTK-VTGFKDEVLETV-VVEVcLADLQGSEDHSFR		13	10	3
no tap	Heat shock protein 26 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP26 PE=1 SV=3	sp|P15992	23880,2	23%	LLGEGGLR-NQILVSGEIPSTLNEESK-VITLPDYPGVDADNIK-VVVPGVK		4	0	4
no tap	60S ribosomal protein L16-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL16B PE=1 SV=3	sp|P26785	22249,9	42%	AEALNISGEFFR-GPFHFR-IFEGIPPPYDK-LSTSVGWK-sQPVVVIDAK-VSSASAAASESDVAK-VVVPQALR-YEDVVAK-YTTLGK		9	0	9
no tap	Keratin 6A - Homo sapiens	sp|A4QPC1,sp|A8K2I0,sp|P02538,sp|	60046,4	7%	AQYEEIAQR-FASFIDK-NLDLDSIIAEVK-YEELQVTAGR		4	3	1
no tap	Inorganic pyrophosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IPP1 PE=1 SV=4	sp|P00817	32301,1	13%	ATNEWFR-GIDLTNVTLPDTPTYSK-VIAIDINDPLAPK		3	0	3
no tap	Cell division control protein 11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC11 PE=1 SV=1	sp|P32458	47650,7	15%	NALLISHLHDLK-NYTHEILYER-QLGSLVNIIPVISK-TEALSGESVAAESIRPNLTK-VQQELLLK		5	0	5
no tap	Nucleolar protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NPL3 PE=1 SV=1	sp|Q01560	45407,3	7%	ENSLETTFSSVNTR-SFANQPLEVVYSK		2	0	2
no tap	Elongation factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EFT1 PE=1 SV=1	sp|P32324	93290,3	19%	ADLMLYVSK-ALLELQVSK-EDLYQTFAR-EGPIFGEEMR-ETVESESSQTALSK-GQVVSEEQRPGTPLFTVK-IKPVVVINK-IQGPNYVPGK-ISPPVVAYR-LFTAIMNFK-NMSVIAHVDHGK-STLTDSLVQR-TGTLTTSETAHNMK-VA		15	0	15
no tap	60S ribosomal protein L9-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL9A PE=1 SV=2	sp|P05738	21568,8	11%	HIDVTFTK-SLVDNmITGVTK		2	0	2
no tap	Protein URA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=URA2 PE=1 SV=5	sp|P07259	245044,8	1%	VVGVNLIELATK		1	0	1
no tap	Mitochondrial outer membrane protein porin 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=POR1 PE=1 SV=4	sp|P04840	30429,5	65%	DFYHATPAAFDVQTTTANGIK-DGPLSTNVEAK-GAFDLcLK-LEFANLTPGLK-LPNSNVNIEFATR-NELITSLTPGVAK-NINDLLNK-QLLRPGVTLGVGSSFDALK-QPVKDGPLSTNVEAK-QTGLGLTQGWSNTNNLQTK-SAVLNTT		15	0	15
no tap	Transposon Ty1-NL2 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-NL2 PE=3 SV=1	sp|Q99337	198206,1	6%	AHNVSTSNNSPSTDNDSISK-DILSVDYTDImK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-STTEPIQLNNK-TVDTTNYVILQGK-VAcQLIMR-VTNIIDR		8	8	0
no tap	ATP-dependent molecular chaperone HSC82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSC82 PE=1 SV=4	sp|P15108	80903,4	26%	AELINNLGTIAK-AILFIPK-APFDLFESK-ELISNASDALDK-GVVDSEDLPLNLSR-HSEFVAYPIQLLVTK-KTFEISPK-LGVHEDTQNR-LLDAPAAIR-NIYYITGESLK-NPSDITQEEYNAFYK-QLETEPDLFIR-RAPFDLFESK-SISNDW		19	18	1
no tap	RNA polymerase II degradation factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DEF1 PE=1 SV=1	sp|P35732	83968,3	3%	QIEQPSLSSK-TESPLENVAELKK		2	0	2
wt	Trypsin precursor - Sus scrofa	sp|P00761	24409,3	29%	APVLSDSScK-IITHPNFNGNTLDNDImLIK-LGEHNIDVLEGNEQFINAAK-LSSPATLNSR-VATVSLPR	c9: Carbamidome	5	0	5
wt	Zuotin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ZUO1 PE=1 SV=1	sp|P32527	49021,5	17%	AFETLTDSNK-AFETLTDSNKR-ATESQIIK-KTPIPSLGNK-LPSSLLSYFV-NHTWSEFER-QSAAGGSLDQDGFFK-TADLYAAMGLSK-TPIPSLGNK		9	0	9
wt	40S ribosomal protein S14-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS14B PE=1 SV=2	sp|P39516	14649,8	70%	ADRDESSPYAAmLAAQDVAAK-ANDLVQAR-cKEVGITAVHVK-DESSPYAAmLAAQDVAAK-DNSQVFGVAR-EVGITAVHVK-IEDVTPVPSDSTR-IEDVTPVPSDSTRK-IYASFNDTFVHVTDLSGK-TKTPGPGGQ	m12: Oxidation (	11	0	11
wt	Protein BMH2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BMH2 PE=1 SV=3	sp|P34730	31061,7	37%	ATNSSLEAYK-AVASSGQELSVEER-DSTLIMQLLR-ISDDILSVLDSHLIPSATTGESK-IVSSIEQK-TASEIATTELPPTHPIR-YEEMVENMK-YLAEFSSGDAR		8	6	2
wt	Pre-mRNA-splicing factor CWC25 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CWC25 PE=1 SV=1	sp|P53854	20375,9	25%	AATTISASGAATSISSQK-ELNELLNESSK-KLDSSILNQPATPPVR-LDSSILNQPATPPVR		4	0	4
wt	Eukaryotic translation initiation factor 5A-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HYP2 PE=1 SV=3	sp|P23301	17114,6	12%	KLEDLSPSTHNMEVPVVK		1	0	1
wt	Heterogeneous nuclear rnp K-like protein 2 OS=Saccharomyces cerevisiae (strain YJM789) GN=HEK2 PE=3 SV=1	sp|A6ZKR5,sp|B3LNH0,sp|C7GND0,	41684,6	8%	LIVANSHISSIIGK-SSGEPTSPSTSSNTR		2	0	2
wt	Branched-chain-amino-acid aminotransferase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BAT2 PE=1 SV=1	sp|P47176	41626	5%	ELVTAPLDGTILEGVTR		1	0	1
wt	37S ribosomal protein S9, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRPS9 PE=1 SV=1	sp|P38120	31927	4%	ALVVFNPLLK		1	0	1
wt	DNA-directed RNA polymerase II subunit RPB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB2 PE=1 SV=2	sp|P08518	138757,2	12%	AGVSQVLNR-EFLPHITQLEGFESR-FISTLQVK-HGTYDKLDDDGLIAPGVR-IPQIGDK-MTVAHLIEcLLSK-QDIPIVIIFR-SAGNIVQVFK-VAALSGNEGDASPFTDITVEGISK-VSGEDVIIGK-YALATGNWGEQK-YGMSITETFEKP		12	0	12
wt	Chromatin structure-remodeling complex subunit RSC7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NPL6 PE=1 SV=1	sp|P32832	49651,9	11%	AITEQQNFEK-FNSDLFYDR-ITADGDLLGGR-QIALVTAR-VLLVDQQGLR		5	0	5
wt	54S ribosomal protein L11, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRPL11 PE=1 SV=2	sp|P36521	28515,7	4%	VENEVLNVEK		1	0	1
wt	DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB5 PE=1 SV=1	sp|P20434	25079,6	5%	ADPVALYLGLK		1	0	1
wt	Protein FAF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FAF1 PE=1 SV=1	sp|P40546	38890,9	3%	ISGGERSGK		1	0	1
wt	Adenosylhomocysteinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SAH1 PE=1 SV=1	sp|P39954	49125,8	3%	VAVVAGYGDVGK		1	0	1
wt	Chromatin structure-remodeling complex protein RSC3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC3 PE=1 SV=1	sp|Q06639	101727	1%	LQLLNAQNQLNNR		1	0	1
wt	30 kDa heat shock protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP30 PE=1 SV=1	sp|P25619	37045,8	8%	NEALGLNPPHGLDmHITK-SITGEVPGIR	m14: Oxidation (	2	0	2
wt	40S ribosomal protein S6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS6A PE=1 SV=1	sp|P0CX37,sp|P0CX38	26997,2	33%	EAAAEYAQLLAK-FFGLSK-GAIVGPDLAVLALVIVK-KGEQELEGLTDTTVPK-LNISYPVNGSQK-QGVLLPTR-VFFDKR		7	0	7
wt	RNA polymerase II degradation factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DEF1 PE=1 SV=1	sp|P35732	83968,3	19%	EQQHSYVPQQHLPNPEDDITYK-HDVPQDSNDNNNEELEAQGQQAQEK-HVPSKPVSNTTSWAAAVSVDTK-KTESPLENVAELK-NNYNYYQTQNGQEQQSPNQGVAQHSEDSQQK-QIEQPSLSSK-TESPLENVAELKK-VPEVDGE		8	0	8
wt	40S ribosomal protein S21-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS21B PE=1 SV=1	sp|Q3E754	9760	61%	ADDHASVQINVAK-AIPGEYITYALSGYVR-GQLVELYVPR-LAQNDGLLK-mENDKGQLVELYVPR		5	0	5
wt	60S ribosomal protein L18-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL18A PE=1 SV=1	sp|P0CX49,sp|P0CX50	20563,7	31%	AGGEcITLDQLAVR-ALFLSK-GQNTLILR-INRPPVSVSR-SDNVYLK-TVVVVGTVTDDAR	c5: Carbamidome	6	0	6
wt	Casein kinase II subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CKA1 PE=1 SV=1	sp|P15790	44669,8	5%	ILTDLSNEK-VLGTSDFEK		2	0	2
wt	Dolichol-phosphate mannosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DPM1 PE=1 SV=3	sp|P14020	30363,4	4%	VIIQYLQQLK		1	0	1
wt	60S ribosomal protein L21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL21A PE=1 SV=1	sp|Q02753	18242	46%	AQGVAVQLK-HGAVHLSTYLK-IVSTEGNVPQTLAPVPYETFI-QEFLER-SSVGVIINK-TGVVYNVTK-VGDIVDIK		7	0	7
wt	Pre-mRNA-splicing factor CLF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CLF1 PE=1 SV=1	sp|Q12309	82449,1	2%	ALLVDSSFIPLWIR		1	0	1

wt	Nucleoporin NUP53 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP53 PE=1 SV=1	sp|Q03790	52621,2	3%	TTPNTASSEASAGSK		1	0	1
wt	60S ribosomal protein L23-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL23A PE=1 SV=1	sp|P0CX41,sp|P0CX42	14473,1	43%	EcADLWPR-ISLGLPVGAIMNcADNSGAR-LPAASLGDMVMATVK-NLYIIAVK-VMPAIVVR	c2: Carbamidome	5	0	5
wt	Chromatin structure-remodeling complex protein RSC6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC6 PE=1 SV=1	sp|P25632	54166,9	11%	IYVYNTTESSPR-LALQLNSSAQK-TSDIYSNNNNDR-VLDTNAAHLPLMNVVQTVNK		4	0	4
wt	Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NDI1 PE=1	sp|P32340	57252,8	3%	STGVENSGAGPTSFK		1	0	1
wt	Protein transport protein SEC61 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEC61 PE=1 SV=1	sp|P32915	52940,2	6%	AFAPTTVNSGR-GQIGIYPIK-TWIEISGTSPR		3	0	3
wt	Pyruvate decarboxylase isozyme 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDC1 PE=1 SV=7	sp|P06169	61496,9	59%	AQYNEIQGWDHLSLLPTFGAK-EVIDTILALVK-GYKPVAVPAR-IYEVEGmR-KLIDLTQFPAFVTPmGK-LIDLTQFPAFVTPmGK-LLQTPIDMSLKPNDAESEK-LLTTIADAAK-ITAATNAK-mIEIMLPVFDAPQNLVEQAK-mSANISE		24	0	24
wt	6-phosphogluconate dehydrogenase, decarboxylating 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GND1 PE=1 SV=1	sp|P38720	53545,3	2%	LPANLLQAQR		1	0	1
wt	26S proteasome regulatory subunit RPN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPN1 PE=1 SV=3	sp|P38764	109495,7	2%	VGQAVETVGQAGRPK		1	0	1
wt	Protein MUK1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MUK1 PE=1 SV=1	sp|Q02866	69542,6	2%	TFKPHQLQTFK		1	0	1
wt	Nucleolar protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOP12 PE=1 SV=1	sp|Q08208	51943,8	8%	ATLGQEITIEGLR-SISFDEALPR-TDETSVPLTSAAK		3	0	3
wt	Tyrosine-protein phosphatase CDC14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC14 PE=1 SV=2	sp|Q00684	61908,2	2%	SSAVPQTSPGQPR		1	0	1
wt	Imidazoleglycerol-phosphate dehydratase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HIS3 PE=1 SV=2	sp|P06633	23833,2	7%	ALAVAIR-ITLHVDcLR		2	0	2
wt	Bromodomain-containing factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BDF1 PE=1 SV=3	sp|P35817	76980,8	1%	LEEVFNSK		1	0	1
wt	Uncharacterized RNA-binding protein YGR250C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YGR250C PE=1 SV=1	sp|P53316	89515,3	40%	AILNTDGYQVSK-cLFIGNLPYHNPEK-DIYLYEHGSQEYEK-DQVLSVSFAQK-EVIEVIKK-FINALMTQNQSQQQVSR-GISVNNSDTETYEFLPDTR-GYGFVSFESPLDAAK-HALTYPGNIFVGGIAK-HIPLSWTDEDLYDFYK-ITDQ		26	0	26
wt	Nuclear segregation protein BFR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BFR1 PE=1 SV=1	sp|P38934	54641,7	46%	ADFDNEFK-DELYSQIR-DLVNIEPIR-DLVNIEPIRK-DVSNQFEENQQK-EELNGLNPK-FKRPDVSVR-IDTEIGLIR-INEIEESIASGDLSLVQEK-INQLKEELNGLNPK-IQADLK-ITVEQLK-KDDFVNVAPSK-KIDTEIGLIR-KLDTLNV		29	0	29
wt	Suppressor protein SRP40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SRP40 PE=1 SV=2	sp|P32583	41016,5	3%	GGSITLESGSYK		1	0	1
wt	Chromatin structure-remodeling complex protein RSC14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LDB7 PE=1 SV=2	sp|P38210	19792	26%	SSQVVFSATELQQLTQQSHATDK-VSLADAAQVEYEVGHSLLGSYVPR		2	0	2
wt	Pre-mRNA-splicing factor CWC21 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CWC21 PE=1 SV=1	sp|Q03375	15762,4	21%	EIEVQVSELR-LTNEWQEQQR-mSSLYTPR		3	0	3
wt	40S ribosomal protein S21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS21A PE=1 SV=1	sp|P0C0V8	9745,9	61%	ADDHASVQINVAK-AIPGEYVTYALSGYVR-GQLVELYVPR-LAQNDGLLK-mENDKGQLVELYVPR		5	4	1
wt	U3 small nucleolar RNA-associated protein 22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UTP22 PE=1 SV=1	sp|P53254	140492,9	3%	FITLENFLAHK-ILLHGFSSYQLFK-TLENISHSYQFYSPVVR		3	0	3
wt	Endoplasmic reticulum transmembrane protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YET1 PE=1 SV=2	sp|P35723	23460,7	12%	GIFSTYNQLTAK-NQPGNVAAAEASK		2	0	2
wt	Trehalose synthase complex regulatory subunit TSL1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TSL1 PE=1 SV=1	sp|P38427	123021,7	1%	LVNDEASEGQVK		1	0	1
wt	Keratin 6A - Homo sapiens	sp|A4QPC1,sp|A8K2I0,sp|P02538,sp|	60046,4	13%	AQYEEIAQR-FASFIDK-FLEQQNK-ISIGGGScAISGGYGSR-QNLEPLFEQYINNLR-YEDEINKR-YEELQVTAGR		7	3	4
wt	Elongator complex protein 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ELP6 PE=1 SV=1	sp|Q04868	30574,6	14%	DKILSDVLAK-DVTGSLHVcR-FITPLLR-ILSDVLAK-SmINLNLNPLK		5	0	5
wt	40S ribosomal protein S2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS2 PE=1 SV=3	sp|P25443	27450,2	30%	AGIIIAK-AVVVVGDSNGHVGLGIK-GSGIVASPAVK-ITTIEEIFLHSLPVK-KLLQLAGVEDVYTQSNGK-LLQLAGVEDVYTQSNGK-LSVIPIR		7	0	7
wt	D-arabinose dehydrogenase [NAD(P)+] heavy chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARA1 PE=1 SV=1	sp|P38115	38885,2	4%	IPALGLGTANPHEK		1	0	1
wt	Glyoxylate reductase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GOR1 PE=1 SV=1	sp|P53839	38831,5	4%	IADVITIPESTTR		1	0	1
wt	60S ribosomal protein L15-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL15A PE=1 SV=3	sp|P05748	24422,6	36%	GATYGKPTNQGVNELK-QGFVIYR-QNTLSLWR-VLNSYWVNQDSTYK-YFEVILVDPQHK-YLEELQR-YNWIcDPVHK		7	0	7
wt	UPF0136 membrane protein YJR085C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YJR085C PE=1 SV=1	sp|P47131	11250,9	22%	FTKPVPVVLTALGGLGSYYYYNK		1	0	1
wt	DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB8 PE=1 SV=1	sp|P20436	16512,1	14%	IEAASTTQDQcK-QENAYLLIR	c11: Carbamidon	2	0	2
wt	Peroxiredoxin type-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AHP1 PE=1 SV=4	sp|P38013	19114,4	49%	ETNPGTDVTVSSVESVLAHL-FASDPGcAFTK-FPAGDYK-FQYIAISQSDADSEScK-mPQTVEWSK-sDLVNKK-WAMVVENGIVTYAAK		7	0	7
wt	Cop9 signalosome complex subunit 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CSN12 PE=1 SV=1	sp|P47130	49484,4	4%	YILQRPTATDEESVR		1	0	1
wt	6-phosphofructokinase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PFK1 PE=1 SV=1	sp|P16861	107972,8	18%	AEVAALAAENK-AQSQGALLK-ASSDASDLLR-AVLEFTPETPSPLIGILENK-DDGSELLPVSDR-GWLSEGGTLIGTAR-HGENSLLSSGTSQDSLR-LNIGIVHVGAPSAALNAATR-LSDTLVFLK-LSEVDASGFR-SVATAIENK-TAIPG		14	0	14
wt	Nucleoporin NSP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NSP1 PE=1 SV=1	sp|P14907	86519,4	3%	DSGSSKPAFSFGAKPDEK-IDQSLQYIER		2	0	2
wt	Uncharacterized protein YEL043W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YEL043W PE=1 SV=1	sp|P32618	106138	1%	EIESLQNEISK		1	0	1
wt	Adenine phosphoribosyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=APT1 PE=1 SV=3	sp|P49435	20588,2	7%	LNAPVFTLLNAQK		1	0	1
wt	U1 small nuclear ribonucleoprotein C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YHC1 PE=1 SV=1	sp|Q05900	27045,8	27%	ELAQTSIDTLK-FDIGDLVK-ILSQWSNTIPK-ITADYYR-LLYDGSPGYSK-TSIFYSVDILQTTIK		6	0	6
wt	NADPH-dependent aldose reductase GRE3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GRE3 PE=1 SV=1	sp|P38715	37120,2	19%	DISALNANIR-FTLTEQELK-LLGNLEIEK-SIGVSNFQGSLIQDLLR-VSQNHPGSTTSQVLLR		5	0	5
wt	Succinyl-CoA ligase [ADP-forming] subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LSC1 PE=1 SV=	sp|P53598	35033,5	3%	AEIEAAQFLK		1	0	1
wt	Vacuolar import and degradation protein 22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VID22 PE=1 SV=1	sp|Q05934	102505,8	1%	LIAPFETFLSK		1	0	1
wt	Nicotinamidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PNC1 PE=1 SV=1	sp|P53184	24993,4	15%	ATAISAAELGYK-TTVLLDYTRPISDDPEVINK		2	0	2
wt	Enhancer of mRNA-decapping protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EDC3 PE=1 SV=1	sp|P39998	61341,7	2%	SNSTSLPAANK		1	0	1
wt	Eukaryotic translation initiation factor 2 subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SUI3 PE=1 SV=2	sp|P09064	31575,7	20%	AGLDNVDAESK-sSDLAAELGFDPALK-TGFQATVGK-TIFSNIQDIAEK-TNNPELAGDR		5	0	5
wt	Eukaryotic translation initiation factor 2 subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GCD11 PE=1 SV=1	sp|P32481	57867,2	38%	AISGVQTVR-EFEEGGGLPEQPLNPDFSK-FAVPGGLIGVGTK-GTIADGAPIVPISAQLK-HVIILQNK-IQcKPIFSNIVSLFAEQNDLK-KLEPNEVLMVNIGSTATGAR-LGDEIEIRPGIVTK-LNPLSAEIINR-LQLTSPAcTEINEK-LVGQV		14	0	14
wt	Mitochondrial inner membrane i-AAA protease complex subunit MGR1 OS=Saccharomyces cerevisiae (strain YJM789) GN=MGR1 PE=3 SV=1	sp|A6ZTE8,sp|P25573	47030,6	4%	TPTSTDQPLPGPTPK		1	0	1
wt	Replication factor A protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RFA2 PE=1 SV=1	sp|P26754	29936,1	4%	VNTLTPVTIK		1	0	1
wt	Mitochondrial acidic protein MAM33 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MAM33 PE=1 SV=1	sp|P40513	30132,7	10%	FSLVETPGKNEAEIVR-VGDILQSELK		2	0	2
wt	Inorganic pyrophosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IPP1 PE=1 SV=4	sp|P00817	32301,1	12%	EETLNPIIQDTK-LNDIEDVEK-VIAIDINDPLAPK		3	0	3
wt	Pre-mRNA-splicing factor CEF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CEF1 PE=1 SV=1	sp|Q03654	67732,9	4%	AALGESTTLTDEYK-VESIEQLQR		2	0	2
wt	Adenosine kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADO1 PE=1 SV=1	sp|P47143	36372,9	9%	LVAGGAAQNTAR-TVIFTHGVEPTVVVSSK		2	0	2
wt	Transposon Ty1-DR5 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-DR5 PE=1 SV=1	sp|P0C2I2,sp|Q03855	198534,8	20%	AHNVSTSNNSPSTDNDSISK-AVSPTDSTPPSTHTEDSKR-DILSVDYTDImK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-GIPGYALHPSR-KYPYPFIHR-KYVRPPPMLTSPNDFPNWVK-LIGLASYVGYK-LNNNGIHINN		25	24	1
wt	NET1-associated nuclear protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAN1 PE=1 SV=1	sp|Q02931	101241,4	4%	LANVFHSEGNYR-TTLNAINLLR-VINPHGISVPITK		3	0	3
wt	Ribosomal RNA small subunit methyltransferase NEP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EMG1 PE=1 SV=1	sp|Q06287	27896,2	15%	ALPASLVPQAPPVLTSK-GILIEVNPTVR-LQVYIQTSR		3	0	3
wt	Nucleoporin POM152 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=POM152 PE=1 SV=1	sp|P39685	151659,4	18%	AIFDGNYGESDIHFR-DSTGcVVGLSQPDAK-EGLYQLVDIR-EHQSELIIK-ELSVTGSAINHHR-FLQGESPFSITFSVYHESTSR-FQNSYKPALK-HGSVTEIPLK-INSIDVPIR-IVNGQTFSYVDSSLQPEYFESPLQSSK-KVDIYSLPLIST		19	0	19
wt	60S ribosomal protein L17-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL17B PE=1 SV=2	sp|P46990	20551,6	40%	FNSSIGR-FVQGLLQNAAANAEAK-INKYESSPSHIELVVTEK-LYVSHIQVNQAPK-YESSPSHIELVVTEK-YGATSTNPAK-YLDQVLDHQR		7	0	7
wt	Protein SOF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SOF1 PE=1 SV=1	sp|P33750	56790,2	8%	NLNPELHPFER-NSSDNDSVTNEEGLIR-YIISGSDDGNVR		3	0	3
wt	60S ribosomal protein L6-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL6B PE=1 SV=4	sp|P05739	19986,9	55%	ALLAEIK-ALLAEIKK-ASLVPGTVLILLAGR-EANLFPEQQTK-FNVEYFAK-HLEDNTLLVTGPFK-KEANLFPEQQTK-QYLSASFSLK-VSVEGVNVEK-WYPSEDVAAPK-YVIATSTK		11	0	11
wt	Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDA1 PE=1 S	sp|P16387	46344,4	40%	ATLLQMYK-AVLAELMGR-DmVIIR-GFcHLSVGQEAIAVGIENAITK-GPLVLEYETYR-GTETPTLR-KYVDEQVELADAAPPPEAK-LDSIITSYR-lSILFEDVYVK-RGQYIPGLK-SSAmTEYFK-TRDEIQHMR-VNGMDILAVYQASK-		16	0	16
wt	ISWI one complex protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IOC2 PE=1 SV=1	sp|Q12072	93448,8	1%	QFDIIYSIIK		1	0	1
wt	Pre-mRNA-splicing factor 38 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP38 PE=1 SV=1	sp|Q00723	27967,7	4%	VNLSNESLR		1	0	1
wt	UBP3-associated protein BRE5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BRE5 PE=1 SV=1	sp|P53741	57675,1	12%	EAETEIKPIEPQVSDAK-IHTETVPSSTK-LAYFYASTAELTHTNYQSK-STNEKDDVLPTVK		4	0	4
wt	Uncharacterized protein YCR016W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YCR016W PE=1 SV=2	sp|P25617	33594,6	8%	GQSNLIDDDPLNITTHLSTGNLTK		1	0	1
wt	Ribonucleoside-diphosphate reductase small chain 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RNR4 PE=1 SV=1	sp|P49723	40056,8	3%	IITEAVEIEK		1	0	1
wt	Transcription initiation factor TFIID subunit 14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF14 PE=1 SV=1	sp|P35189	27440,7	20%	SGSTEETTANTGTIGK-TQQHILPEVPPVENFPVR-VIYHLHPTFANPNR		3	0	3
wt	Pentafunctional AROM polypeptide OS=Saccharomyces cerevisiae (strain YJM789) GN=ARO1 PE=3 SV=1	sp|A6ZY89,sp|B3LGE9,sp|C7GIN5,sp	174810,3	1%	YFGILSPTQVAR		1	0	1
wt	Pre-mRNA-splicing factor PRP11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP11 PE=1 SV=1	sp|Q07350	29921,2	4%	IVSGLELSDTK		1	0	1
wt	U6 snRNA-associated Sm-like protein LSm8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LSM8 PE=1 SV=2	sp|P47093	12386,1	11%	NTNLFITNVFNR		1	0	1
wt	Transcription initiation factor TFIID subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF1 PE=1 SV=1	sp|P46677	120701,7	1%	LPVGETHVLGVQDK		1	0	1
wt	1,3-beta-glucan synthase component FKS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FKS1 PE=1 SV=2	sp|P38631,sp|P40989	214859,4	1%	VQLSGNPILGDGK		1	0	1
wt	Alcohol dehydrogenase 3, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADH3 PE=1 SV=2	sp|P07246	40369,8	6%	DIPVPEPKPNEILINVK-YVVDTSK		2	1	1
wt	Thioredoxin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TRX2 PE=1 SV=3	sp|P22803	11203,8	34%	AEVSSmPTLIFYK-FAEQYSDAAFYK-VVGANPAAIK	m6: Oxidation (+	3	0	3
wt	Ferrochelatase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HEM15 PE=1 SV=1	sp|P16622	44597,7	5%	SHLQSNQLYSNQLPLDFALGK		1	0	1
wt	DNA-directed RNA polymerase I subunit RPA12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA12 PE=1 SV=1	sp|P32529	13660,6	12%	VVTTTADDAFPSSLR		1	0	1
wt	Nuclear and cytoplasmic polyadenylated RNA-binding protein PUB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PUB1 PE=1 S	sp|P32588	50762	7%	QIENNIVK-QYFQVGGPIANIK-VLYVGNLDK		3	0	3
wt	60S ribosomal protein L6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL6A PE=1 SV=2	sp|Q02326	19962,1	48%	ALIAEIK-ALIAEIKK-ASLVPGTVLILLAGR-EANLFPEQQNK-FNVEYFAK-HLEDNTLLISGPFK-QYLSASFSLK-VSVEGVNVEK-YVIATSTK		9	7	2
wt	60S ribosomal protein L1-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL1A PE=1 SV=1	sp|P0CX43,sp|P0CX44	24486,3	48%	FPTPVSHNDDLYGK-KYNAFIASEVLIK-LLGPQLSK-LPNcPRPNmSIcIFGDAFDVDR-NFLETVELQVGLK-NWQNVGSLVVK-ScGVDAMSVDDLKK-SSmGPAFR-YNAFIASEVLIK		9	0	9
wt	Small nuclear ribonucleoprotein Sm D3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMD3 PE=1 SV=1	sp|P43321	11224,3	62%	DVIATEPQGAVTHMDQIFVR-FIVVPDLLK-LLNEAQGHIVSLELTTGATYR-LVESEDSmNVQLR		4	0	4
wt	Protein CAF40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CAF40 PE=1 SV=1	sp|P53829	41156,3	3%	LTSLGVIGALVK		1	0	1
wt	Cell division control protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC3 PE=1 SV=3	sp|P32457	60056,2	7%	QLELSINSASPNVNHSPVPTK-VEPGLGmGITSSQSEK		2	0	2
wt	60S ribosomal protein L12-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL12A PE=1 SV=1	sp|P0CX53,sp|P0CX54	17823,2	47%	AVGGEVGASAALAPK-EILGTAQSVGcR-HSGNIQLDEIIEIAR-IGPLGLSPK-QAAASVVPSASSLVITALK-VGEDIAK		6	0	6
wt	Heat shock protein homolog SSE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSE1 PE=1 SV=4	sp|P32589	77368,6	15%	GAAFIcAIHSPTLR-GIDIVVNEVSNR-IAGLNPVR-QSISEAFGKPLSTTLNQDEAIAK-sTPFGLDLGNNNSVLAVAR-STPSVVGFGPK-YEELASLGNIIR-YNIADAAR	c6: Carbamidome	8	0	8
wt	Heat shock protein SSB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSB1 PE=1 SV=3	sp|P11484	66602,8	56%	AADEAFAK-ARFEDLNAALFK-AVITVPAYFNDAQR-DAGAISGLNVLR-ENTLLGEFDLK-FDDESVQK-FEDLNAALFK-IEAALSDALAALQIEDPSADELR-IEAALSDALAALQIEDPSADELRK-IINEPTAAAIAYGLGAGK-KTGLD		31	0	31
wt	DNA-directed RNA polymerases I, II, and III subunit RPABC2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPO26 PE=1 SV=1	sp|P20435	17910,4	27%	ALQISmNAPVFVDLEGETDPLR-TIVTGGNGPEDFQQHEQIR	m6: Oxidation (+	2	0	2
wt	Nuclear polyadenylated RNA-binding protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HRP1 PE=1 SV=1	sp|Q99383	59650,6	2%	IFVGGIGPDVRPK		1	0	1
wt	Elongation factor 1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EFB1 PE=1 SV=4	sp|P32471	22627,5	10%	AFQSAYPEFSR-QLNASLADK		2	0	2
wt	40S ribosomal protein S30-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS30A PE=1 SV=1	sp|P0CX33,sp|P0CX34	7118,5	18%	FVNVTLVNGK-RFVNVTLVNGK		2	0	2
wt	Saccharopepsin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PEP4 PE=1 SV=1	sp|P07267	44501	8%	FDGILGLGYDTISVDK-VVPPFYNAIQQDLLDEKR		2	0	2
wt	PAB-dependent poly(A)-specific ribonuclease subunit PAN2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PAN2 PE=1 SV=1	sp|P53010	127045,6	1%	LLPSLSISGINK		1	0	1
wt	40S ribosomal protein S24-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS24A PE=1 SV=1	sp|P0CX31,sp|P0CX32	15329	45%	ANVSKDELR-DAVSVFGFR-KQFVVDVLHPNR-KVISNPLLAR-LAEVYK-QFVVDVLHPNR-SVGFGLVYNSVAEAK-VISNPLLAR		8	0	8
wt	40S ribosomal protein S7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS7A PE=1 SV=4	sp|P26786	21622,7	62%	AELRPLQFK-ALAIFVPVPSLAGFHK-DVQQIDYK-HVIFLAER-ILEDLVFPTEIVGK-ILPKPSR-ILSQAPTELELQVAQAFVELENSSPELK-LESFQAVYNK-QIVFEIPSETH-YLVGGNK		10	0	10
wt	T-complex protein 1 subunit epsilon OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CCT5 PE=1 SV=3	sp|P40413	61916,5	2%	IYEQEFGTTK		1	0	1
wt	ATP synthase subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ATP1 PE=1 SV=5	sp|P07251	58609,4	15%	AQPTEVSSILEER-GPIDAAGR-IGEFESSFLSYLK-TAVALDTILNQK-TGNIVDVPVGPGLLGR-VLAVGDGIAR-VVDALGNPIDGK		7	0	7
wt	Proteasome component PUP3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PUP3 PE=1 SV=1	sp|P25451	22605,7	17%	AIEPETFTQLVSSSLYER-FGPYFVGPVVAGINSK		2	0	2
wt	FACT complex subunit POB3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=POB3 PE=1 SV=1	sp|Q04636	62995,2	31%	ADDIHHLLVLAIEPPLR-EEQQLLEQFLK-GSTTFANISK-GSTTFANISKEEQQLLEQFLK-INNTNLTSK-ISTSGGSAANQAR-IVSLPK-KEESSNEVVPK-KPFLLPATELSTVQWSR-NQGVIQLDGFSQDDYNLIK-QGQTTYPFLVLQFQ		16	0	16
wt	Thioredoxin reductase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TRR1 PE=1 SV=3	sp|P29509,sp|P38816	34239,2	6%	VTIIGSGPAAHTAAIYLAR		1	0	1
wt	ATP-dependent helicase NAM7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAM7 PE=1 SV=1	sp|P30771	109432,6	16%	ANEQQAIGFLR-ILVcAPSNVAVDHLAAK-LITPSQISK-LPNSFQDTFTLELKPSK-NANWDTDQWQPLIEDR-NLYQEEASHLNSNFAR-QVILVGDHQQLGPVILER-SEAVVVLLcR-TPPPTHLTTGFTAEFIWK-VEVASVDAFQGR-YGL		11	0	11
wt	Carboxypeptidase S OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CPS1 PE=1 SV=2	sp|P27614	64599,3	2%	FVGSIIDIDLLK		1	0	1
wt	60S ribosomal protein L43-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL43A PE=1 SV=1	sp|P0CX25,sp|P0CX26	10090,8	29%	KLEIQQHAR-TVAGGAYTVSTAAAATVR		2	0	2
wt	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VIP1 PE	sp|Q06685	129761,4	3%	LDIGLLTSLPLAK-VLFDFIcPK-YITELSDEEK		3	0	3
wt	Mitochondrial DNA replication protein YHM2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YHM2 PE=1 SV=1	sp|Q04013	34185,2	27%	IGASALGGGLSAWNQPIEVIR-LVEDGIR-MTGETPVAK-NFTFLESVK-PSTTNTAAANVIEK-QmTNWGSR-SASAGGVPQSSWSVFK		7	0	7
wt	mRNA transport regulator MTR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MTR2 PE=1 SV=1	sp|P34232	20783,9	17%	LAQFVQLFNPNNcR-mGQDATVPIQPNNTGNR	c13: Carbamidon	2	0	2
wt	60S ribosomal protein L13-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL13B PE=1 SV=1	sp|P40212	22525,5	49%	AAGLTAAYAR-APEAEQVLSAAATFPIAQPATDVEAR-AVQDNGESAFR-DGKAPEAEQVLSAAATFPIAQPATDVEAR-GFTLAEVK-IIVFPR-NLPILK-NQEIFDANVQR-TIGIAVDHR-VHFDQAGK		10	0	10
wt	Transcription elongation factor SPT6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPT6 PE=1 SV=1	sp|P23615	168298,5	1%	ATDNNYYASALK-VLIVDNQK		2	0	2
wt	U1 small nuclear ribonucleoprotein 70 kDa homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNP1 PE=1 SV=1	sp|Q00916	34449,2	45%	ETSSSAYSADR-FASASTSNPAER-FGEIEK-GNRPLLSAATPTAAVTSVYK-GYAFIVFK-GYAFIVFKDPISSK-IcIVDIER-LFKPRPPLSYK-LQNWNPNVDPHIK-NAQLLDR-QTNPNITGVANLLSTSLK-YGSSTLDAR-YPDDVSR		13	0	13
wt	60S ribosomal protein L10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL10 PE=1 SV=1	sp|P41805	25362,1	52%	DAFHLR-DSNKDVVVEGLR-DVVVEGLR-EAGEVKDDGAFVK-GAWGKPHGLAAR-GSLENNIR-IYDLGK-KWGFTNLDRPEYLK-mLScAGADR-vDIGQIIFSVR-VHPFHVLR-WGFTNLDRPEYLK-YKFPGQQK-YmTTVSGR		14	0	14
wt	60S ribosomal protein L8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL8A PE=1 SV=4	sp|P17076	28125,5	51%	HWGGGILGNK-LGTLVNQK-LKVPPTIAQFQYTLDR-LVSTIDANFADK-LVSTIDANFADKYDEVK-mGVPYAIVK-NFGIGQAVQPK-NTAAETFK-QDASPKPYAVK-SKQDASPKPYAVK-TSAVAALTEVR-VAPAPFGAK-VPPTIAQF		15	13	2
wt	Exosome complex component RRP40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RRP40 PE=1 SV=2	sp|Q08285	26557	5%	QLLFNNDFPLLK		1	0	1
wt	40S ribosomal protein S15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS15 PE=1 SV=1	sp|Q01855	16002,2	30%	LAAPENEKPAPVR-LLEMSTEDFVK-NmIIVPEmIGSVVGIYNGK		3	0	3
wt	Protein MMF1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MMF1 PE=1 SV=1	sp|P40185	15908,1	24%	AEQVFQNVK-NFAEFNSVYAK-NILAESNSSLDNIVK		3	0	3
wt	SWI5-dependent HO expression protein 3 OS=Saccharomyces cerevisiae (strain YJM789) GN=SHE3 PE=3 SV=1	sp|A6ZL74,sp|B3LN26,sp|C7GY13,sp	47533,6	3%	NSSAIEQScSEK	c9: Carbamidome	1	0	1
wt	RuvB-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RVB1 PE=1 SV=1	sp|Q03940	50454	6%	ENPGVNSSNSGAVTR-GLGLDESGVAK		2	0	2
wt	ATP-dependent RNA helicase DBP2 OS=Saccharomyces cerevisiae (strain YJM789) GN=DBP2 PE=3 SV=1	sp|A6ZRX0,sp|P24783	60987,1	14%	ELAVQIQTEcSK-GSEIVIATPGR-KIVDQIRPDR-LIDMLEIGK-SDSEIAQFR-SPImVATDVAAR-VTYLVLDEADR	c10: Carbamidon	7	0	7
wt	Phosphoglycerate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PGK1 PE=1 SV=2	sp|P00560	44739,6	53%	AHSSMVGFDLPQR-ALENPTRPFLAILGGAK-ALLDEVVK-ASAPGSVILLENLR-ELPGVAFLSEK-ELQSLLGK-GVEVVLPVDFIIADAFSADANTK-HELSSLADVYINDAFGTAHR-ISHVSTGGGASLELLEGK-IVAALPTIK-LSVQD		17	0	17
wt	Phenylalanyl-tRNA synthetase alpha chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FRS2 PE=1 SV=3	sp|P15625	57514	2%	LIQELGQLQIK		1	0	1
wt	Pre-mRNA-splicing helicase BRR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BRR2 PE=1 SV=2	sp|P32639	246193,9	2%	FMNTSQNPQR-GLNDLVEQYK-VAELTGDSR-VSLPEGSFK		4	0	4
wt	114 kDa U5 small nuclear ribonucleoprotein component OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNU114 PE=1 SV=1	sp|P36048	114047,2	30%	cYQPFELFDNK-EGPLAEEPIYGVQYK-EVEVLmETK-GISTGGFmSNDGPTLEK-GQVPVIESAGFETDLR-HVLQLIFR-IDDFTTR-IINVGVIGPLHSGK-ILDTSQSESR-IVLQPLLPR-LGFTFTIK-LKPAPINSLSR-LLD	c1: Carbamidome	27	0	27
wt	General negative regulator of transcription subunit 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOT3 PE=1 SV=2	sp|P06102	94405,4	2%	VTSASSTISNTSTK		1	0	1
wt	40S ribosomal protein S16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS16A PE=1 SV=1	sp|P0CX51,sp|P0CX52	15847,9	65%	AFTSYDR-fSNIDIR-GLVAYHQK-sAVPSVQTFGK-TLLIADSR-VNGSPITLVEPEILR-VTGGGHVSQVYAIR-VYEPLLLVGLDK-VYEPLLLVGLDKFSNIDIR-YVDEQSKNELK		10	0	10
wt	Uncharacterized protein YNL134C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YNL134C PE=1 SV=1	sp|P53912	41165,7	33%	cAADDLDATVVQLTVLTEK-DKLPEGPVK-FAIGDYIYGVIHGASVR-FPSNGAFAEYSAISSETAYKPAR-IGPQGALLGcDAAGQIVK-IIVVASR-LGPNVDAAR-LVAVLK-QDIPIPELEEGFVLIK	c1: Carbamidome	9	0	9
wt	U2 small nuclear ribonucleoprotein A' OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LEA1 PE=1 SV=1	sp|Q08963	27194,2	31%	LLPmNVQNLTLSNNSIR-LVPHLETLDFQNVTAEER-QADGDTLGPVNTAIR-QLAEATSLEEIAR-RDDIHTLLLGR	m4: Oxidation (+	5	0	5

wt	mRNA 3'-end-processing protein RNA15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RNA15 PE=1 SV=1	sp|P25299	32791,1	5%	QSGVNAGVQNNPPSR		1	0	1
wt	Cerevisin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRB1 PE=1 SV=1	sp|P09232	69623,2	2%	AITVGASTLSDDR		1	0	1
wt	Transketolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TKL1 PE=1 SV=4	sp|P23254	73807,9	5%	HTPSIIALSR-ILAVDTVSK-SFVVPQEVYDHYQK		3	0	3
wt	60S ribosomal protein L20-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL20A PE=1 SV=1	sp|P0CX23,sp|P0CX24	20437,1	49%	ASGEIVSINQINEAHPTK-DLKFPLPHR-EYQVIGR-FPLPHR-IFASNEVIAK-KASGEIVSINQINEAHPTK-LPTESVPEPK-NFGVWVR-RLPTESVPEPK-VAAVETLYQDmAAR-YWYFLQK		11	0	11
wt	THO complex subunit MFT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MFT1 PE=1 SV=1	sp|P33441	44997,2	3%	LQGLYDSVQVINR		1	0	1
wt	Replication factor C subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RFC2 PE=1 SV=1	sp|P40348	39743,3	5%	FISEQENVK-ILDISAGDLR		2	0	2
wt	Pre-mRNA-splicing factor PRP21 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP21 PE=1 SV=1	sp|P32524	33053,9	6%	LLEDER-TFTDFVAQYK		2	0	2
wt	U3 small nucleolar ribonucleoprotein protein IMP3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IMP3 PE=1 SV=1	sp|P32899	21886,1	8%	VGPNLINDPAYLVTR		1	0	1
wt	Cold sensitive U2 snRNA suppressor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CUS1 PE=1 SV=1	sp|Q02554	50254,3	9%	FQVQENDTPK-IAGLNWDITNLK-NLFEETNWK-YPGLLASIK		4	0	4
wt	Protein ISD11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ISD11 PE=1 SV=1	sp|Q6Q560	11266,4	10%	LVVEPLQGR		1	0	1
wt	DNA-directed RNA polymerase II subunit RPB11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB11 PE=1 SV=1	sp|P38902	13616,4	8%	IQTTEGYDPK		1	0	1
wt	Transposon Ty1-ML1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-ML1 PE=3 SV=2	sp|Q04711	198533	19%	AHNVSTSNNSPSTDNDSISK-AVSPTDSTPPSTHTEDSKR-DILSVDYTDImK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-GIPGYALHPSR-KYPYPFIHR-KYVRPPPMLTSPNDFPNWVK-LIGLASYVGYK-LNNNGIHINN		25	25	0
wt	Meiotic activator RIM4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RIM4 PE=1 SV=1	sp|P38741	80110,6	2%	GTVTTTSTSTESR		1	0	1
wt	Heat shock protein SSC1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSC1 PE=1 SV=1	sp|P12398	70628,8	13%	ADQLANDTENSLK-AQFETLTAPLVK-DAGQIVGLNVLR-GQTYSPAQIGGFVLNK-TEELQTSSmK-TTPSVVAFTK-VQGGEEVNAEELK		7	0	7
wt	60S ribosomal protein L36-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL36B PE=1 SV=3	sp|O14455	11135,9	37%	EIAGLSPYER-LIDLIR-TGIAIGLNK-VEEmNNIIAASR		4	0	4
wt	HMG2-induced ER-remodeling protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HER1 PE=1 SV=1	sp|Q12276	139464,3	4%	IPTGAELR-ISGSLTPDSSVAGGK-TATLPSTAAVPTK-VSQQGQVPTR		4	0	4
wt	U3 small nucleolar RNA-associated protein 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UTP5 PE=1 SV=1	sp|Q04177	72002,9	1%	VGVQPTQR		1	0	1
wt	Farnesyl pyrophosphate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ERG20 PE=1 SV=2	sp|P08524	40485,3	3%	ADVLTAFLNK		1	0	1
wt	Nuclear cap-binding protein complex subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STO1 PE=1 SV=2	sp|P34160	100023,3	66%	AFEDDIK-AGIFTEPGESIAQLIATYEENPLAPTFK-AIAPVFGR-DQLINYYQSLFTGYTVEEDSVR-EmMPDIR-EYNGEPPYEMVELVR-FFYSHLDSLDFELK-FIANIDNAIPHESTR-FLSEAIMNEYGHEDYFNNALLSTLNAVVVEQP		49	0	49
wt	DNA topoisomerase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TOP2 PE=1 SV=2	sp|P06786	164223,8	3%	GLGTSLAQEVR-NAIIQELENLGFPR-QYEPGTVLDPTLK		3	0	3
wt	V-type proton ATPase catalytic subunit A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VMA1 PE=1 SV=3	sp|P17255	118639,8	7%	ANELVESYR-ETFLAGLIDSDGYVTDEHGIK-FTcNATHELVVR-IVELVK-LADSTGDVK-LSADYPLLTGQR-NVSMIADSSSR		7	0	7
wt	Ribosome-associated complex subunit SSZ1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSZ1 PE=1 SV=2	sp|P38788	58239,5	42%	AIPSALSYVGEDEYHGGQALQQLIR-cANGAPAVEVDGK-DVNVVVADFGGIR-EAVLTVPTNFSEEQK-GEFHPVLLAETSFPVQK-KPIGLIGAK-LAAEDYIGSAVK-LISDYDADELAEALQPVIVNTPHLK-LMELGIK-LTTNLEYTLP		17	0	17
wt	H/ACA ribonucleoprotein complex subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NHP2 PE=1 SV=2	sp|P32495	17122,1	12%	QDLGAAGATK-TVDNYEAR		2	0	2
wt	Protein STU2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STU2 PE=1 SV=1	sp|P46675	100923	3%	TLPNFSIASGSTHSTIETNK-VLSLENELR		2	0	2
wt	60S ribosomal protein L4-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL4B PE=1 SV=2	sp|P49626	39062	55%	AGHQTSAESWGTGR-AVGAHSDLLK-FVIWTEAAFTK-GPLVVYAEDNGIVK-IINSSEIQSAIRPAGQATQK-IPEIPLVVSTDLESIQK-LDQVWGSETVASSK-NVPGVETANVASLNLLQLAPGAHLGR-QAYAVSEK-RGPLVVYAEDNG		15	13	2
wt	FK506-binding nuclear protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FPR3 PE=1 SV=2	sp|P38911	46554,2	17%	DLEEGPTKPK-IIIPAPYAYGK-ITMAALNPEAIDEENKPSTLR-QALPGIPANSELTFDVK-VLEGGIVIEDR		5	0	5
wt	60S ribosomal protein L42-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL42A PE=1 SV=1	sp|P0CX27,sp|P0CX28	12211,5	8%	HFELGGEK		1	0	1
wt	60S ribosomal protein L9-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL9A PE=1 SV=2	sp|P05738	21568,8	36%	FIEVR-FLDGIYVSHK-HIDVTFTK-SLVDNmITGVTK-YIQTEQQIEVPEGVTVSIK-YVYAHFPINVNIVEK		6	0	6
wt	Actin-related protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARP4 PE=1 SV=1	sp|P80428	54833,5	9%	ATLAHNVVLTGGTSSIPGLSDR-IFSEQSIGIPR-YGFAEELFLPK		3	0	3
wt	Casein kinase II subunit alpha' OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CKA2 PE=1 SV=2	sp|P19454	39405	10%	ILTNLTGGPNVVGLYDIVQDADSK-IPALIFEEIK		2	0	2
wt	Pre-mRNA-splicing factor CWC26 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BUD13 PE=1 SV=1	sp|P46947	30473,2	8%	AQEPLVTVADK-LSTLQQEQEK		2	0	2
wt	Acetyl-coenzyme A synthetase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ACS2 PE=1 SV=1	sp|P52910	75492,2	5%	GVVHTTGGYLLGAALTTR-IITFGELLR-TGTEGIPMK		3	0	3
wt	Vacuolar protein sorting-associated protein 17 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VPS17 PE=1 SV=2	sp|P32913	63205,9	6%	QLAPPYDEITELAEFRPLVK-SIYVVSQSLQEK		2	0	2
wt	FK506-binding protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FPR4 PE=1 SV=1	sp|Q06205	43904,6	6%	LGQGEVIK-QALPGIPANSELTFDVK		2	1	1
wt	ABC transporter ATP-binding protein ARB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARB1 PE=1 SV=1	sp|P40024	68379,5	2%	IMTGELTPQSGR		1	0	1
wt	Phosphoglycerate mutase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GPM1 PE=1 SV=3	sp|P00950	27609,7	47%	AIQTANIALEK-FNTYR-HLEGISDADIAK-LLPYWQDVIAK-LWIPVNR-NLFTGWVDVK-RSFDVPPPPIDASSPFSQK-sFDVPPPPIDASSPFSQK-TVmIAAHGNSLR-VYPDVLYTSK-YVDPNVLPETESLALVIDR		11	0	11
wt	Small nuclear ribonucleoprotein-associated protein B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMB1 PE=1 SV=1	sp|P40018	22379,9	42%	DGTTLNIK-EIAQPSSSR-FNNEAPPQTR-GEQILSTVVEDKPLLSK-LANLIDYK-VLGLTILR-VYIGQLMAFDK-YNGGNDNIGANR		8	0	8
wt	60S ribosomal protein L27-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL27A PE=1 SV=1	sp|P0C2H6,sp|P0C2H7	15531,2	59%	IKPFIK-KVVIVKPHDEGSK-NQWFFSK-SHPFGHALVAGIER-SVVSTETFEQPSQR-VAVVVR-VVIVKPHDEGSK-VVNYNHLLPTR-YTLDVEAFK		9	0	9
wt	Nucleolar complex protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOC2 PE=1 SV=2	sp|P39744	81605,1	3%	LIPTPQFFPLR-LNQNSTFIQEK		2	0	2
wt	Probable oxidoreductase AIM17 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AIM17 PE=1 SV=2	sp|P23180	53137,1	2%	LFQTLVNLQK		1	0	1
wt	60S ribosomal protein L17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL17A PE=1 SV=4	sp|P05740	20549,6	40%	FNSSIGR-FVQGLLQNAAANAEAK-INKYESSPSHIELVVTEK-LYVSHIQVNQAPK-YESSPSHIELVVTEK-YGATSTNPAK-YLEQVLDHQR		7	6	1
wt	Transcription initiation factor TFIID subunit 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF5 PE=1 SV=1	sp|P38129	88970,6	2%	IAAAGFQDSYIK		1	0	1
wt	Cytochrome b5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CYB5 PE=1 SV=2	sp|P40312	13297,1	8%	GLYIGDVDK		1	0	1
wt	Aconitate hydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ACO1 PE=1 SV=2	sp|P19414	85371,6	2%	TIFTVTPGSEQIR		1	0	1
wt	Small nuclear ribonucleoprotein F OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMX3 PE=1 SV=1	sp|P54999	9660,1	40%	cNNVLYIR-FNSTEYR-sESSDISAmQPVNPKPFLK	c1: Carbamidome	3	0	3
wt	60S ribosomal protein L22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL22A PE=1 SV=3	sp|P05749	13693,4	41%	TFTVDVSSPTENGVFDPASYAK-VEGAVGNLGNAVTVTEDGTVVTVVSTAK		2	0	2
wt	Ribosome biogenesis protein BMS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BMS1 PE=1 SV=1	sp|Q08965	135576,8	3%	FPIVMGGLLPTEIK-FYNPVTSLLLK-ILMSDIVILR		3	0	3
wt	Ribose-phosphate pyrophosphokinase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRS3 PE=1 SV=1	sp|P38689	35125,1	15%	AAEILLENR-AIENINNSK-ITAIIPNFPYAR-LGLQLTSSK-MVLVGDVTDK		5	0	5
wt	Protein PCF11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PCF11 PE=1 SV=2	sp|P39081	71900,4	5%	GSQNTANTGISNSNLNTTTTR-TYLLVDNTTR		2	0	2
wt	Heat shock protein 42 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP42 PE=1 SV=1	sp|Q12329	42817,5	5%	EKPLNQLEESSRPPLAK		1	0	1
wt	Nucleoporin NUP192 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP192 PE=1 SV=1	sp|P47054	191546,8	4%	IIAELSFLK-NGALVSNILSAFK-VFSDVLFEFTK-VLSDQVGSEK-VNVTLDNPLLVDK-VTGILLLDSLIQLANR		6	0	6
wt	56 kDa U1 small nuclear ribonucleoprotein component OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNU56 PE=1 SV=1	sp|Q03782	56500,3	26%	ALELILNILEH-AYNEISGLQGDQFPR-FmNELSNFFSQVEFGK-GQLSQGHYPTTSNDGQR-HAVNKPSNVLNSSNR-NINLTGSFYLPK-SSYQILK-TRPIIETSK-VGNSEAFQSFDIWK-VISIGGVGEYIVK		10	0	10
wt	DNA-directed RNA polymerase I subunit RPA34 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA34 PE=1 SV=1	sp|P47006	26876,5	7%	IPAIDYSK-VFSVSETAK		2	0	2
wt	Protein SCP160 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SCP160 PE=1 SV=3	sp|P06105	134813,7	46%	AEYGVEMDFLQK-ANESLNSLR-APSATYAGYVWGADTR-DITVQGPQK-DKVGEAITYAR-DLPSLGSNAAFANVK-DNEIVTIR-EAADVIINVPR-EVDVPASIYEYVSER-FAcQIDIPNEENNNASK-FHGSLIGPHGTYR-FNMIVGPG		50	0	50
wt	UPF0202 protein KRE33 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KRE33 PE=1 SV=1	sp|P53914	119353,8	5%	EISLDEPIR-FTAVQALSVIESSK-GTPHPSQcNLFVVNR-LFVLLPPIDPK		4	0	4
wt	Superoxide dismutase [Mn], mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SOD2 PE=1 SV=1	sp|P00447	25774,9	16%	AIDEQFGSLDELIK-AIWNVVNWK-LAGVQGSGWAFIVK		3	0	3
wt	Histone deacetylase HOS3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HOS3 PE=1 SV=1	sp|Q02959	79201,4	4%	AAAQIPESAK-AVVVLSPYSLQHVFPR		2	0	2
wt	Signal recognition particle receptor subunit alpha homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SRP101 PE=1 SV=2	sp|P32916	69279,7	3%	LTQQLITK-SGAVEQLR		2	0	2
wt	Acetyl-CoA acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ERG10 PE=1 SV=3	sp|P41338	41728,6	10%	FGQTVLVDGVER-TPIGSFQGSLSSK-VVVTLLSILQQEGGK		3	0	3
wt	U1 small nuclear ribonucleoprotein component SNU71 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNU71 PE=1 SV=1	sp|P53207	71385,1	31%	AAAITLPEGTVK-ADIMSAENYEEHLEK-ASEFYSVFK-DKEASIADNNSANK-ETFDEDGETIADR-LPFTADELNIR-NIEDQTDER-NSLSETLLNSNDDGSIHNSDQNTGLNK-QALLNELR-QFLPISLDQQIHTVSLQGVSSSFSR-SAA		15	0	15
wt	40S ribosomal protein S8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS8A PE=1 SV=1	sp|P0CX39,sp|P0CX40	22490,4	53%	AAIVQIDATPFR-cDGYILEGEELAFYLR-IAGVVYHPSNNELVR-IESSVESQFSAGR-IETGNFSWASEGISK-IETGNFSWASEGISKK-KFELGR-LYAcISSRPGQSGR-QWFEAHYGQTLGK		9	0	9
wt	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RIP1 PE=1 SV=1	sp|P08067	23365,4	18%	TPHEIQEANSVDmSALK-TPNFDDVLK-VEVNLAAIPLGK	m13: Oxidation (	3	0	3
wt	Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TDH3 PE=1 SV=3	sp|P00359	35746,6	69%	DPANLPWGSSNVDIAIDSTGVFK-eLDTAQK-ETTYDEIK-IALSRPNVEVVALNDPFITNDYAAYMFK-IATYQER-IATYQERDPANLPWGSSNVDIAIDSTGVFK-IVSNASCTTNcLAPLAK-KVVITAPSSTAPmFVmGVNEEK-LTGMAF		19	7	12
wt	Heat shock protein SSB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSB2 PE=1 SV=2	sp|P40150	66595,7	54%	AADEAFAK-ARFEDLNAALFK-AVITVPAYFNDAQR-DAGAISGLNVLR-ENTLLGEFDLK-FDDESVQK-FEDLNAALFK-IEAALSDALAALQIEDPSADELR-IEAALSDALAALQIEDPSADELRK-IINEPTAAAIAYGLGAGK-KTGLD		30	30	0
wt	Nucleolar protein NET1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NET1 PE=1 SV=1	sp|P47035	128535,1	1%	SAVSESSVTNSK		1	0	1
wt	Nucleoporin NUP188 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP188 PE=1 SV=1	sp|P52593	188591	1%	FALFAESHDVLQK		1	0	1
wt	Pre-mRNA-splicing factor SNT309 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNT309 PE=1 SV=1	sp|Q06091	20710,5	19%	HQEIVLDTLLPQTVSNQWR-IPDGYKNEIDQLVK		2	0	2
wt	Protein URA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=URA2 PE=1 SV=5	sp|P07259	245044,8	3%	AIMGLPLTPYPVEK-DSLPLLLAAVEEGK-FLDSNEVAIR-TADLASVLLLTSLQNR-TITLPGLINIATYVPNASHVIK		5	0	5
wt	40S ribosomal protein S1-A OS=Saccharomyces cerevisiae (strain YJM789) GN=RPS1A PE=3 SV=1	sp|A7A1W1,sp|B3RHV0,sp|B5VNY0	28743,8	61%	APSTFENR-DIFPLQNIHVR-EVQGSTLAQLTSK-FDVGALmALHGEGSGEEK-HSYAQSSHIR-IFAIAFTR-KVISEILTK-LIPEVINK-LRVDEVQGK-NLLTNFHGmDFTTDK-TSDDYVLR-VISEILTK-VTGFKDEVLETV-VVDPFTR-VV		16	12	4
wt	Cytochrome c1, heme protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CYT1 PE=1 SV=1	sp|P07143	34055,4	4%	TLVGVSHTNEEVR		1	0	1
wt	60S acidic ribosomal protein P2-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP2A PE=1 SV=1	sp|P05319	10746,2	10%	VSSVLSALEGK		1	0	1
wt	Vacuolar protein sorting-associated protein 29 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VPS29 PE=1 SV=1	sp|P38759	31013,1	13%	FVNQISNNITIVR-ISQVALLGNSTK-NDPLSLLALAR		3	0	3
wt	RNA 3'-terminal phosphate cyclase-like protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RCL1 PE=1 SV=1	sp|Q08096	40172,3	3%	YTTFQGSQNFR		1	0	1
wt	Activator of SKN7 protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ASK10 PE=1 SV=2	sp|P48361,sp|Q06108	126868	1%	YSALIDSEAR		1	0	1
wt	T-complex protein 1 subunit delta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CCT4 PE=1 SV=2	sp|P39078	57605,6	11%	GLIAGGGAPEIEISR-IGLIQFQISPPKPDTENNIIVNDYR-IVSQYSSFLAPLAVDSVLK		3	0	3
wt	Regulation of enolase protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=REE1 PE=1 SV=1	sp|P40893	21966,8	7%	VTFSEWSLTAPLGK		1	0	1
wt	ISWI one complex protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IOC3 PE=1 SV=1	sp|P43596	90901,4	5%	LQEFFLGR-QQLPSDQDISKPK-STTDNNPSINTNPLPK		3	0	3
wt	Ribosomal RNA-processing protein 9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RRP9 PE=1 SV=1	sp|Q06506	65056,4	2%	SEANDILTDNR		1	0	1
wt	6-phosphofructokinase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PFK2 PE=1 SV=4	sp|P16862	104619,8	8%	AFVVMEGYEGLVR-AIDYVEATANSHSR-ISNEQYER-ITTLGHVQR-LAEVITAEADGR-NAVSTKPTPPPAPEASAESGLSSK		6	0	6
wt	Endoplasmic reticulum transmembrane protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YET3 PE=1 SV=1	sp|Q07451	22904,2	5%	ASPPVASSDVK		1	0	1
wt	Nucleoporin NUP84 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP84 PE=1 SV=1	sp|P52891	83639,8	1%	LPASNILR		1	0	1
wt	60S ribosomal protein L28 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL28 PE=1 SV=3	sp|P02406	16721,9	39%	ETAPVIDTLAAGYGK-GRIPNVPVIVK-IPNVPVIVK-lWTLIPEDK-LWTLIPEDKR-QQAHFWKPVLNLDK-YHPGYFGK		7	0	7
wt	DNA-directed RNA polymerases I, II, and III subunit RPABC4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPC10 PE=1 SV=1	sp|P40422	7716,2	10%	LVQFEAR		1	0	1
wt	Fructose-bisphosphate aldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FBA1 PE=1 SV=3	sp|P14540	39621,5	45%	DYImSPVGNPEGPEKPNK-DYImSPVGNPEGPEKPNKK-FAIPAINVTSSSTAVAALEAAR-FFDPR-GAIAAAHYIR-GISNEGQNASIK-KTGVIVGEDVHNLFTYAK-LLPWFDGmLEADEAYFK-SIAPAYGIPVVLHSDH	m4: Oxidation (+	13	0	13
wt	Peptidyl-prolyl cis-trans isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CPR1 PE=1 SV=3	sp|P14832	17390,7	29%	GFGYAGSPFHR-HVVFGEVVDGYDIVK-KVESLGSPSGATK-LYNDIVPK-VESLGSPSGATK		5	0	5
wt	Vacuolar transporter chaperone 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VTC4 PE=1 SV=2	sp|P47075	83157,5	3%	ISLDTELTMVR-VKEVQEQVQHTVR		2	0	2
wt	40S ribosomal protein S4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS4A PE=1 SV=1	sp|P0CX35,sp|P0CX36	29411,2	45%	AILmQR-DSLDNTFVTR-ESLPLIVFLR-GVPYVVTHDGR-HDGGFDLVHIK-IDLASGK-ITDEEASYK-ITDFIK-KGVPYVVTHDGR-LAAPHHWLLDK-LNNVFVIGEQGKPYISLPK-LRESLPLIVFLR-LSIAEER-LVY	m4: Oxidation (+	14	0	14
wt	Homoserine dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HOM6 PE=1 SV=1	sp|P31116	38503,2	10%	EIIQTGDEVEK-ISGVEVESPTSFPVQSLIPKPLESVK		2	0	2
wt	C-1-tetrahydrofolate synthase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MIS1 PE=1 SV=1	sp|P09440	106220,5	9%	IEVSPEAQK-IIQVGARPDSSTYVR-LPAEITEVELLK-LVGDVDFDSVK-QITIGEAATEK-QPSLGPTLGVK-VVDINDR-YVLVAGITPTPLGEGK		8	2	6
wt	V-type proton ATPase subunit d OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VMA6 PE=1 SV=2	sp|P32366	39792,4	8%	AALANVYEYR-LYPLATFHLAQAQDFEGVR		2	0	2
wt	ATP-dependent RNA helicase MAK5 OS=Saccharomyces cerevisiae (strain YJM789) GN=MAK5 PE=3 SV=1	sp|A6ZL85,sp|P38112	86611	4%	LAGELADHEIASNSLR-YDNSGQIVIATPGR		2	0	2
wt	Small COPII coat GTPase SAR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SAR1 PE=1 SV=1	sp|P20606	21451,5	26%	DVPFVILGNK-FTTFDLGGHIQAR-IDAPNAVSEAELR-SALGLLNTTGSQR		4	0	4
wt	40S ribosomal protein S12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS12 PE=1 SV=1	sp|P48589	15470,9	34%	KVVGASVVVVK-LVEGLANDPENK-LVEGLANDPENKVPLIK-QLGEWAGLGK-TALVHDGLAR		5	0	5
wt	Translationally-controlled tumor protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TMA19 PE=1 SV=1	sp|P35691	18741,3	7%	LQETNPEEVPK		1	0	1
wt	DnaJ homolog 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MDJ1 PE=1 SV=1	sp|P35191	55562	3%	TITVDLPHGLQDGDVVR		1	0	1
wt	Heat shock protein SSA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSA1 PE=1 SV=4	sp|P10591	69659,4	55%	ARFEELcADLFR-ATAGDTHLGGEDFDNR-DAGTIAGLNVLR-EEFDDKLK-ELQDIANPIMSK-ETAESYLGAK-FELSGIPPAPR-IINEPTAAAIAYGLDK-IINEPTAAAIAYGLDKK-ITITNDK-KSEIFSTYADNQPGVL	c7: Carbamidome	28	1	27
wt	Vacuolar protein sorting-associated protein 30 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VPS30 PE=1 SV=1	sp|Q02948	63264,4	1%	LLDQLLR		1	0	1
wt	(DL)-glycerol-3-phosphatase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RHR2 PE=1 SV=3	sp|P41277	27948,2	6%	VVVFEDAPAGIAAGK		1	0	1
wt	Ubiquitin-40S ribosomal protein S31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS31 PE=1 SV=3	sp|P05759	17216,6	31%	EcSNPTcGAGVFLANHK-ESTLHLVLR-LIFAGK-mQIFVK-TLSDYNIQK	c2: Carbamidome	5	0	5
wt	Probable quinone oxidoreductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ZTA1 PE=1 SV=1	sp|P38230	37020,5	4%	VILIDEIGGYDVIK		1	0	1
wt	Thiosulfate sulfurtransferase TUM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TUM1 PE=1 SV=1	sp|Q08686	34220	4%	TALELAGVPNVR		1	0	1
wt	Eukaryotic translation initiation factor 3 subunit C OS=Saccharomyces cerevisiae (strain YJM789) GN=NIP1 PE=3 SV=1	sp|A6ZN26,sp|P32497	93225,2	3%	ISLNSSNNASADER-VQVESLK		2	0	2
wt	Nucleolar protein 56 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOP56 PE=1 SV=1	sp|Q12460	56867,3	17%	APIEYLLFEEPTGYAVFK-GLQSGDLER-LEFYNTGKPTLK-LISHAGSLTNLSK-LVPDNYTFAK-QAASTVQILGAEK-YGLIYHSGFISK		7	0	7
wt	Lanosterol 14-alpha demethylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ERG11 PE=1 SV=1	sp|P10614	60722,4	2%	SYVPLIAEEVYK		1	0	1
wt	Elongator complex protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IKI3 PE=1 SV=1	sp|Q06706	152994,2	39%	ASGLVGNQLR-DVLIFAAVPSIEEMK-DVLIFAAVPSIEEMKK-EAFIVcR-EAMGAYQSAK-EAMSIAVQK-EAVALYcK-EIYSISEK-EYLPFLQELQDNEPLR-EYLPFLQELQDNEPLRR-FLIDDYLGNYEK-FPQLVR-GKHPSIVcEFPK-G		45	0	45
wt	Eukaryotic initiation factor 4F subunit p130 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TIF4632 PE=1 SV=1	sp|P39936	103901,5	28%	AcDEPHWSSMYAQLcGK-AEEQAPKEEIAPLVPSANR-AQPISDIYEFAYPENVERPDIK-DTLTETSNEK-EAPKPTGEANEVVIDGK-EATPVLPANEAVK-EEIAPLVPSANR-ETEPSTSDIEMPTVSQLLETLGK-FRPDP	c2: Carbamidome	20	4	16
wt	High mobility group protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HMO1 PE=1 SV=1	sp|Q03973	27545,1	17%	AGLPPLSSTEITQEISKK-DSLVSSLFELSK-QAYNVELENYQR		3	0	3
wt	Proteasome component PRE3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE3 PE=1 SV=2	sp|P38624	23548,1	5%	TTTGAYIANR		1	0	1
wt	60S acidic ribosomal protein P2-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP2B PE=1 SV=2	sp|P02400	11050,3	11%	GSLEEIIAEGQK		1	0	1
wt	Nucleoporin SEH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEH1 PE=1 SV=1	sp|P53011	39123,8	5%	AHDSSIVAIDWASPEYGR		1	0	1
wt	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=OST3 PE	sp|P48439	39485,6	6%	NTQLAGVGPK-SPAYPFPLLR		2	0	2
wt	Putative fatty aldehyde dehydrogenase HFD1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HFD1 PE=1 SV=1	sp|Q04458	59981,9	9%	IDEIVEISR-IESVLNETTK-SLTPcVLELGGK-SPTFITENFK-VGSIVAEK		5	0	5
wt	Putative glycosyltransferase HOC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HOC1 PE=1 SV=3	sp|P47124	46298,8	2%	IIETTLQR		1	0	1
wt	Partitioning protein REP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=REP2 PE=1 SV=1	sp|P03872	33197,1	8%	LQNTITEGPK-TEVNHANTNEEVPSR		2	0	2
wt	Structural maintenance of chromosomes protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMC3 PE=1 SV=1	sp|P47037	141342,9	3%	IKDVQQQIESNEEQR-LQTVLETLLSDVNQNQR-VNAVDSTFQK		3	0	3
wt	60S ribosomal protein L8-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL8B PE=1 SV=3	sp|P29453	28112,8	56%	AKNPLTHSTPK-HWGGGILGNK-LGTLVNQK-LKVPPTIAQFQYTLDR-LVSTIDANFADK-LVSTIDANFADKYDEVK-mGVPYAIIK-NFGIGQAVQPK-NTAAETFK-QDASPKPYAVK-SKQDASPKPYAVK-TSAVAALTEVR-VAPAPFG		17	0	17
wt	Protein MLP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MLP1 PE=1 SV=2	sp|Q02455	218464,7	2%	IESETVNEAK-ILEAQER-VAQGNNQLEAIR		3	0	3
wt	Elongation factor 1-gamma 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TEF4 PE=1 SV=1	sp|P36008	46521,9	12%	IDNLAAVFDAR-IVDLEQSSEFASLFPLK-LLGSDVIEK-WFNTVAASPIVK		4	0	4
wt	40S ribosomal protein S28-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS28B PE=1 SV=1	sp|P0C0X0,sp|Q3E7X9	7564,7	42%	ENDILVLMESER-TPVTLAK-VEFLEDTSR		3	0	3
wt	Pre-mRNA-splicing factor CWC2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CWC2 PE=1 SV=1	sp|Q12046	38432,2	10%	FVSPFALQPQLHSGK-HLKPAQIESR-WSQGFAGNTR		3	0	3

wt	Aspartate-semialdehyde dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HOM2 PE=1 SV=1	sp|P13663	39544,7	14%	EQDVPLIVPVVNPEHLDIVAQK-QTIHVLEQPDRPQPR-VAVSDGHTEcISLR		3	0	3
wt	Clustered mitochondria protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CLU1 PE=1 SV=1	sp|Q03690	145171,1	34%	ALEHITVTQGIFTK-ALTNLAILEFSNESPYNATVVYNR-AVEQDNKEYEDWEK-DANTGEEVTEDFVNDINVK-DLTTSTLQDR-DSLAYGYTESR-ELDSQIVHYEQNLK-EQLESYK-FGIQLLNK-FISHVQAFEK-FNEMVHEVFSSFK-		34	0	34
wt	Acetolactate synthase small subunit, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ILV6 PE=1 SV=2	sp|P25605	33986,7	11%	QFHPANLPASEVLR-VVDISETScIVELSAKPTR		2	0	2
wt	Protein phosphatase 1 regulatory subunit SDS22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SDS22 PE=1 SV=1	sp|P36047	38890,2	3%	LTTLDVTSNK		1	0	1
wt	Prohibitin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PHB2 PE=1 SV=2	sp|P50085	34407,2	36%	AVVAQFNASQLITQR-DLQMVNITcR-ILASSPNR-NVASLTGTK-SAELIGEAIK-SAELIGEAIKK-SPGEFQR-TLGQDYDER-VILDNEALLLNTVVDAR-VLPSIVNEVLK-VLSRPDVVQLPTIYR		11	0	11
wt	Chromo domain-containing protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CHD1 PE=1 SV=1	sp|P32657	168249,1	1%	EILDELIADGTLPVK		1	0	1
wt	ATP-dependent RNA helicase MSS116, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MSS116 PE=1 SV=1	sp|P15424	76272,5	7%	FANSIFAAVEHIK-IDQSVVISEK-LIDVLEK-TIKPILSSEDHDVIAR		4	0	4
wt	FACT complex subunit SPT16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPT16 PE=1 SV=1	sp|P32558	118636	43%	AIDLFKDPESK-ALADVVQQDK-AVDEELK-DLGFQGVPNR-DSNFILNVK-DSQLPTNIR-DSQSANNYALQLADTVQIPLDETEPPR-DVNEQAFLSVSSK-EASDMSVDETGGGR-EIVTNILKPGR-ENEFNVIDISLGLSK-EVYESVIEY		40	0	40
wt	Ribosome biogenesis protein BRX1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BRX1 PE=1 SV=2	sp|Q08235	33532,5	6%	QYVSPNVVR-TLLISSR		2	0	2
wt	Mitochondrial phosphate carrier protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MIR1 PE=1 SV=1	sp|P23641	32813,9	22%	ASEFYYGFAGPK-EEGIGSFYSGFTPILFK-IQLEPTVYNK-KAPGQSTVGLLAQLAK-QLGFFGSFAGLPTR		5	0	5
wt	Polyamine N-acetyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PAA1 PE=1 SV=1	sp|Q12447	21948,7	8%	IVLIAHEPLIPFYER		1	0	1
wt	40S ribosomal protein S17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS17A PE=1 SV=1	sp|P02407,sp|P14127	15788,9	58%	DQYVPEVSALDLSR-IAGYTTHLmK-KDQYVPEVSALDLSR-LcDEIATIQSK-LPLSVINVSAQR-LTLDFQTNK-LTLDFQTNKR-SLGLKLPLSVINVSAQR-SNGVLNVDNQTSDLVK		9	0	9
wt	Enolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ENO1 PE=1 SV=3	sp|P00924	46817,4	47%	AADALLLK-AVDDFLISLDGTANK-GNPTVEVELTTEK-IATAIEK-IGLDcASSEFFK-IGSEVYHNLK-LGANAILGVSLAASR-LNQLLR-SGETEDTFIADLVVGLR-SIVPSGASTGVHEALEmR-TAGIQIVADDLTVTNPK-TFAEALR-VN		15	11	4
wt	ADP-ribosylation factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARF1 PE=1 SV=3	sp|P11076	20530,1	21%	ILMVGLDGAGK-LFSNLFGNK-mLNEDELR-NAAWLVFANK		4	3	1
wt	Pre-mRNA-processing factor 39 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP39 PE=1 SV=1	sp|P39682	74752,2	31%	ANTFLPLDFK-FATIEYQLFGLK-FIEFEVGQK-FVTDPSK-GLDTQFLQDNTALVQAYR-ILETSITNYINNQIDAK-IYEYIIEVPLHQYAR-LALETILWQILR-NIDIVLR-NISDEVVVDIYQK-NLSIVVVELIK-NSVPFWLTYYK-SIAVLATS		16	0	16
wt	ATP-dependent RNA helicase DHH1 OS=Saccharomyces cerevisiae (strain YJM789) GN=DHH1 PE=3 SV=1	sp|A6ZXG9,sp|P39517	57545,4	29%	ELALQTSQVVR-ELLmGIFEAGFEKPSPIQEEAIPVAITGR-GNTFEDFYLK-IEQELGTEIAAIPATIDK-IQALImVPTR-KDTRPQTDDVLNTK-LNETVHILVGTPGR-TAAFVIPTLEK-TAETYLHR-TLVcSDLLTR-VFHEFR-VLDLASR		12	0	12
wt	DNA topoisomerase 2-associated protein PAT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PAT1 PE=1 SV=4	sp|P25644	88515,5	2%	SYVAATAEGISGPR		1	0	1
wt	DNA-directed RNA polymerases I and III subunit RPAC2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPC19 PE=1 SV=1	sp|P28000	16150,9	11%	IQTYGETTAVDALQK		1	0	1
wt	U3 small nucleolar RNA-associated protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UTP4 PE=1 SV=1	sp|Q06679	87803,7	3%	LVVSWSESTVK-TDQIASGDSTGSIK		2	0	2
wt	Heat shock protein STI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STI1 PE=1 SV=1	sp|P15705	66267,6	2%	TSEMMKDPQLVAK		1	0	1
wt	ATP-dependent RNA helicase HAS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HAS1 PE=1 SV=1	sp|Q03532	56720,2	17%	ALIIDEADR-ELALQIFGVAR-GVNmLIATPGR-IANVQSQLEK-LLDHLQNTK-TLAFLIPAIELLHSLK-VNITIGASGK-VPLNEYEFPENK		8	0	8
wt	H/ACA ribonucleoprotein complex subunit 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CBF5 PE=1 SV=1	sp|P33322	54706,3	10%	DSAVNAVcYGAK-SIIQPLETLLVGYK-SLENLTGALFQRPPLISAVK	c8: Carbamidome	3	0	3
wt	Ketol-acid reductoisomerase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ILV5 PE=1 SV=1	sp|P06168	44369,9	22%	AAIEDGWVPGK-EVNSDLYGER-GINSSYAVWNDVTGK-NALKPVFQDLYESTK-NLFTVEDAIK-SLEFNSQPDYR-TLYFSHGFSPVFK		7	0	7
wt	40S ribosomal protein S22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS22A PE=1 SV=2	sp|P0C0W1,sp|Q3E7Y3	14626,5	54%	cGVISPR-FLQVMQK-HGYIGEFEYIDDHR-IGDIEK-QFGYVILTTSAGImDHEEAR-SSVLADALNAINNAEK	c1: Carbamidome	6	0	6
wt	Mitochondrial 2-oxodicarboxylate carrier 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ODC2 PE=1 SV=1	sp|Q99297	34007,9	5%	FQLEVTTPTAAAVGK		1	0	1
wt	Nuclear cap-binding protein subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CBC2 PE=1 SV=1	sp|Q08920	23775,7	58%	FDFDASR-FDNSSSQSNTNNYIPPPDAMGTFRPGFDEER-gGFAIPFAER-IImGLDR-LDTPSR-NPNGLQELR-RIIMGLDR-RNPNGLQELR-SGGQVSDELR-SGGQVSDELRFDFDASR-sLEEFDEVK-sLEEFDEVKYDHSTK-TITIDLDP		14	0	14
wt	Protein CBP3, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CBP3 PE=1 SV=1	sp|P21560	39085,4	13%	AGPVAGSYYYK-SSHLNSKPLDVSNK-TFSDIELR-YIYSQLYVLSR		4	0	4
wt	Transcription initiation factor TFIID subunit 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF3 PE=1 SV=1	sp|Q12297	40297,8	2%	ISILQLLK		1	0	1
wt	Cytochrome b-c1 complex subunit 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=QCR7 PE=1 SV=2	sp|P00128	14565,7	7%	PQSFTSIAR		1	0	1
wt	Repressible alkaline phosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PHO8 PE=1 SV=2	sp|P11491	63004,9	5%	IDHAGHQNDPASQVR-LAGYLTGLVVTTR		2	0	2
wt	60S ribosomal protein L7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL7A PE=1 SV=3	sp|P05737	27639,6	54%	AAGSYYVEAQHK-AIILER-ATLELLK-HFIQGGSFGNR-ILTPESQLKK-INSGTFVK-LIEPYVAYGYPSYSTIR-LSNPSGGWGVPR-LVFVVR-QANNFLWPFK-QRVPLSDNAIIEANLGK-RAIILER-TAEQVAAER-VLQLLR-VPLSDNAI		15	0	15
wt	RNA-binding protein SGN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SGN1 PE=1 SV=1	sp|P40561	28955	13%	GYGYIEFESPAYR-ITLLYDR-LSIEGTPQVSQK		3	0	3
wt	Transcription factor CSR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CSR2 PE=1 SV=1	sp|Q12734	124852,9	1%	STTLSDIK		1	0	1
wt	Peptidyl-prolyl cis-trans isomerase CPR6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CPR6 PE=1 SV=1	sp|P53691	42073,2	10%	IVFELYNDIVPK-LIENQQcDQENNKPLR-TKPDVPLSYK		3	0	3
wt	40S ribosomal protein S10-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS10B PE=1 SV=1	sp|P46784,sp|Q08745	12738,7	38%	ALQSLTSK-eYLNLPEHIVPGTYIQER-IHQYLFQEGVVVAK		3	0	3
wt	Uncharacterized protein YHR127W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YHR127W PE=1 SV=1	sp|P38833	27132	20%	KLFHGALVDGR-LAYPTTQSLEK-LVSSNDVGVLLR-NVLENISQVQIAQIR		4	0	4
wt	60S ribosomal protein L33-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL33B PE=1 SV=2	sp|P41056	12168,2	45%	IAYVYR-IEGVATPQEAQFYLGK-IFLYPSNI-RVNNPNVSLIK-TFGASVR-VNNPNVSLIK		6	0	6
wt	Nucleoporin NUP82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP82 PE=1 SV=2	sp|P40368	82089,5	6%	IVFIQDNIIR-LEDIATIER-TLTFQNISSDmKPQSTAAETSISTEK		3	0	3
wt	78 kDa glucose-regulated protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KAR2 PE=1 SV=1	sp|P16474	74470,2	37%	ALSSQMSTR-DAGTIAGLNVLR-DGKPAVEVSVK-DVDDIVLVGGSTR-FASEDASIK-FELTGIPPAPR-HLPFNVVNK-ITPSYVAFTDDER-IVNEPTAAAIAYGLDK-LIGDAAK-LTQEEIDR-NKLENYAHSLK-NQVAANPQNTIFDIK-N		23	2	21
wt	Mannose-1-phosphate guanyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PSA1 PE=1 SV=2	sp|P41940	39566,6	19%	ETFPILVEEK-GLILVGGYGTR-IGPDVVIGPNVTIGDGVR-KLATGANIVGNALIDPTAK-SVVLcNSTIK		5	0	5
wt	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit SWP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SW	sp|Q02795	31654,6	4%	LDAALLQEASR		1	0	1
wt	H/ACA ribonucleoprotein complex non-core subunit NAF1 OS=Saccharomyces cerevisiae (strain YJM789) GN=NAF1 PE=3 SV=1	sp|A6ZRW0,sp|P53919	54840,4	10%	AFIVTPDAHWIDTFELK-IKLPDSK-SAFENNIIIHATmSGEK-TIITPIGVLK		4	0	4
wt	60S ribosomal protein L34-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL34B PE=1 SV=1	sp|P40525,sp|P87262	13641,1	26%	AFLIEEQK-cGDcGSALQGISTLRPR-TPGGILR		3	0	3
wt	Respiratory growth induced protein 1 OS=Saccharomyces cerevisiae (strain YJM789) GN=RGI1 PE=3 SV=1	sp|A6ZR21,sp|B3LRI4,sp|C7GRP9,sp	18988,8	8%	VQTVTTEDGETVK		1	0	1
wt	T-complex protein 1 subunit zeta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CCT6 PE=1 SV=1	sp|P39079	59925,9	2%	IITDGFEIAR		1	0	1
wt	Elongation factor 3B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HEF3 PE=1 SV=2	sp|P53978	115871,6	8%	ATETVDNKDIER-EALASGQFR-LSSAELR-QHAFAHIESHLDK-QINENDAEAMNK-STLINVLTGELLPTSGEVYTHENcR-TPSEYIQWR		7	6	1
wt	Plasma membrane ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PMA1 PE=1 SV=2	sp|P05030	99621,6	15%	ADTGIAVEGATDAAR-DDTAQTVSEAR-GYLVAmTGDGVNDAPSLK-GYLVAMTGDGVNDAPSLKK-LSAIESLAGVEILcSDK-mLTGDAVGIAK-QLGLGTNIYNAER-SVEDFMAAMQR-TLANTAVVIR-VLEFHPFDPVSK-VTAVVE		12	0	12
wt	Hsp90 co-chaperone AHA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AHA1 PE=1 SV=1	sp|Q12449	39436,2	3%	LVGVEAGSVK		1	0	1
wt	Probable mannosyltransferase KTR3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KTR3 PE=1 SV=1	sp|P38130	47484,6	11%	LDIPYGSSVPYR-NSDLWNLVK-SPEVPIAQGTSVSR-VTSALVSGK		4	0	4
wt	Single-stranded DNA-binding protein RIM1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RIM1 PE=1 SV=1	sp|P32445	15386,6	6%	YSIASQPR		1	0	1
wt	Pre-mRNA-splicing factor 19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP19 PE=1 SV=2	sp|P32523	56572,3	36%	DVGTLAYPTYTIPEFK-EEFLQGLLQSSR-FPVDEEAK-GTIGFQSYEDDSQYIVHSAK-LLLLYPGNQITILDSK-LSTVMYER-LVAAQLLmEK-NLELLQAQNYSR-SDVEYSSGVLHK-SSQQAVAITR-STLDSLTK-TGGEHPAIISR-TGT		15	0	15
wt	mRNA transport factor GFD1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GFD1 PE=1 SV=1	sp|Q04839	21572,1	15%	ATEISPPPVSPSK-ISPVSESLAINPFSQK		2	0	2
wt	60S ribosomal protein L3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL3 PE=1 SV=4	sp|P14126	43757,9	44%	AGmTTIVR-AHLAEIQLNGGSISEK-ALEEVSLK-FQTPAEK-GHGFEGVTHR-HAFmGTLK-HGHLGFLPR-KALEEVSLK-SKPVALTSFLGYK-SLTTVWAEHLSDEVK-SLYTNTSR-TITPmGGFVHYGEIK-TVAVDSV	m3: Oxidation (+	17	0	17
wt	Trehalose-phosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TPS2 PE=1 SV=3	sp|P31688	102978,9	1%	QILDGLVGANR		1	0	1
wt	ER-derived vesicles protein ERV14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ERV14 PE=1 SV=3	sp|P53173	15931,3	8%	VQLLDATEIFR		1	0	1
wt	Importin subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SRP1 PE=1 SV=1	sp|Q02821	60442,5	16%	AVGNIVTGNDLQTQVVINAGVLPALR-DTQQVELR-GLNINENADFIEK-LLEVAEYK-LVELLSHESTLVQTPALR-TATWTLSNLcR		6	0	6
wt	Protein ERP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ERP1 PE=1 SV=1	sp|Q05359	24724	12%	DASEAVNSR-GSASGDLTFLASDSGEHK		2	0	2
wt	Chromatin structure-remodeling complex subunit RSC2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC2 PE=1 SV=1	sp|Q06488	102303,9	3%	GPSVIVNER-STTPSHSGTPQPLGPR		2	0	2
wt	54S ribosomal protein IMG1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IMG1 PE=1 SV=1	sp|P25626	19394,6	6%	VPLFSPLIER		1	0	1
wt	Poly(A) polymerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PAP1 PE=1 SV=1	sp|P29468	64554	8%	ILQELAQR-TETALNALK-VFGITGPVSTVGATAAENK-VILQEFVR		4	0	4
wt	Pumilio homology domain family member 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PUF6 PE=1 SV=1	sp|Q04373	75109	7%	FAPMFLSTISK-NLIGTITASVEK-QTIINELHGSLR-YQQVLNNILTTFK		4	0	4
wt	Down-regulator of invasive growth 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DIG1 PE=1 SV=1	sp|Q03063	49356,9	2%	TTAEDTSIAK		1	0	1
wt	Cystathionine gamma-lyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CYS3 PE=1 SV=2	sp|P31373	42542,8	10%	EASGVFDDLVR-LVWIETPTNPTLK-QSSPANPIGTYEYSR		3	0	3
wt	Uncharacterized protein YDR179W-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDR179W-A PE=1 SV=2	sp|Q03983,sp|Q3E765	53733,7	1%	LLIYR		1	0	1
wt	Keratin, type I cytoskeletal 10 - Homo sapiens	sp|P13645	59512,4	33%	AETEcQNTEYQQLLDIK-ALEESNYELEGK-GSLGGGFSSGGFSGGSFSR-LAADDFR-LASYLDK-LENEIQTYR-LKYENEVALR-NQILNLTTDNANILLQIDNAR-NVSTGDVNVEMNAAPGVDLTQLLNNMR-QSLE	c5: Carbamidome	17	0	17
wt	Vacuolar membrane protein PEP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PEP5 PE=1 SV=2	sp|P12868	117484	1%	ILLFNTTGR		1	0	1
wt	60S ribosomal protein L31-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL31A PE=1 SV=1	sp|P0C2H8	12953,2	53%	AGLKDVVTR-EYTINLHK-LAPELNQAIWK-LHMGTDDVR-NEEEDAKNPLFSYVEPVLVASAK-NPLFSYVEPVLVASAK		6	0	6
wt	Histone H2B.1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HTB1 PE=1 SV=2	sp|P02293,sp|P02294	14253	31%	EIQTAVR-ETYSSYIYK-KETYSSYIYK-LILPGELAK-SMSILNSFVNDIFER		5	0	5
wt	Non-classical export protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NCE102 PE=1 SV=1	sp|Q12207	18967,7	13%	mLALADNILR-RTGQVGVPTISQV	m1: Oxidation (+	2	0	2
wt	Eukaryotic translation initiation factor 3 subunit G OS=Saccharomyces cerevisiae (strain YJM789) GN=TIF35 PE=3 SV=1	sp|A6ZZ25,sp|Q04067	30474,6	4%	GSPAGPSAVTAR		1	0	1
wt	V-type proton ATPase subunit B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VMA2 PE=1 SV=2	sp|P16140	57751,6	32%	AIVQVFEGTSGIDVK-GIYPPINVLPSLSR-IPIFSASGLPHNEIAAQIcR-IPVSEDMLGR-IYPEEMISTGVSAIDTMNSIAR-LSLEFLEK-QGQVLEIR-TFITQGAYEDR-TSLFLNLANDPTIER-TTVEFTGESLR-TVFESLDQAWSLLR-YNE		12	0	12
wt	Ribosome biogenesis protein 15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOP15 PE=1 SV=1	sp|P53927	25448,1	6%	TLEEYSGIIYVSR		1	0	1
wt	Exosome complex component RRP4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RRP4 PE=1 SV=1	sp|P38792	39427,8	4%	STGPTGAVSLNPSITR		1	0	1
wt	Protein EMP47 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EMP47 PE=1 SV=1	sp|P43555	50332,5	3%	ILANDINALETK		1	0	1
wt	Pre-mRNA-processing factor 31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP31 PE=1 SV=2	sp|P49704	56304,9	5%	ILQQQEIDFIK-LLPFFNEIIPLIK		2	0	2
wt	Fumarate hydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FUM1 PE=1 SV=2	sp|P08417	53152,6	3%	AIQQAADEVASGK		1	0	1
wt	Aspartyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DPS1 PE=1 SV=3	sp|P04802	63517,8	7%	GEEILSGAQR-IHDHALLQER-LPLIQSR-QQASLIQGLVK		4	0	4
wt	Altered inheritance rate of mitochondria protein 38 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AIM38 PE=1 SV=1	sp|P53721	25345,2	5%	ILTQDEIEAHR		1	0	1
wt	Uncharacterized protein YMR086W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YMR086W PE=1 SV=1	sp|Q04279	105876,3	1%	LPQAQEVSVTK		1	0	1
wt	Nucleoporin NUP133 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP133 PE=1 SV=1	sp|P36161	133327,5	2%	EVFNILVEELK-GIFQTWQLSATNSHPTK		2	0	2
wt	2-isopropylmalate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LEU4 PE=1 SV=1	sp|P06208,sp|Q12166	68409,3	1%	TVEALTGAK		1	0	1
wt	DNA-directed RNA polymerase I subunit RPA135 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA135 PE=1 SV=1	sp|P22138	135745,4	24%	EcGSILTTQQSVPR-EIFDGIIGNDVK-FQELQTVSIK-FVGGNETTTVAIPFVLK-IFIDDSQIWEDGQGNK-IGSISTVccR-IIADTLR-ISTQQSDVSR-KNEYLVPVVMILK-LLNSSDYTQASVcR-LQTGQTPIVK-LSVSVE	c2: Carbamidome	20	0	20
wt	40S ribosomal protein S20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS20 PE=1 SV=3	sp|P38701	13906,8	44%	EKVEEQEQQQQQIIK-ITLTSTK-QLENVSSNIVK-TWETYEmR-VEEQEQQQQQIIK-YIDLEAPVQIVK		6	0	6
wt	GTP-binding protein RHO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RHO1 PE=1 SV=3	sp|P06780	23152	5%	NDPQTIEQLR		1	0	1
wt	Elongation factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EFT1 PE=1 SV=1	sp|P32324	93290,3	33%	ADLMLYVSK-AFNmFILDPIFR-ALLELQVSK-ATYAGFLLADPK-AVQYLHEIK-AYLPVNESFGFTGELR-EDLYQTFAR-EGPIFGEEMR-ETVESESSQTALSK-GQVVSEEQRPGTPLFTVK-IKPVVVINK-IQGPNYVPGK-ISPPVVAYR-		23	0	23
wt	Nuclear protein SNF4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNF4 PE=1 SV=1	sp|P12904	36402,5	4%	LVGVLTLSDILK		1	0	1
wt	Polyadenylate-binding protein, cytoplasmic and nuclear OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PAB1 PE=1 SV=4	sp|P04147	64345,4	72%	AHYTNLYVK-AIEQLNYTPIK-ALYDTFSVFGDILSSK-AVEALNDSELNGEK-dSQLEETK-EAIDALNGmLLNGQEIYVAPHLSR-EASAAYESFK-EASAAYESFKK-FGPIVSASLEK-FGPIVSASLEKDADGK-GFGFVcFSTPEEATK-GF		38	0	38
wt	Cytochrome B pre-mRNA-processing protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CBP2 PE=1 SV=2	sp|P03874	73864,9	3%	ILANEEGKPFYLDANSATTR		1	0	1
wt	54S ribosomal protein L2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRP7 PE=1 SV=1	sp|P12687	43229	7%	DIELATSYLIR-KYEGQDVSTGEIImR		2	0	2
wt	U6 snRNA-associated Sm-like protein LSm6 OS=Saccharomyces cerevisiae (strain YJM789) GN=LSM6 PE=3 SV=1	sp|A6ZYX7,sp|Q06406	9398	33%	ASTEGSVTTEFLSDIIGK-LASGLLYSGR		2	0	2
wt	Probable alpha-1,6-mannosyltransferase MNN11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MNN11 PE=1 SV=2	sp|P46985	47860,9	5%	SAGASYSPSHGLYINEIPASSR		1	0	1
wt	Replication factor C subunit 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RFC4 PE=1 SV=1	sp|P40339	36150,5	3%	TLSLQLPWVEK		1	0	1
wt	ATP-dependent molecular chaperone HSP82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP82 PE=1 SV=1	sp|P02829	81410,2	38%	AELINNLGTIAK-AILFIPK-APFDLFESK-EILGDQVEK-ELISNASDALDK-GVVDSEDLPLNLSR-HSEFVAYPIQLVVTK-LEEVDEEEEKKPK-LFLKDDQLEYLEEK-LGVHEDTQNR-LIEAFNEIAEDSEQFEK-LLDAPAAIR-LLYETAI		24	0	24
wt	External NADH-ubiquinone oxidoreductase 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NDE1 PE=1 SV=1	sp|P40215	62776,5	30%	AIADLAVGEAK-EISDAQEIR-GALAYIGSDK-KVDATTITAK-LQLLGAK-NLDTTLYNVVVVSPR-NNDYDLDLK-NYFLFTPLLPSTPVGTIELK-TGDGDIENIPYGVLVWATGNAPR-TLVILGSGWGSVSLLK-TQSQIEDFK-VTLVEAI		14	0	14
wt	Magnesium-activated aldehyde dehydrogenase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ALD6 PE=1 SV=4	sp|P54115	54415,5	21%	ANFQGAITNR-GYFIRPTVFYDVNEDMR-IVKEEIFGPVVTVAK-SAHLVFDDANIKK-SVAVDSSESNLK-SVAVDSSESNLKK-TLPNLVNGIFK-TVGAALTNDPR-VGIPAGVVNIVPGPGR		9	0	9
wt	54S ribosomal protein L3, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRPL3 PE=1 SV=2	sp|P36516	44001,2	3%	STVNEIPESVASK		1	0	1
wt	Casein kinase I homolog HRR25 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HRR25 PE=1 SV=1	sp|P29295	57342	5%	YASVNTHLGIEQSR-YLSGGVGIPFIR		2	0	2
wt	Putative COX1/OXI3 intron 1 protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=aI1 PE=1 SV=2	sp|P03875	96085	1%	TIINNYK		1	0	1
wt	Poly(A) RNA polymerase protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PAP2 PE=1 SV=1	sp|P53632	66033,5	4%	AFAGAFDLLTNR-NLATEVEVVAK		2	0	2
wt	Suppressor protein STM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STM1 PE=1 SV=3	sp|P39015	29995,4	44%	EAQADAAAEIAEDAAEAEDAGKPK-GNNTANATNSANTVQK-KADVPPPSADPSK-KVELDAER-NRPRPSGNEGAIR-sNPFDLLGNDVEDADVVVLPPK-TAQLSLQDYLNQQANNQFNK-TAQLSLQDYLNQQANNQFNKVPEAK		8	0	8
wt	Mitochondrial peculiar membrane protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MPM1 PE=1 SV=1	sp|P40364	28471,4	4%	STAVEPLAR		1	0	1
wt	Mannan polymerase complexes subunit MNN9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MNN9 PE=1 SV=3	sp|P39107	45956,7	3%	ELIELGFITPR		1	0	1
wt	U1 small nuclear ribonucleoprotein A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MUD1 PE=1 SV=1	sp|P32605	34379,9	43%	GNDETYNLDIK-IKNQLGSTYK-LQNNDVTIGFAK-MTNQAFLTFVTQEEADRFLEK-NLAFVEYETVADATK-NQLGSTYK-sALYFQNLPSRPANK-TNSLLGLSIEmQK-VSNTMENPPNK-YAINPSLPLPHNK-YTTTALK		11	0	11
wt	13 kDa ribonucleoprotein-associated protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNU13 PE=1 SV=1	sp|P39990	13569,4	37%	AcGVSRPVIAASITTNDASAIK-DKIETLLI-NVPYVFVPSR-TQIYAVK	c2: Carbamidome	4	0	4
wt	Protein transport protein SEC31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEC31 PE=1 SV=3	sp|P38968	138720,8	1%	SLPAQNPATATTSK		1	0	1
wt	40S ribosomal protein S23-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS23A PE=1 SV=1	sp|P0CX29,sp|P0CX30	16038,3	28%	AKGDIPGVR-LGIESK-LLGTAFK-VSGVSLLALWK-WAENNYK		5	0	5
wt	THO complex subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=THO2 PE=1 SV=1	sp|P53552	183940,5	31%	AFEENVLPFVELNNR-AISLVENDDETR-ALSIDTIAK-ANPYQASSYK-DDNSVISSR-DILVTGISHQR-DLFTTFWR-ELIITVGGIR-EPYPDTTSSYSEAAAPEYTK-EPYPDTTSSYSEAAAPEYTKR-FFIALLR-FPEKPFQEGK-FQTQDY		44	0	44
wt	DNA replication licensing factor MCM4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MCM4 PE=1 SV=2	sp|P30665	105006,4	1%	ELGTSNLNLDAR		1	0	1
wt	40S ribosomal protein S29-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS29A PE=1 SV=3	sp|P41057	6660,7	38%	AHENVWFSHPR-VcSSHTGLIR		2	0	2
wt	5'-3' exoribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KEM1 PE=1 SV=1	sp|P22147	175468	8%	EVQIIFSGHEVPGEGEHK-FIAVSLESDSLTK-FTTDSEEK-GAFPVLLQTFK-GPIPIEEEFPLNSK-IGPmEAIATVFPVTGLVR-LIEAMQPYLR-LVSLTDGK-QLENISLEGER-QTFPDFFFR-VVYIQDSGK		11	0	11
wt	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=COQ5 PE=1 S	sp|P49017	34685,8	4%	LVGDVFSSVANR		1	0	1
wt	Sterol 24-C-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ERG6 PE=1 SV=4	sp|P25087	43431,6	6%	LGLAPEGSK-YVQNLANLATFFR		2	0	2
wt	Translation initiation factor eIF-2B subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GCD7 PE=1 SV=1	sp|P32502	42570,3	3%	TPVFAVAGLYK		1	0	1
wt	Elongator complex protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ELP3 PE=1 SV=1	sp|Q02908	63658,8	27%	EINLNGLITK-EYFENPDFR-FQHQGFGTLLMEEAER-GTGLYELWK-ISVISGVGVR-IYPTLVIR-LEIGVQSLYEDVAR-LHNALSGFNGNDIDEAILYSQQSLTK-LTDIINSIPDQYKK-SVcETFAVSK-SYSANALVDLVAR-VQPDQVELIR		12	0	12
wt	Nucleolar protein 9 OS=Saccharomyces cerevisiae (strain YJM789) GN=NOP9 PE=3 SV=1	sp|A6ZPV9,sp|B3LQ92,sp|C7GV42,s	77725,5	3%	LVTSQITSK-SDISQSTITK		2	0	2
wt	60S ribosome subunit biogenesis protein NOP8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOP8 PE=1 SV=1	sp|Q08287	56967	3%	EIGQGTISNTETLR		1	0	1
wt	54S ribosomal protein L8, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRPL8 PE=1 SV=4	sp|P22353	26946	6%	AITTSNSVAQAELK		1	0	1
wt	Eukaryotic translation initiation factor 1A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TIF11 PE=1 SV=1	sp|P38912	17435,7	7%	NQGELPENAK		1	0	1
wt	Protein MKT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MKT1 PE=1 SV=2	sp|P40850	94499,4	33%	EINLLTQPINR-ENIQNYQR-EQYLDAIGGFPTSLK-FILGMEFPNK-FLLEISK-GWTQWNNLISSNQNSYIDQPIQPQEPFR-LDEEVQPPAPSALSQATLR-LIDENVFK-LNELNIDSK-LNSPFNLLSTNFLR-LSLDNFGWAR-mSPSmFETIN		22	0	22
wt	Inorganic phosphate transporter PHO86 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PHO86 PE=1 SV=1	sp|P46956	34883,2	18%	GFTYIQSIR-INQLVGSK-LLIDVYSFDSTLK-NTGSVAGWFYQLAR-VFGINLNDLVAR		5	0	5

wt	Serine/threonine-protein kinase PTK2/STK2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PTK2 PE=1 SV=1	sp|P47116	91403,5	1%	LADPNPATR		1	0	1
wt	Eukaryotic translation initiation factor 5B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FUN12 PE=1 SV=2	sp|P39730	112271,5	13%	ALLTPQPLR-APFVVALNK-GPMIIGVDVLEGTLR-IAANDLEK-IPVMSIGLGPVYK-LEDPSGQQPIWGR-QTFDVPGLLVIDTPGHESFSNLR-QTNVQGGEAGGITQQIGATYFPIDAIK-VPAGLAALR		9	0	9
wt	60S ribosomal protein L33-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL33A PE=1 SV=3	sp|P05744	12154,2	45%	IAYVYR-IEGVATPQDAQFYLGK-IFLYPSNI-RVNNPNVSLIK-TFGASVR-VNNPNVSLIK		6	5	1
wt	Pre-mRNA-splicing factor SLT11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ECM2 PE=1 SV=1	sp|P38241	40927,1	8%	FQSSELGER-ISETLVTPK-ITDTVSQLLGIK		3	0	3
wt	40S ribosomal protein S27-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS27A PE=1 SV=1	sp|P35997,sp|P38711	8879,3	38%	LSEGTSFR-TLVQGPR-VLVQDLLHPTAASEAR		3	0	3
wt	Pre-mRNA-splicing factor CWC22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CWC22 PE=1 SV=1	sp|P53333	67297,9	6%	ESLETLFEIR-LTEEEScPQGR-YILQTQELSSTLR		3	0	3
wt	Nascent polypeptide-associated complex subunit alpha OS=Saccharomyces cerevisiae (strain YJM789) GN=EGD2 PE=3 SV=1	sp|A6ZT99,sp|P38879	18709,1	29%	DNQIYAIEKPEVFR-LAAAQQQAQASGImPSNEDVATK-SAGGNYVVFGEAK		3	0	3
wt	mRNA-binding protein PUF3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PUF3 PE=1 SV=1	sp|Q07807	98070	2%	ELATSPASEK-FASNVVEK		2	0	2
wt	Target of rapamycin complex 1 subunit KOG1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KOG1 PE=1 SV=2	sp|P38873	177614,5	1%	STGLLTEWLQIR		1	0	1
wt	Pyruvate dehydrogenase complex protein X component, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDX1 PE=1	sp|P16451	45363,8	12%	ITPVEFEEQLVFHAPASIPFDK-KPSADSTEATQQHLK-LPQEANTANAK		3	0	3
wt	Protein LSM12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LSM12 PE=1 SV=1	sp|P38828	21314	41%	DIIILDDVK-LYSFNSSNNTLTIQTTK-QQIKPSYVNVER-sVSLEQTLGFR-VLHEGSNQSITLIQR-VTNVLDVVTEGR		6	0	6
wt	Mitochondrial import inner membrane translocase subunit TIM44 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TIM44 PE=1 SV	sp|Q01852	48855,7	1%	DLASGK		1	0	1
wt	Citrate synthase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CIT1 PE=1 SV=2	sp|P00890	53362,3	8%	ANQEVLEWLFK-GLVWEGSVLDPEEGIR-ITSTDPNADYGK		3	0	3
wt	Keratin, type I cytoskeletal 9 - Homo sapiens	sp|P35527	62131	28%	EIETYHNLLEGGQEDFESSGAGK-FSSSSGYGGGSSR-GGSGGSYGGGGSGGGYGGGSGSR-HGVQELEIELQSQLSK-IKFEmEQNLR-LASYLDK-mTLDDFR-QEYEQLIAK-QGVDADINGLR-QVLDNLTMEK-SGGGGGGGLGSGG		14	1	13
wt	Uncharacterized protein YDR132C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDR132C PE=1 SV=1	sp|Q03900	57198,7	2%	ISQVQTLLTDK		1	0	1
wt	Sphingolipid long chain base-responsive protein LSP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LSP1 PE=1 SV=1	sp|Q12230	38071,6	5%	APTAAELQAPPPPPSSTK		1	0	1
wt	DNA topoisomerase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TOP1 PE=1 SV=2	sp|P04786	89998,9	7%	FYQEVEVDK-LAANSSLK-TVAILcNHQR-VNPEDIVLNLSK-YLQNYMPGLTAK		5	0	5
wt	Suppressor of yeast profilin deletion OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SYP1 PE=1 SV=3	sp|P25623	96140,1	2%	SPYEATETIR-VILNQAFIER		2	0	2
wt	Nucleoporin NUP57 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP57 PE=1 SV=1	sp|P48837	57499,3	6%	LGTQLATLK-NISSQLDSK-NQVQTENVAQAR		3	0	3
wt	Peroxisomal acyl-coenzyme A thioester hydrolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TES1 PE=1 SV=1	sp|P41903	40260,6	4%	ILELVPLSPTSFVTK		1	0	1
wt	Proteasome component Y13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE9 PE=1 SV=1	sp|P23638	28715,8	3%	TTIFSPEGR		1	0	1
wt	Single-stranded nucleic acid-binding protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SBP1 PE=1 SV=2	sp|P10080	32989,9	15%	ATKEEVAEFFGTDADSISLPMR-EEVAEFFGTDADSISLPMR-IFTSDSANR-SKDTLYINNVPFK		4	0	4
wt	Probable inosine-5'-monophosphate dehydrogenase IMD3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IMD3 PE=1 SV=1	sp|P50095	56586,2	32%	EQAANLIAAGADGLR-FGFSGFPVTEDGKR-GMGSIDAMQK-LDGLSVQELMDSK-LLIVDDNGNLVSMLSR-LmGIVTSR-NPVTGAQGITLSEGNEILK-NPVTGAQGITLSEGNEILKK-NQNYPLASK-QLLcGAAIGTIDADKER-TAL		13	0	13
wt	cDNA FLJ75925, highly similar to Homo sapiens keratin 16 - Homo sapiens	sp|A8K488,sp|P08779	51269	20%	APSTYGGGLSVSSR-GScGIGGGIGGGSSR-IIAATIENAQPILQIDNAR-LAADDFR-LASYLDK-LLEGEDAHLSSQQASGQSYSSR-VTMQNLNDR		7	3	4
wt	Myosin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MYO2 PE=1 SV=1	sp|P19524	180687	32%	AcGVLETIR-AINAVVISESLPGFSAGETSGFLNK-DAQLELEDMVK-EHLIDIDNQK-ELGWIGAEVIK-GELEPHLFAIAEEAYR-GFEVPDAGVAIQLSK-GHEHSSSIFITPETGPFTDPFSLIK-GIcYSLTPAQLQK-GLQLN	c2: Carbamidome	38	0	38
wt	Triosephosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TPI1 PE=1 SV=2	sp|P00942	26795,6	47%	ADVDGFLVGGASLKPEFVDIINSR-ASGAFTGENSVDQIK-ILYGGSANGSNAVTFK-KPQVTVGAQNAYLK-QLNAVLEEVK-SYFHEDDKFIADK-TFFVGGNFK-TLDVVER-WVILGHSER		9	0	9
wt	UTP--glucose-1-phosphate uridylyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UGP1 PE=1 SV=1	sp|P32861	55989,9	49%	AKFENELDSFFTLFR-DGHEINVLQLETAcGAAIR-EGNTFLDLSVR-EHIDEFK-FENELDSFFTLFR-FGPNPLIK-FTNFNTNNLWINLK-GGTLISYDGQVR-GTVIIVcSDGHK-HFDGAHGVVVPR-ILNHMIETGAEYImELTDK-IVELDI		22	0	22
wt	Protein CWC16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YJU2 PE=1 SV=1	sp|P28320	32313,3	9%	NYVPQKPNDDLNAK-TPLFNPTSTK		2	0	2
wt	Protein PSP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PSP2 PE=1 SV=2	sp|P50109	65586,3	3%	QNNEEGLTSDSSLDASGNKK		1	0	1
wt	Transcription initiation factor TFIID subunit 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF10 PE=1 SV=1	sp|Q12030	23019,3	7%	SSVAVSNANNSQAR		1	0	1
wt	E3 ubiquitin-protein ligase RSP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSP5 PE=1 SV=1	sp|P39940	91817,4	1%	GNQLNANTELER		1	0	1
wt	Actin-related protein 2/3 complex subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARC35 PE=1 SV=1	sp|P53731	39567,7	3%	VFLQEFVDAR		1	0	1
wt	Pre-mRNA-splicing factor NTC20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NTC20 PE=1 SV=1	sp|P38302	15970,4	7%	LAPImEVLEK	m5: Oxidation (+	1	0	1
wt	Heat shock protein 60, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP60 PE=1 SV=1	sp|P19882	60753	26%	AAVEEGILPGGGTALVK-GSIDITTTNSYEK-GVETLAEAVAATLGPK-ISSIQDILPALEISNQSR-LLASAMEK-LLQEVASK-NVLIEQPFGPPK-TNEAAGDGTTSATVLGR-VEFEKPLLLLSEK-VGGASEVEVGEK-VLDEVVVDNFDQK		11	0	11
wt	40S ribosomal protein S5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS5 PE=1 SV=3	sp|P26783	25038,5	43%	AQcPIIER-DASLVDYVQVR-GSSTSYAIK-KAQcPIIER-LTNSLMmNGR-QAVDVSPLR-QPIFVAHTAGR-TIAETLAEELINAAK-vNQAIALLTIGAR-WSFEEVEVK	c3: Carbamidome	10	0	10
wt	60S ribosomal protein L35-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL35A PE=1 SV=1	sp|P0CX84,sp|P0CX85	13910,2	44%	EQLASQLVDLK-EQLASQLVDLKK-FEASQVTEK-KSIAcVLTVINEQQR-LSRPSLPK-QIAFPQR-SIAcVLTVINEQQR-SKEQLASQLVDLK		8	0	8
wt	Eukaryotic translation initiation factor 3 subunit A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPG1 PE=1 SV=1	sp|P38249	110348,5	9%	FQQVDVSVK-GHVYIDPNEAK-QAALQSLHDFITAR-QVIIAEVSK-TAGGSSPATPATPATPATPTPSSGPK-WATPSTVEPVVFK		6	0	6
wt	Ribosome biogenesis protein RLP7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RLP7 PE=1 SV=1	sp|P40693	36560,6	3%	LVETNTGVFVK		1	0	1
wt	THO complex subunit HPR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HPR1 PE=1 SV=2	sp|P17629	87834	20%	ALEEEASFPER-ALPVSFDSIR-INSASQTEGDELKSEQTQPK-IPTGLDKIEQEVK-ISSETSGGEAKDEIIR-KPEGVYEAAQAK-KVEALDDSFK-LENNDILNTVK-NLISSDETR-SSEVSSQDPDSGVAGEFAPQNTTAQLENPK-TGVDGL		11	0	11
wt	Mitochondrial peroxiredoxin PRX1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRX1 PE=1 SV=1	sp|P34227	29496,7	9%	LIFTYPSTVGR-NVGFPIIGDTFR		2	0	2
wt	Nucleoporin NUP170 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP170 PE=1 SV=1	sp|P38181	169483,7	1%	IDNDPIEK		1	0	1
wt	Alcohol dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADH1 PE=1 SV=5	sp|P00330	36848,7	58%	aNELLINVK-ANGTTVLVGmPAGAK-ATDGGAHGVINVSVSEAAIEASTR-ccSDVFNQVVK-EALDFFAR-EELFR-EKDIVGAVLK-GVIFYESHGK-IGDYAGIK-LPLVGGHEGAGVVVGmGENVK-SANLmAGHWVA	n-term: Acetyl (+	17	0	17
wt	Small nuclear ribonucleoprotein G OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMX2 PE=1 SV=1	sp|P40204	8482,4	12%	ILLNINGSR		1	0	1
wt	37S ribosomal protein S17, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRPS17 PE=1 SV=1	sp|Q03246	27636	4%	FFAIAEIIR		1	0	1
wt	Elongator complex protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ELP4 PE=1 SV=1	sp|Q02884	51157,7	7%	APGNVPLSDTTAR-LPVFTDR-RAPGNVPLSDTTAR-VTVQNLNETQR		4	0	4
wt	Protein LUC7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LUC7 PE=1 SV=1	sp|Q07508	30195,1	19%	EYLAILSR-IGLmGQEIDSLIR-LQELISK-NITENVGQSAQQK-TATTLPGR		5	0	5
wt	ADP-ribosylation factor-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARL1 PE=1 SV=4	sp|P38116	20435,3	6%	ILILGLDGAGK		1	0	1
wt	Branchpoint-bridging protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MSL5 PE=1 SV=1	sp|Q12186	53035,8	3%	AVTSPEGQNDLKR		1	0	1
wt	Prohibitin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PHB1 PE=1 SV=2	sp|P40961	31427,9	34%	AEGEAESAEFISK-LEDVSITHMTFGPEFTK-LIDVITK-QIAQQDAER-QQVVGEGTHFLVPWLQK-SIVAQFDAAELITQR-VGDGLLLIR-VLPSIGNEVLK		8	0	8
wt	40S ribosomal protein S11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS11A PE=1 SV=1	sp|P0CX47,sp|P0CX48	17748,8	56%	cPFTGLVSIR-ILTGTVVSTK-NVPVHVSPAFR-QPHIFNNPK-RAYLHYIPK-sTELTVQSER-TAIEGSYIDK-TAIEGSYIDKK-VQVGDIVTVGQcRPISK	c1: Carbamidome	9	0	9
wt	Vacuolar protein sorting-associated protein 35 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VPS35 PE=1 SV=2	sp|P34110	109147,8	2%	LQLTSSTTAPPNSPVTSK		1	0	1
wt	Eukaryotic translation initiation factor 3 subunit B OS=Saccharomyces cerevisiae (strain YJM789) GN=PRT1 PE=3 SV=1	sp|A6ZPJ1,sp|P06103	88330,8	5%	MVGDSLIVHDATK-NINDNNDVSASLK-TQFSNLQIcR		3	0	3
wt	Sphingolipid long chain base-responsive protein PIL1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PIL1 PE=1 SV=1	sp|P53252	38350,3	8%	APTASQLQNPPPPPSTTK-IALIAGYGK		2	0	2
wt	60S acidic ribosomal protein P0 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP0 PE=1 SV=2	sp|P05317	33717,4	36%	AGAVAPEDIWVR-AVNTGMEPGK-AVVLMGK-EYLEEYK-GFLSDLPDFEK-GNVGFVFTNEPLTEIK-GTIEIVSDVK-LREYLEEYK-NVIVSNR-SLFVVGVDNVSSQQmHEVR-TSFFQALGVPTK		11	0	11
wt	Vesicle-associated membrane protein-associated protein SCS2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SCS2 PE=1 SV=3	sp|P40075	26924,8	8%	YLISPDVHPAQNQNIQENK		1	0	1
wt	[NU+] prion formation protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NEW1 PE=1 SV=1	sp|Q08972	134335,5	1%	LIVDTLQDPSKVPESVK		1	0	1
wt	DNA-directed RNA polymerase II subunit RPB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPO21 PE=1 SV=2	sp|P04050	191615,1	1%	EGLIDTAVK-TAETGYIQR		2	1	1
wt	Ubiquitin carboxyl-terminal hydrolase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UBP3 PE=1 SV=1	sp|Q01477	101920,1	7%	GIEPLGSIALR-LPQVLLIQFK-TSSPSPSPPAAK-VIQEPQATVLPVVDKK-YGHELIIPEESMSSITLK		5	0	5
wt	Bifunctional purine biosynthetic protein ADE5,7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADE5,7 PE=1 SV=1	sp|P07244	86068,6	2%	VLSVTSTAQDLR		1	0	1
wt	Protein transport protein SEC23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEC23 PE=1 SV=1	sp|P15303	85387,6	5%	FIDTEAGGSQAR-VQGLIGHASAVK-YADYNKDDPQSFR		3	0	3
wt	Importin subunit beta-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KAP95 PE=1 SV=1	sp|Q06142	94778,6	5%	ImVDNTGAEQPENVKR-TNALTALVSIEPR-WITQVSPEAK	m2: Oxidation (+	3	0	3
wt	60S ribosomal protein L32 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL32 PE=1 SV=1	sp|P38061	14771,8	39%	DLETLTmHTK-GIDSVVR-TFLVANVK-TYAAEIAHNISAK-VAENWR-VVILAR	m7: Oxidation (+	6	0	6
wt	Helicase SEN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEN1 PE=1 SV=2	sp|Q00416	252506,4	0%	VAIELVDYLFR		1	0	1
wt	Bud site selection protein 31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BUD31 PE=1 SV=1	sp|P25337	18448,1	8%	IKPTLTDFEIQLR		1	0	1
wt	60S ribosomal protein L38 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL38 PE=1 SV=1	sp|P49167	8827,2	41%	GSSSLYTLVINDAGK-LIQSLPPTLK-QFLELTR		3	0	3
wt	Transposon Ty1-DR1 Gag polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1A-DR1 PE=1 SV=1	sp|Q03856	49057,2	43%	AHNVSTSNNSPSTDNDSISK-DILSVDYTDImK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-HDLHLRPGTY-KYVRPPPMLTSPNDFPNWVK-LNNNGIHINNK-mESQQLSNYPHISHGSAcASVTSK-MQSDTQEANDIVTL		13	12	1
wt	Orotidine 5'-phosphate decarboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=URA3 PE=1 SV=2	sp|P03962	29240,4	16%	ELLELVEALGPK-LQYSAGVYR-SDKDFVIGFIAQR-YNFLLFEDR		4	0	4
wt	Transcription initiation factor TFIID subunit 11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF11 PE=1 SV=1	sp|Q04226	40625,1	7%	LLVTNLDKDQTNR-TGGTSINNQLNK		2	0	2
wt	Cytochrome c oxidase subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=COX2 PE=1 SV=1	sp|P00410	28568,3	18%	FVVTAADVIHDFAIPSLGIK-IEAVSLPK-LLDTDTSmVVPVDTHIR		3	0	3
wt	Pre-mRNA-splicing factor RSE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSE1 PE=1 SV=1	sp|Q04693	153790,1	3%	LTVSPDTNDR-SQIVSDSPLSIATK-TLVNQPLTR-YPLDVITLQQK		4	0	4
wt	Cell division control protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC10 PE=1 SV=1	sp|P25342	37026,3	26%	ISTHTLVEDR-LTEIANVIPVIGK-mDPLSSVQPASYVGFDTITNQIEHR-SDTLTLDER-STLINTLFASHLIDSATGDDISALPVTK		5	0	5
wt	Pre-mRNA-splicing factor ISY1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ISY1 PE=1 SV=2	sp|P21374	28024,2	3%	ALELPEVK		1	0	1
wt	DNA polymerase V OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=POL5 PE=1 SV=1	sp|P39985	115901,8	1%	ISQLTLDSIVK		1	0	1
wt	Acetyl-CoA carboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ACC1 PE=1 SV=2	sp|Q00955	250359,5	21%	AHLMGTTYVYDFPELFR-AIQVEGQPIILTGAPAINK-ALINNVSGYVIK-cDIILR-DLLQTMFPVDFIHEGK-EEDFIALYHQAANEIPGSPIFIMK-EILIQGALPSVK-ELLPIYGQISLQFADLHDR-FQLPSAAFSTFPTVK-GSFFETLSGWAI		33	0	33
wt	Heat shock protein SSA4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSA4 PE=1 SV=3	sp|P22202	69652,7	37%	ARFEELcADLFR-ATAGDTHLGGEDFDSR-DAGTIAGLNVLR-DAVVTVPAYFNDSQR-ETAENFLGTEVK-FELSGIPPAPR-GGKPVVQVEYK-IINEPTAAAIAYGLDK-IINEPTAAAIAYGLDKK-ITITNDK-KSEVFST	c7: Carbamidome	22	9	13
wt	Nuclear migration protein NUM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUM1 PE=1 SV=2	sp|Q00402	313042,2	0%	LTNLSmEcR	m6: Oxidation (+	1	0	1
wt	RNA annealing protein YRA2 OS=Saccharomyces cerevisiae (strain YJM789) GN=YRA2 PE=3 SV=1	sp|A7A075,sp|B3LQP5,sp|B5VLV2,sp	23836,6	46%	aFDEIIGNSHTDSSSNHK-EFGSPIFSK-EREEPPLPK-IEVEIYQPQR-IEVEIYQPQRK-IPLDVSDYTLDDmIK-LGFAPSDAASR-NNTPTSVEALDAELDAYmKG	n-term: Acetyl (+	8	0	8
wt	Glucose-6-phosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PGI1 PE=1 SV=3	sp|P12709	61300,4	31%	ANKPmYVDGVNVAPEVDSVLK-EANVTGLR-ELDNSSTISTHDASTNGLINQFK-FGIDTK-HFAALSTNETEVAK-LATELPAWSK-LIPSDFILAAQSHNPIENK-mLASNFFAQAEALmVGKDEEQVK-NmFGFESWVG	m5: Oxidation (+	12	0	12
wt	3-methyl-2-oxobutanoate hydroxymethyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ECM31 PE=1 SV=1	sp|P38122	34465,5	4%	QAVNMTDIATQGLK		1	0	1
wt	Pre-tRNA-processing protein PTA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PTA1 PE=1 SV=1	sp|Q01329	88478	2%	VLESLGPFLENK		1	0	1
wt	Multiprotein-bridging factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MBF1 PE=1 SV=2	sp|O14467	16404	58%	AIPNQQVLSK-GNNIGSPLGAPK-INEKPTVVNDYEAAR-KLDPNVGR-QGLVVSVDKK-RQGLVVSVDK-sDWDTNTIIGSR-sQGQINAAR-VDRETDIVKPK		9	0	9
wt	60S ribosomal protein L5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL5 PE=1 SV=4	sp|P26321	33716,1	21%	ADPAFKPTEK-eQYAAESK-FQTPFR-FSELFK-GASDGGLYVPHSENR-LGLDETYK-VFLDIGLQR		7	0	7
wt	Structural maintenance of chromosomes protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMC1 PE=1 SV=1	sp|P32908	141288,4	4%	IDDLSANQR-LDTQLNDLR-LQFETDR-LSALNSEISSLK-LVGLELSNFK		5	0	5
wt	La protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LHP1 PE=1 SV=2	sp|P33399	32104,9	4%	RVPLDLTAAR		1	0	1
wt	Serine hydroxymethyltransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SHM1 PE=1 SV=2	sp|P37292	53688	18%	ALELYGLDPAK-AVmDLLGSELQNK-HSITLIPSENFTSK-IGTPAmTTR-SALFPSGLR-SESLcQAR-VETILSALNIAANK-YSEGYPGER		8	0	8
wt	ATP-dependent RNA helicase SUB2 OS=Saccharomyces cerevisiae (strain YJM789) GN=SUB2 PE=3 SV=1	sp|A6ZXP4	50280,1	9%	AAEAGETGAATSATEGDNNNNAAAGDKK-TAVFYGGTPISK		2	0	2
wt	37S ribosomal protein MRP4, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRP4 PE=1 SV=1	sp|P32902	44153,9	7%	GIHIIDLNQTLSYLK-SVNFLLGVLAR		2	0	2
wt	60S ribosomal protein L26-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL26B PE=1 SV=2	sp|P53221	14235,3	41%	DDEVLVVR-FAVQVDK-ISSVYR-KAYFTAPSSER-QSLDVSSDR-QSLDVSSDRR-RDDEVLVVR-VLLSAPLSK		8	0	8
wt	ATP-dependent RNA helicase eIF4A OS=Saccharomyces cerevisiae (strain YJM789) GN=TIF1 PE=3 SV=1	sp|A6ZQJ1,sp|P10081	44698,3	31%	AIMPIIEGHDVLAQAQSGTGK-APQALmLAPTR-DAQIVVGTPGR-ELALQIQK-GVFGYGFEEPSAIQQR-ILISTDLLAR-KDELTLEGIK-TGTFSIAALQR-VFDNIQR-VHAcIGGTSFVEDAEGLR		10	0	10
wt	Small nuclear ribonucleoprotein Sm D1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMD1 PE=1 SV=1	sp|Q02260	16275,9	45%	LRNEQVTIELK-LTLPQPR-NEQVTIELK-NGTTVWGTLQSVSPQmNAILTDVK-QIILPDSNLSDSLLVDQK-QLNSLR		6	0	6
wt	Phosphoglucomutase-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PGM1 PE=1 SV=1	sp|P33401,sp|P37012	63114,7	2%	LSGTGSSGATIR		1	0	1
wt	mRNA turnover protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRT4 PE=1 SV=1	sp|P33201	27058,8	23%	APLTFTIPEGIVYSR-GGQIPAEEDVPmIHSLEPTmR-TPVLQEIR-YVWVLHLDDVR		4	0	4
wt	Protein BUR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BUR2 PE=1 SV=1	sp|Q05949	45723,3	5%	DRFPIEVTPENFANIFTDYK		1	0	1
wt	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP43 PE=1 SV=	sp|P53131	87564,8	5%	SNLSSTVLELK-TYPVELYYTPEFQR-YFNDAPLLAVPGR		3	0	3
wt	H/ACA ribonucleoprotein complex subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GAR1 PE=1 SV=1	sp|P28007	21481,3	8%	VDEILGPLNEVFFTIK		1	0	1
wt	Protein PBP4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PBP4 PE=1 SV=1	sp|Q07362	19881,4	24%	LFQSYTAGEK-QVLSETASGR-TTTSTTSVDGR-VSTATDWGTVSSSK		4	0	4
wt	Elongator complex protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ELP2 PE=1 SV=1	sp|P42935	89413,8	2%	LFAPWIYDASGR		1	0	1
wt	Mitochondrial outer membrane protein porin 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=POR1 PE=1 SV=4	sp|P04840	30429,5	68%	DFYHATPAAFDVQTTTANGIK-DGPLSTNVEAK-GAFDLcLK-LEFANLTPGLK-LPNSNVNIEFATR-lSEPVHK-NELITSLTPGVAK-NINDLLNK-QLLRPGVTLGVGSSFDALK-QPVKDGPLSTNVEAK-QTGLGLTQGWSNTNNLQTK-		16	0	16
wt	Cohesin subunit SCC3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IRR1 PE=1 SV=1	sp|P40541	133016,5	1%	LESTIAETQGSK		1	0	1
wt	Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IDH1 PE=1 SV=2	sp|P28834	39325,3	15%	DYAVFEPGSR-FAFDFAK-FTVTLIPGDGVGK-HVGLDIK-IPDIDLIVIR-LGDGLFR		6	0	6
wt	Protein HRB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HRB1 PE=1 SV=2	sp|P38922	52143	9%	ELDSTYEEK-GDYGPLLAR-NLPASVNWQALK-SDLYDLFETIGK		4	0	4
wt	Neutral trehalase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NTH1 PE=1 SV=3	sp|P32356	85882,8	1%	INENPVNR		1	0	1
wt	Uncharacterized GTP-binding protein YGR210C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YGR210C PE=1 SV=1	sp|P42942	45215,2	3%	AVLTSAVTEVFLR		1	0	1
wt	Pre-mRNA-splicing factor 8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP8 PE=1 SV=1	sp|P33334	279514,8	26%	AINGcIFTLNPK-ALNNAIPGGPK-AmLDPLEVHmLDFPNIAIRPTELR-ANPALYVLR-AQDVALAK-ATDLAGPANNPNEFMQFK-AVFWEIQSR-DLILTEYGR-DRHTLAYDR-EELALIEEAYDNPHDTLNR-ELGGLG	c5: Carbamidome	54	0	54
wt	Isocitrate dehydrogenase [NAD] subunit 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IDH2 PE=1 SV=1	sp|P28241	39740,6	30%	ENTEGEYSGIEHIVcPGVVQSIK-GPLATPIGK-ISIFEAVHGSAPDIAGQDK-LADGLFVNVAK-TGDLAGTATTSSFTEAVIK-TTYENVDLVLIR-YTVSFIEGDGIGPEISK	c15: Carbamidom	7	0	7
wt	RNA-binding protein NAB6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAB6 PE=1 SV=1	sp|Q03735	126143	1%	VLPTGDDAYR		1	0	1
wt	26S protease regulatory subunit 8 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPT6 PE=1 SV=4	sp|Q01939	45272,6	19%	GVILYGPPGTGK-LDILDPALLRPGR-LLQEPGSYVGEVIK-tAAVTSSNIVLETHESGIKPYFEQK-VEGSGGGDSEVQR		5	0	5
wt	mRNA-decapping enzyme subunit 2 OS=Saccharomyces cerevisiae (strain YJM789) GN=DCP2 PE=3 SV=1	sp|A6ZRW5,sp|P53550	108661,2	1%	GAAIFNENLSK		1	0	1
wt	rRNA biogenesis protein RRP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RRP5 PE=1 SV=1	sp|Q05022	193141,4	2%	APESVADFER-FIGLVLPSYAVDSR-VFGLVSGVVNVSHLR		3	0	3
wt	DNA-binding protein REB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=REB1 PE=1 SV=2	sp|P21538	91875,9	1%	FINEYEAIER		1	0	1
wt	Elongator complex protein 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IKI1 PE=1 SV=1	sp|P38874	35220,9	46%	aSSSHNPVILLK-FLSEIASPHcTMVATYHK-GLNNDIFQLR-HMVIIDSLNYISTEYITR-ILSLTESSPFILcLDSIAQTSYK-LIQEFVHQSK-QIISYLPAATATQAK-SLEYDFIVNSNTHEYELLSTTK-TVIPDWNNNYPDK	n-term: Acetyl (+	9	0	9
wt	rRNA-processing protein EBP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EBP2 PE=1 SV=1	sp|P36049	49735,3	2%	QSLDAVLVAR		1	0	1
wt	Heat shock protein 104 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP104 PE=1 SV=2	sp|P31539	102039,6	25%	ALTILTLAQK-DKETVNVVLK-DSKPEELDSK-EAQVDIEAIK-GADTNTPLEYLSK-IEVAEPSVR-IIDDDVPTILQGAK-ILDSALVTAAQLAK-IPQQQPAPAEITPSYALGK-ISSIVIFNK-LEDQVAEEERR-LFSLDLAALTAGAK-LIQNEI		20	0	20
wt	Keratin, type II cytoskeletal 5 - Homo sapiens	sp|P13647	62379,6	6%	FASFIDK-FLEQQNK-QNLEPLFEQYINNLR-YEDEINKR		4	4	0
wt	40S ribosomal protein S25-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS25B PE=1 SV=1	sp|P0C0T4,sp|Q3E792	12009,9	43%	AQHAVILDQEK-AQHAVILDQEKYDR-EGIIKPISK-IGGSLAR-QAIYTR-YVSVSVLVDR		6	0	6
wt	Serine/threonine-protein phosphatase PP1-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GLC7 PE=1 SV=1	sp|P32598	35909	11%	AHQVVEDGYEFFSK-QPILLELEAPIK-YPENFFILR		3	0	3
wt	66 kDa U4/U6.U5 small nuclear ribonucleoprotein component OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNU66 PE=1 SV=1	sp|Q12420	66432,4	4%	KDTILTLK-TSSNNELKGPEDLAR		2	0	2
wt	Nucleolar protein 58 OS=Saccharomyces cerevisiae (strain YJM789) GN=NOP58 PE=3 SV=1	sp|A6ZPE5,sp|Q12499	56959,8	5%	LIAHSGSLISLAK-SSSLIQDLDSSDK		2	0	2
wt	DnaJ-like chaperone JEM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=JEM1 PE=1 SV=3	sp|P40358	75147,9	2%	ILGVSPSASSK		1	0	1
wt	Chromatin structure-remodeling complex subunit RSC4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC4 PE=1 SV=2	sp|Q02206	72294,7	5%	LIQQIYIFSSK-QNLEIGQYSK-TPHVDYNAPLNPK		3	0	3

wt	Eukaryotic translation initiation factor 3 subunit I OS=Saccharomyces cerevisiae (strain YJM789) GN=TIF34 PE=3 SV=1	sp|A6ZMK5,sp|P40217	38756,2	36%	DTNSFLVDVSTLQVLK-EFIILGGGQEAK-IITHEGLDAATVAGWSTK-KYETDcPLNTAVITPLK-NPGSINIYEIER-SISDmQFSPDLTYFITSSR-VQGHFGPLNTVAISPQGTSYASGGEDGFIR		7	0	7
wt	mRNA 3'-end-processing protein RNA14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RNA14 PE=1 SV=2	sp|P25298	79964,2	20%	FGNLNNVYSLEK-FPQENLIEVFTSR-ISGLSAAR-LVNFLNDQVEIPTVESTK-NNLITGGQEAR-QNILYTALLANPDSPSLTFK-TLFETSVEK-VAEPSDNIHGDELR-VQDLTQLK-YFQNDGVYINK-YTQWEQEINSLTAR		11	0	11
wt	Keratin, type II cytoskeletal 1 - Homo sapiens	sp|P04264	66019,2	39%	AEAESLYQSK-FLEQQNQVLQTK-FVSTTYSGVTR-GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR-IEISELNR-LALDLEIATYR-LDSELK-LNDLEDALQQAK-mSGEcAPNVSVSVSTSHTTISGGGSR-NMQDmVEDYR-QISNLQ		21	0	21
wt	Transposon Ty1-NL2 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-NL2 PE=3 SV=1	sp|Q99337	198206,1	20%	AHNVSTSNNSPSTDNDSISK-AVSPTDSTPPSTHTEDSKR-DILSVDYTDImK-EVDPNISKSDILPSK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-GIPGYALHPSR-KYPYPFIHR-LIGLASYVGYK-LNNNGIHINNK-LVAISD		24	23	1
wt	GTP-binding protein YPT7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YPT7 PE=1 SV=1	sp|P32939	23043,1	6%	SLGDIPLFLTSAK		1	0	1
wt	Histone H4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HHF1 PE=1 SV=2	sp|P02309	11368,9	52%	DNIQGITKPAIR-DSVTYTEHAK-ISGLIYEEVR-KTVTSLDVVYALK-SFLESVIR-TVTSLDVVYALK-TVTSLDVVYALKR		7	0	7
wt	Tat-binding homolog 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YTA7 PE=1 SV=2	sp|P40340	157413,2	1%	ALAAScSSDER	c6: Carbamidome	1	0	1
wt	ARS-binding factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ABF1 PE=1 SV=4	sp|P14164	81753,2	4%	ETAQLAIDK-GLDDESGPTHGNDSGNHR		2	0	2
wt	ATP-dependent RNA helicase DBP9 OS=Saccharomyces cerevisiae (strain YJM789) GN=DBP9 PE=3 SV=1	sp|A7A1G0,sp|Q06218	68062,5	4%	SLEGEPENDKKPSK-TGTAISFVVPLK		2	0	2
wt	Histone H2A.1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HTA1 PE=1 SV=2	sp|P04911,sp|P04912	13989,9	30%	AGLTFPVGR-HLQLAIR-LLGNVTIAQGGVLPNIHQNLLPK		3	0	3
wt	Nuclear polyadenylated RNA-binding protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAB3 PE=1 SV=1	sp|P38996	90438,5	27%	ADLSKPITEEEHDR-DAIEcESQEMNFGK-DGTGLETDmIFLKPR-DVDEAIKK-EENDNTHFPTNmENVNYDLLQK-FRDGTGLETDMIFLKPR-HTVScNIFVK-IFSPYGHIMQINIK-LFIGNLPLK-NAFGFIQFDNPQSVR-RHTVScNIFV		17	0	17
wt	ISWI chromatin-remodeling complex ATPase ISW1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ISW1 PE=1 SV=2	sp|P38144	131109,5	17%	DIISPLLLNPTK-FVFLLTTR-IAGILADEmGLGK-IIENEEEK-INWEYIIIDEAHR-IPGPFLVIAPK-IQAIDDYNAPDSK-LLDILEDYcYFR-LSVNNSQPLTEEEEK-LVTDNSVEEK-NSIQAIAR-SDVETSLLPK-STLNNWLR-TLQTISFLGY		18	0	18
wt	Target of rapamycin complex subunit LST8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LST8 PE=1 SV=1	sp|P41318	34033,2	9%	GNVTSVSFQQDNR-sVILVSAGYDHTIR		2	0	2
wt	Transposon Ty1-PR1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY1B-PR1 PE=3 SV=1	sp|P0C2I9,sp|Q03612	198575,8	21%	AHNVSTSNNSPSTDNDSISK-AVSPTDSTPPSTHTEDSKR-DILSVDYTDImK-EVHTNQDPLDVSASK-FLQNSNLGGIIPTVNGKPVR-GIPGYALHPSR-KYPYPFIHR-KYVRPPPMLTSPNDFPNWVK-LIGLASYVGYK-LNNNGIHINN		26	0	26
wt	Processing of GAS1 and ALP protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PGA2 PE=1 SV=3	sp|P53903	15053,6	7%	kQLAAQVEK	n-term: Acetyl (+	1	0	1
wt	DNA-directed RNA polymerase I subunit RPA43 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA43 PE=1 SV=2	sp|P46669	36224	4%	VGGVVLGYEGLK		1	0	1
wt	60S ribosomal protein L30 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL30 PE=1 SV=3	sp|P14120	11416	69%	KSELEYYAMLSK-LALVIK-LIIIAANTPVLR-SELEYYAMLSK-VGVVSILEAGDSDILTTLA-VYYFQGGNNELGTAVGK-YTLGYK		7	0	7
wt	ATP-dependent rRNA helicase RRP3 OS=Saccharomyces cerevisiae (strain YJM789) GN=RRP3 PE=3 SV=1	sp|A6ZSX1,sp|P38712	55955,4	2%	TAAFAIPILNR		1	0	1
wt	NADPH-dependent alpha-keto amide reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDL124W PE=1 SV=1	sp|Q07551	35562	20%	LPGIIHIDAAEIYR-NIGVSNFAVEDLQR-SEAQIILR-VAEVKPQVNQIEFSPFLQNQTPGIYK		4	0	4
wt	Protein YRO2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YRO2 PE=1 SV=1	sp|P38079,sp|Q12117	38721,3	4%	INPPTGADFHITSR		1	0	1
wt	Glutamine synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GLN1 PE=1 SV=4	sp|P32288	41767,1	4%	IIAEYVWIDGTGNLR		1	0	1
wt	U3 small nucleolar RNA-associated protein 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UTP7 PE=1 SV=1	sp|P40055	62318,4	2%	GPVNSIAIDR		1	0	1
wt	C-1-tetrahydrofolate synthase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADE3 PE=1 SV=1	sp|P07245	102207,3	23%	ANVTIEGSR-cVGDVEFNEAIK-DVDGFGPTNIGELNK-EQGFGNLPIcIAK-FETDTEGEIAAIR-GVPTGFTFPIR-LLTPVPSDIDISR-LNIDPDTITIK-LVGTEPEAK-QITIGQAPTEK-QMEESSKPLQIPPLPLK-QPSLGPTLGVK-SDIVGSI		18	0	18
wt	40S ribosomal protein S19-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS19A PE=1 SV=2	sp|P07280,sp|P07281	15917,4	38%	DVAAQDFINAYASFLQR-HIDASGSINR-IGIVEISPK-LEVPGYVDIVK-VLQALEK		5	0	5
wt	Glucan 1,3-beta-glucosidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BGL2 PE=1 SV=1	sp|P15703	34118,6	6%	AALQTYLPK-NDLTASQLSDK		2	0	2
wt	40S ribosomal protein S1-B OS=Saccharomyces cerevisiae (strain YJM789) GN=RPS1B PE=3 SV=1	sp|A6ZM02,sp|B3LLJ2,sp|B5VP69,sp	28812,9	61%	APSTFENR-DIFPLQNIHVR-EVQNSTLAQLTSK-FDVGALmALHGEGSGEEK-HSYAQSSHIR-IFAIAFTR-KVISEILTR-KVVDPFTR-LIPEVINK-LRVDEVQGK-NLLTNFHGmDFTTDK-TSDDYVLR-VSGFKDEVLETV-VVDPFTR-V		16	0	16
wt	Cofilin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=COF1 PE=1 SV=1	sp|Q03048	15901,2	29%	FILFGLNDAK-IVFFTWSPDTAPVR-SGVAVADESLTAFNDLK		3	0	3
wt	U6 snRNA-associated Sm-like protein LSm5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LSM5 PE=1 SV=1	sp|P40089	10423,2	41%	mLLSGNNIAILVPGGK-sLPEILPLEVIDK-VLIVLQSNR	m1: Oxidation (+	3	0	3
wt	Imitation switch two complex protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ITC1 PE=1 SV=1	sp|P53125	145648,7	3%	NSEGISEATR-VNPLIELTPIQK-VQFNATINPESR		3	0	3
wt	60S ribosomal protein L4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL4A PE=1 SV=4	sp|P10664	39092	55%	AGHQTSAESWGTGR-AVGAHSDLLK-FVIWTEAAFTK-GPLVVYAEDNGIVK-IINSSEIQSAIRPAGQATQK-IPEIPLVVSTDLESIQK-LDQVWGSETVASSK-NVPGVETANVASLNLLQLAPGAHLGR-QAYAVSEK-RGPLVVYAEDNG		15	0	15
wt	Aspartokinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HOM3 PE=1 SV=2	sp|P10869	58111	2%	FPVQIVDDIVK		1	0	1
wt	Cell division control protein 48 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC48 PE=1 SV=3	sp|P25694	91998,4	25%	ATQGFSGADLLYIVQR-AVATEVSANFISVK-EMVELPLR-ETVEYPVLHPDQYTK-EVDIGIPDATGR-FALGNSNPSALR-GGSLGDAGGASDR-GVLFYGPPGTGK-GVLmYGPPGTGK-KTPLEPGLELTAIAK-LGDLVTIHPcPDIK-LSII		17	0	17
wt	Ribosome biogenesis protein MAK21 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MAK21 PE=1 SV=1	sp|Q12176	116682	13%	AFPFAQIPASVYEVHmETLFK-ASDIMHDQGPVNTEDWLTK-EALALGASEEDLK-FMSQILSDGTLNDK-ISAVTLLIQDSPLHNTK-LFSALLTGINR-NQPGLSMMLNK-QDALNVER-TYFTLFEK-VNDSVLVK	m16: Oxidation (	10	0	10
wt	Cleavage factor two protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CFT2 PE=1 SV=1	sp|Q12102	96258,8	2%	IVEFSTTIK-QIQNEEITAK		2	0	2
wt	DNA-directed RNA polymerase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPO41 PE=1 SV=2	sp|P13433	153053,6	1%	VSVQGVDPVTK		1	0	1
wt	60S acidic ribosomal protein P1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPP1B PE=1 SV=3	sp|P10622	10668,1	15%	AAGANVDNVWADVYAK		1	0	1
wt	U1 small nuclear ribonucleoprotein component PRP42 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP42 PE=1 SV=1	sp|Q03776	65149,7	34%	ALLPLAHYDLVWIK-DTVEFVEK-FYALWLQR-GLQAFNQR-IDDIMDLK-IDINYSGR-ILEIPLHSFSK-KSGQEILLNNLVQFYSK-LIYFDTSR-LLYSVIcK-LNEYVLLR-NVLLmGLK-QLSQLTSK-SLAYWEK-SLLLWTSYLK-STEPQI		19	0	19
wt	LAS seventeen-binding protein 3 OS=Saccharomyces cerevisiae (strain YJM789) GN=LSB3 PE=3 SV=2	sp|A7A261,sp|P43603	49346,1	3%	ISSASTPQTSQGR		1	0	1
wt	Pre-mRNA-splicing factor SYF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SYF1 PE=1 SV=1	sp|Q04048	100234,4	3%	AESTLGPSVTR-SLQQTLR-TPQNILTWK		3	0	3
wt	Protein AIR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AIR2 PE=1 SV=1	sp|Q12476	39343,7	3%	AYILVDDNEK		1	0	1
wt	Mitochondrial import receptor subunit TOM40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TOM40 PE=1 SV=1	sp|P23644	42039,4	6%	AFSMNPAFQTSHTFSIGSQALPK		1	0	1
wt	Serine hydroxymethyltransferase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SHM2 PE=1 SV=2	sp|P37291	52219,7	9%	AVEFAQQVQQSLPK-VLVAGTSAYcR-VNPETGIIDYDTLEK		3	0	3
wt	Pre-mRNA-processing protein PRP40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP40 PE=1 SV=1	sp|P33203	69068,5	34%	ALGDEDNIR-ELGESLEYK-ELISQEELLLR-ETSWTIPAFEK-IISELGTR-IVNTIENDLQNK-KHYFWLLLQR-LIADEPIYK-MYIFAQR-QIFEDFKPESSAPTAESATANLTLTASK-SIAQQTLIDQNFEWNDADSDEITK-TINEEESQYANN		16	0	16
wt	37S ribosomal protein MRP1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRP1 PE=1 SV=2	sp|P10662	36730,9	13%	EVSYIPLLAIDASPK-LGPEALLQTPDFNR-TISNEPLTTGNER		3	0	3
wt	Protein BOI2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BOI2 PE=1 SV=1	sp|P39969	115693,3	2%	QQFTDNAAR-QTSAFIEGLR		2	0	2
wt	Translation machinery-associated protein 46 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TMA46 PE=1 SV=2	sp|Q12000	39515,5	7%	ITLEEFIETER-LTPITIANFAQWK		2	0	2
wt	60S ribosomal protein L16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL16A PE=1 SV=3	sp|P26784	22201,6	48%	AEELNISGEFFR-LASVVAK-LSTSVGWK-RVVVPQALR-SVEPVVVIDGK-VASANATAAESDVAK-VFEGIPPPYDK-VSSAEYYAK-VVVPQALR-YEDVVAK-YHDFLR		11	5	6
wt	3-isopropylmalate dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LEU2 PE=1 SV=4	sp|P04173	38954,2	3%	LSLNLPEEGK		1	0	1
wt	Reticulon-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RTN1 PE=1 SV=1	sp|Q04947	32916,5	4%	LAADVPLEPESK		1	0	1
wt	Suppressor of mar1-1 protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SUM1 PE=1 SV=2	sp|P46676	118205,7	1%	LVSNAASVNLK		1	0	1
wt	60S ribosomal protein L24-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL24A PE=1 SV=1	sp|P04449	17614,4	36%	AQRPITGASLDLIK-GITEEVAK-GTLFVR-IAWTVLFR-KGITEEVAK-mKVEIDSFSGAK-SASLFK		7	0	7
wt	GLC7-interacting protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GIP1 PE=1 SV=2	sp|P38229,sp|REVERSED_P33302,sp	73357,4	1%	LLIYK		1	0	1
wt	60S ribosome subunit biogenesis protein NIP7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NIP7 PE=1 SV=1	sp|Q08962	20381,1	5%	NISFLVDNK		1	0	1
wt	Proteasome component Y7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE8 PE=1 SV=1	sp|P23639	27163,1	9%	LTSQEINDR-YSFSLTTFSPSGK		2	0	2
wt	Fatty acid synthase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FAS1 PE=1 SV=2	sp|P07149	228696	1%	ALDTVTNVLNFIK		1	0	1
wt	Translation initiation factor RLI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RLI1 PE=1 SV=1	sp|Q03195	68343,3	4%	LLAGALKPDEGQDIPK-LNAAQIIR		2	0	2
wt	60S ribosomal protein L25 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL25 PE=1 SV=4	sp|P04456	15758,2	35%	ELYEVDVLK-KVEDGNILVFQVSmK-LTADYDALDIANR-VEDGNILVFQVSmK-VIEQPITSETAMK-VIEQPITSETAmKK		6	0	6
wt	Pre-mRNA-processing ATP-dependent RNA helicase PRP5 OS=Saccharomyces cerevisiae (strain YJM789) GN=PRP5 PE=3 SV=1	sp|A6ZLH6,sp|P21372	96416,4	3%	FIDILTLNDGK-VYINDLPQIVR		2	0	2
wt	Probable chaperone protein HSP31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP31 PE=1 SV=1	sp|Q04432	25670,6	7%	TGVFVVEALHPFNTFR		1	0	1
wt	60S ribosomal protein L16-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL16B PE=1 SV=3	sp|P26785	22249,9	43%	aEALNISGEFFR-iFEGIPPPYDK-LSTSVGWK-RVVVPQALR-SAEYYAK-sQPVVVIDAK-VSSASAAASESDVAK-VVVPQALR-YEDVVAK-YHDFLR	n-term: Acetyl (+	10	0	10
wt	U6 snRNA-associated Sm-like protein LSm3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LSM3 PE=1 SV=1	sp|P57743	10030,5	17%	LNLDER-mETPLDLLK		2	0	2
wt	Aromatic/aminoadipate aminotransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARO8 PE=1 SV=1	sp|P53090	56180,5	6%	LLYTIPTGQNPTGTSIADHR-SANPSNDIPLSR		2	0	2
wt	Pre-mRNA-splicing factor 18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP18 PE=1 SV=3	sp|P33411	28378,8	8%	ALFPLLLQLR-IQEAIAQDK		2	0	2
wt	2-oxoglutarate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=KGD1 PE=1 SV=2	sp|P20967	114419,3	1%	LISEGTFSK		1	0	1
wt	U3 small nucleolar RNA-associated protein 9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UTP9 PE=1 SV=1	sp|P38882	65273,8	6%	FAFQASVAQK-LIQSWPVQVK-NNVDIYPLNETK		3	0	3
wt	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=QCR2 PE=1 SV=1	sp|P07257	40479,7	48%	DGVAHLLNR-DLSPAINYTK-DQDSAVVSSNIK-ENLEVSGENVVEADLKR-ESELLGGTFK-FIGDSVAAIGIPVNK-FNFQNTNTR-FTDGGLFTLFVR-FVDESLLSTLPAGK-GKDLSPAINYTK-GLGNPLLYDGVER-LDKFTDGGLFTLI		15	0	15
wt	Small nuclear ribonucleoprotein Sm D2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMD2 PE=1 SV=2	sp|Q06217	12853,3	36%	GDSVIVVLK-HGPmSLINDAmVTR-sSQIIDRPK-TPVIISLR		4	0	4
wt	60S ribosomal protein L2-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL2A PE=1 SV=1	sp|P0CX45,sp|P0CX46	27408,9	45%	ASGNYVIIIGHNPDENK-ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR-GAGSIFTSHTR-GVIGVIAGGGR-KASLNVGNVLPLGSVPEGTIVSNVEEKPGDR-KGAGSIFTSHTR-LREEIFIANEGVHTGQFIYAGK-TLDYAER-VDKPLLK		10	0	10
wt	Proteasome component PRE6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE6 PE=1 SV=1	sp|P40303	28438,7	19%	LTLEDPVTVEYLTR-SLLEVVQTGAK-YTQSGGVRPFGVSTLIAGFDPR		3	0	3
wt	Replication factor C subunit 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RFC5 PE=1 SV=1	sp|P38251	39943,7	2%	IVIQELLK		1	0	1
wt	CBK1 kinase activator protein MOB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MOB2 PE=1 SV=2	sp|P43563	33276,6	8%	STPQSQQLTSTTPQSQQQEASER		1	0	1
wt	60S ribosomal protein L39 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL39 PE=1 SV=3	sp|P04650	6342	20%	QNRPLPQWIR		1	0	1
wt	40S ribosomal protein S7-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS7B PE=1 SV=1	sp|P48164	21634,7	52%	ALVLFVPVPALSAYHK-DVQQIDYK-HVIFLAER-ILPKPSR-ILSQAPSELELQVAK-LESFQAVYNK-TFIDLESSSPELK-VLEDmVFPTEIVGK-YLVGGNK		9	5	4
wt	Elongation factor 3A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YEF3 PE=1 SV=4	sp|P16521	115948,1	27%	AIANGQVDGFPTQEEcR-ALLPHLTNAIVETNK-ATETVDNKDIER-AYEELSNTDLEFK-DKEIQSVASETLISIVNAVNPVAIK-EALASGQFRPLTR-EFEGGVIIITHSAEFTK-EIQSVASETLISIVNAVNPVAIK-FPEPGYI	c16: Carbamidon	23	0	23
wt	Nuclear localization sequence-binding protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NSR1 PE=1 SV=1	sp|P27476	44536,1	21%	AIQEMQGK-ALDALQGEYIDNRPVR-GYGYVDFENK-IPTHPETEQPK-KEFEHIGGVIGAR-LSWSIDDEWLK-QKNEETEEPATIFVGR		7	0	7
wt	Eukaryotic translation initiation factor 2 subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SUI2 PE=1 SV=1	sp|P20459	34718,7	22%	FQIPLEELYK-GIEQLESAIEK-ITEVITK-LSIIDETVWEGIEPPSKDVLDELK-LVAAPLYVLTTQALDK		5	0	5
wt	Protein TBF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TBF1 PE=1 SV=2	sp|Q02457	62826,6	7%	FNDIIQSLPAR-GHEAFIITAIR-ILDLYGPGGK-SQAILYLDLK		4	0	4
wt	26S proteasome regulatory subunit RPN13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPN13 PE=1 SV=1	sp|O13563	17902,5	7%	IFALVFSSNER		1	0	1
wt	DNA-directed RNA polymerase I subunit RPA49 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA49 PE=1 SV=2	sp|Q01080	46653,2	15%	AIADLER-APSDTTFDLYK-APVLVSK-GATVAQAEAFGIPK-KELQFIR-LNSPPEILVDGILSR		6	0	6
wt	Flavohemoprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YHB1 PE=1 SV=2	sp|P39676	44647,2	36%	ALQIKPEHYPIVGEYLLK-ATVPVLEQQGTVITR-FGSGIELESLPITPGQYITVNTHPIR-IIVHTDTEPLINAAFLK-LSAPAGDFAINK-NIDDLSVLMDHVK-NMLTEHTELLNIFNR-QENQYDALR-VGAQPNALATTVLAAAK		9	0	9
wt	Asparaginyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DED81 PE=1 SV=1	sp|P38707	62208,6	3%	SVQYVLEDPIAGPLVK		1	0	1
wt	60S ribosomal protein L19-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL19A PE=1 SV=1	sp|P0CX82,sp|P0CX83	21704,6	34%	ALNEEAEAR-ALVEHIIQAK-HLYHVLYK-KVWLDPNETSEIAQANSR-LAASVVGVGK-LPSQVVWIR-VWLDPNETSEIAQANSR		7	0	7
wt	Threonyl-tRNA synthetase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=THS1 PE=1 SV=2	sp|P04801	84522,6	3%	IYNTLVDLLR-QVLVVPVGVK		2	0	2
wt	Protein CAF130 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CAF130 PE=1 SV=1	sp|P53280	128788,4	1%	QGPIVLSDIETK		1	0	1
wt	Transposon Ty2-LR1 Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY2B-LR1 PE=3 SV=1	sp|P0C2J3,sp|P25384,sp|Q03494,sp|Q	202130,3	6%	ENNINVSDR-GIPGYALHPSR-IMNLNKPSQYK-LIGLASYVGYK-LKENNINVSDR-LVAISDASYGNQPYYK-NSNLGDIIPNDQGEIKR-NSYGYIIYLPSLK-SDGTVLAPIVK-YDEAITYNK		10	6	4
wt	40S ribosomal protein S9-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS9A PE=1 SV=3	sp|O13516,sp|P05755	22443,9	40%	ISFQLSK-KLDYVLALK-LAGEFGLK-LDAELK-LDYVLALK-LFEGNALIR-LQTQVYK-QIVNIPSFMVR-VEDFLER-VGVLSEDK-VGVLSEDKK-VLITQR		12	0	12
wt	Serine/threonine-protein kinase BUR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SGV1 PE=1 SV=1	sp|P23293	74241,6	11%	APELVLGDK-FHPETNVSSK-FSGNSTAPNNSR-VPLPLGPQSR-YLPGAELTTTNYKPTLR-YVNKPETNFNR		6	0	6
wt	Nuclear polyadenylated RNA-binding protein NAB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAB2 PE=1 SV=1	sp|P32505	58319,6	24%	ADLLAAK-ALGMAGESNMNFTPTK-ALGMAGESNMNFTPTKK-FGALcSNPScPFGHPTPANEDAK-FNPLAK-IDcLFGHPINEDcR-IKEVKPISQK-KPVQTGIVLcK-LFPHcPLGR-NLTcDNPEcR-RKPVQTGIVLcK-sQEQYTENLK-VI		13	0	13
wt	60S ribosomal protein L7-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL7B PE=1 SV=3	sp|Q12213	27697,8	54%	AAGSYYVEAQHK-AIILER-ATLELLK-HFIQGGSFGNR-ILTPESQLKK-INSGTFVK-LIEPYVAYGYPSYSTIR-LSNPSGGWGVPR-LVFVVR-QANNFLWPFK-QRVPLSDNAIIEANLGK-RAIILER-TAEQIAAER-VLQLLR-VPLSDNAII		15	14	1
wt	TATA-box-binding protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPT15 PE=1 SV=3	sp|P13393	27004,3	11%	DGTKPATTFQSEEDIKR-IVLLIFVSGK		2	0	2
wt	Pre-mRNA-splicing factor 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP6 PE=1 SV=1	sp|P19735	104235,1	12%	AIDLESTTVNK-FPSNALLWVEQIK-IQEQLNR-LLQSQIDENLAQLTK-NASNPIQVNKPNAATDALSYLK-NNPDIPVDK-NPDDVLFYIAK-SLQLDELR-YQDLNEEAIK		9	0	9
wt	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDB1 PE=1 SV	sp|P32473	40054,2	39%	cQMVFR-EGTDISIVTYTR-ELEDFAFPDTPTIVK-GPNGAAVGVGAQHSQDFSPWYGSIPGLK-KYGVSAEVINLR-NVQFSLEAAEILQK-RVVDTPITEYGFTGLAVGAALK-SIRPLDTEAIIK-VLVPYSAEDAR-VTGA	c1: Carbamidome	12	0	12
wt	Histone H3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HHT1 PE=1 SV=2	sp|P61830	15356,8	19%	fQKSTELLIR-KLPFQR-kSAPSTGGVK-STELLIR	n-term: Acetyl (+	4	0	4
wt	ATP-dependent RNA helicase DED1 OS=Saccharomyces cerevisiae (strain YJM789) GN=DED1 PE=3 SV=1	sp|A6ZP47,sp|P06634	65554,5	53%	AcVVYGGSPIGNQLR-aELSEQVQNLSINDNNENGYVPPHLR-AGGASAGGWGSSR-AGNTGLATAFFNSENSNIVK-AYPTAVIMAPTR-DAMMSAPGSR-DLmAcAQTGSGK-ELATQIFDEAK-FTKPTPVQK-GcDLL	c2: Carbamidome	23	0	23
wt	General negative regulator of transcription subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC39 PE=1 SV=3	sp|P25655	240289,7	0%	LEIVVPFVTK		1	0	1
wt	Protein BMH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BMH1 PE=1 SV=4	sp|P29311	30092	38%	ATNASLEAYK-DSTLIMQLLR-ISDDILSVLDSHLIPSATTGESK-IVSSIEQK-TASEIATTELPPTHPIR-TVASSGQELSVEER-YEEMVENMK-YLAEFSSGDAR		8	0	8
wt	Phosphomannomutase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEC53 PE=1 SV=1	sp|P07283	29064,1	22%	EKPETLVLFDVDGTLTPAR-ELASQSFINWLGEEK-LTVSEEVR-TIGHSVQSPDDTVK		4	0	4
wt	DNA-directed RNA polymerase I subunit RPA190 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPA190 PE=1 SV=2	sp|P10964	186435,3	19%	ADSFFMDVLVVPPTR-AVLDNEREQLDSPSAR-EGLIDTAVK-GSFTATVNDER-GSLENEVLFK-GSNVNVSQIMcLLGQQALEGR-IFETALNEK-LGEEVHENSQNQLLSK-LNNVGTGSFDVLAK-LQTDVANSSSNSK-LTYPEPVTAYN		22	0	22
wt	Heat shock protein 26 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSP26 PE=1 SV=3	sp|P15992	23880,2	43%	DIDIEYHQNK-KDIDIEYHQNK-KIEVSSQESWGN-LLGEGGLR-NQILVSGEIPSTLNEESK-NQILVSGEIPSTLNEESKDK-SVAVPVDILDHDNNYELK-VITLPDYPGVDADNIK-VVVPGVK		9	0	9
wt	Pre-mRNA-splicing factor CWC15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CWC15 PE=1 SV=1	sp|Q03772	19935,2	6%	DSLQELLVTQK		1	0	1
wt	Dihydrolipoyl dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LPD1 PE=1 SV=1	sp|P09624	54010,9	11%	INVANFQK-IVSSTGALSLK-QLTGGIELLFK-RPYIAGLGAEK-VTPVDGLEGTVK		5	0	5
wt	ATP-dependent RNA helicase DOB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MTR4 PE=1 SV=1	sp|P47047	122058,7	15%	ELVDVANTIGNSSLK-GATFTQIcK-GLTNSETLQVEQDGK-GVVWEETIILLPDK-IEVVEKDYVESFR-IFNNAIALLPETDR-ISESQAVIQLDDLR-NADTNVGDTPDHTQDKK-QVVTHPANALSFLQPGR-SIcAVIPITLDSIK-VVVPVLA		11	0	11
wt	Myosin light chain 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MLC1 PE=1 SV=1	sp|P53141	16445,3	39%	AIGYNPTNQLVQDIINADSSLR-DIFTLFDK-FIEDVLRQ-LTDAEVDELLK-YMLTGLGEK		5	0	5
wt	Protein transport protein SEB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEB2 PE=1 SV=1	sp|P52871	9606,5	15%	QAGYGGSSSSILK		1	0	1
wt	Guanine nucleotide-binding protein subunit beta-like protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ASC1 PE=1 SV=4	sp|P38011	34805,9	55%	AmYTLSAQDEVFSLAFSPNR-ASMIISGSR-aSNEVLVLR-DGEImLWNLAAK-DKTLISWK-FGVPVR-GQcLATLLGHNDWVSQVR-GTLEGHNGWVTSLATSAGQPNLLLSASR-KAmYTLSAQDEVFSLAFSPNR-LW	m2: Oxidation (+	16	0	16
wt	Glutaredoxin-2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GRX2 PE=1 SV=3	sp|P17695	15862,1	26%	ATLSTLFQELNVPK-HIGGNSDLETLKK-LAEILKPVFQ		3	0	3
wt	Enolase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ENO2 PE=1 SV=2	sp|P00925	46915,1	63%	AADALLLK-AAQDSFAANWGVMVSHR-AVDDFLLSLDGTANK-GNPTVEVELTTEK-GVmNAVNNVNNVIAAAFVK-IATAIEK-IEEELGDK-IGLDcASSEFFK-IGSEVYHNLK-LGANAILGVSmAAAR-LNQLLR-NVPLYQHLADLSI		20	0	20
wt	Histone H1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HHO1 PE=1 SV=1	sp|P53551	27805,3	23%	ASSPSSLTYK-ELIIEGLTALK-GPSGIIK-GVEAGDFEQPK-QAATSVSATASK-SMPQLNDGK		6	0	6
wt	Protein HSH49 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSH49 PE=1 SV=1	sp|Q99181	24504,9	23%	ITVDYAFK-NLADSIDSDQLVK-QVTNSTGTTNLPSNISK-SLNNQLVANNR		4	0	4
wt	Uncharacterized oxidoreductase YJR096W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YJR096W PE=1 SV=1	sp|P47137	32344,9	5%	IPSIALGTYDIPR		1	0	1
wt	Tricalbin-3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TCB3 PE=1 SV=1	sp|Q03640	171081,4	6%	FIGSVQIPTSNVFK-FLYTPTSVK-LQGSFNPEYIKPSFDIVK-SPSNLNSTSVTPR-TNQLPGPNPQGSIGAVPLEGLRPK-YLLLNTLEQK		6	0	6
wt	Nucleoporin NIC96 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NIC96 PE=1 SV=2	sp|P34077	96180,3	6%	DLQTNQFLEPNPPK-FANILANYTK-IPGVIEER-NAQLLESWK-NmNEGLATNVNK		5	0	5
wt	Transcriptional modulator WTM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=WTM1 PE=1 SV=1	sp|Q12363	48383,6	6%	IIDNAGKPGEILR-TVHVPGTTVTHTVR		2	0	2
wt	40S ribosomal protein S0-B OS=Saccharomyces cerevisiae (strain YJM789) GN=RPS0B PE=3 SV=1	sp|A7A0V3,sp|B3LT19,sp|P46654	27962,3	51%	FAAHTGATPIAGR-FTPGSFTNYITR-IIAAIPNPEDVVAISSR-LDAQAIK-LVIVTDPR-LVLAAR-NVQVHQEPYVFNARPDGVHVINVGK-sLPATFDLTPEDAQLLLAANTHLGAR-TQPWSImPDLYFYR		9	0	9
wt	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=COR1 PE=1 SV=1	sp|P07256	50229	15%	EGLALSSNISR-NLSLQTGTKPVLK-QVQDFEENDHPNR-SLDFLNQSFIQQK-VLEHLHSTAFQNTPLSLPTR		5	0	5
wt	DNA-directed RNA polymerase II subunit RPB7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB7 PE=1 SV=1	sp|P34087	19058,4	8%	ILPTDGSAEFNVK		1	0	1
wt	Actin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ACT1 PE=1 SV=1	sp|P60010	41690,4	44%	AGFAGDDAPR-APEALFHPSVLGLESAGIDQTTYNSImK-cDVDVR-DLTDYLMK-DSYVGDEAQSK-EITALAPSSMK-GYSFSTTAER-HQGIMVGMGQK-IIAPPER-QEYDESGPSIVHHK-SYELPDGQVITIGNER-VAPEEHPVLLTEA		13	0	13
wt	Cytochrome b2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CYB2 PE=1 SV=1	sp|P00175	65541,2	5%	LLGVTSIAELKPDLLDLSTLK-LPIVIK		2	0	2
wt	U6 snRNA-associated Sm-like protein LSm2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LSM2 PE=1 SV=1	sp|P38203	11163,2	36%	GTLQSVDQFLNLK-mLFFSFFK-NmVDTNLLQDATR		3	0	3
wt	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Saccharomyces cerevisiae (strain AT	sp|P12695	51819,7	30%	ADIESYLEK-ADVPAFK-AQPAEPQAEK-DFKLEDSGSDSK-DIPVNKPIAVYVEDK-GLSQISNEIK-iFASPLAK-ILVPEGTK-LLQSTQGIPSYIVSSK-lSINDLLVK-QSLNATANDK-QSLNATANDKYK-RVPDANAYWLPNENVIR-TVIE		15	0	15

wt	UPF0674 endoplasmic reticulum membrane protein YNR021W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YNR021W PE=1 S	sp|P53723	47095,1	6%	FVTSIVNK-VNSLNAPYQALSYDEQK		2	0	2
wt	NAD-dependent malic enzyme, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MAE1 PE=1 SV=1	sp|P36013	74377,4	7%	GLILQSYEANSTPAQHVYAK-GSAFTQEER-IEQEQVPGGAPGETVK		3	0	3
wt	T-complex protein 1 subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CCT3 PE=1 SV=2	sp|P39077	58814,7	2%	TLIQNAGGDPIR		1	0	1
wt	Heat shock protein SSA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSA2 PE=1 SV=3	sp|P10592	69471,8	56%	ARFEELcADLFR-ATAGDTHLGGEDFDNR-DAGTIAGLNVLR-ELQEVANPIMSK-ETAESYLGAK-FELSGIPPAPR-IINEPTAAAIAYGLDK-IINEPTAAAIAYGLDKK-ITITNDK-KSEVFSTYADNQPGVLIQVFEGER-I	c7: Carbamidome	29	23	6
wt	PWWP domain-containing protein YLR455W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YLR455W PE=1 SV=1	sp|Q06188	35509,9	4%	IVAGEDPFVGR		1	0	1
wt	S-adenosylmethionine synthase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SAM1 PE=1 SV=2	sp|P10659,sp|P19358	41819,4	6%	FVIGGPQGDAGLTGR-YFIQPSGR		2	0	2
wt	Keratin, type II cytoskeletal 2 epidermal - Homo sapiens	sp|P35908	65866,4	18%	AQYEEIAQR-FASFIDK-FLEQQNQVLQTK-GFSSGSAVVSGGSR-GGSISGGGYGSGGGK-IEISELNR-SKEEAEALYHSK-TAAENDFVTLK-VDLLNQEIEFLK-YEDEINKR-YEELQVTVGR		11	3	8
wt	GMP synthase [glutamine-hydrolyzing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GUA1 PE=1 SV=4	sp|P38625	58483,4	2%	TYDQVIALR		1	0	1
wt	Isocitrate dehydrogenase [NADP], mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IDP1 PE=1 SV=1	sp|P21954	48192,8	24%	EPIVIPR-FKDIFQEVYEAQYK-GSGVAmAmYNTDESIEGFAHSSFK-LIDDmVAQmIK-LILPYLDVDLK-LNLFLSTK-SAYVTTEEFLDAVEKR-TFESEAAHGTVTR		8	0	8
wt	Proteasome component PRE5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE5 PE=1 SV=1	sp|P40302	25605	15%	QGSVTVGLR-SGAHLLEFQPSGNVTELYGTAIGAR		2	0	2
wt	Pre-mRNA-splicing factor SYF2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SYF2 PE=1 SV=1	sp|P53277	24803,3	4%	EIQEVSANR		1	0	1
wt	Ribonuclease 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RNT1 PE=1 SV=1	sp|Q02555	54073,2	4%	LPEIQDLAIR-VPVQILPSLSR		2	0	2
wt	T-complex protein 1 subunit theta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CCT8 PE=1 SV=1	sp|P47079	61663,6	13%	AIDDGVAAVK-IIITNDAATMLR-TLAETAGLDVNEVLPNLYAAHNVTEPGAVK-TPGLLQLAIK-VLVMATEQQK		5	0	5
wt	Transcriptional activator/repressor MOT3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MOT3 PE=1 SV=1	sp|P54785	54380,6	3%	mNADHHLQQQQQQR	n-term: Acetyl (+	1	0	1
wt	MAP kinase kinase PBS2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PBS2 PE=1 SV=4	sp|P08018	72721,5	4%	ITATTIGVNTGLPATDITPSVSNTASATHK		1	0	1
wt	ADP,ATP carrier protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PET9 PE=1 SV=2	sp|P18239	34428	48%	AmFGFK-GcGANILR-GFLPSVVGIVVYR-IVAAEGVGSLFK-KESNFLIDFLmGGVSAAVAK-KIVAAEGVGSLFK-LLIQNQDEMLK-MMMTSGQAVK-QFNGLIDVYK-QFNGLIDVYKK-SDGVAGLYR-TAASPIER-T	m2: Oxidation (+	16	0	16
wt	Transcription initiation factor TFIID subunit 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF6 PE=1 SV=1	sp|P53040	57904	6%	FFLGNLNNWAR-GVSVLEGESIR-LINEPLPQVPR		3	0	3
wt	26S proteasome regulatory subunit RPN11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPN11 PE=1 SV=1	sp|P43588	34398,1	4%	AVAVVVDPIQSVK		1	0	1
wt	UPF0368 protein YPL225W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YPL225W PE=1 SV=1	sp|Q08971	17445,2	7%	LQFYAFEIAR		1	0	1
wt	Proteasome component PRE2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE2 PE=1 SV=3	sp|P30656	31636,9	3%	ILSNLVYQYK		1	0	1
wt	RNA annealing protein YRA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YRA1 PE=1 SV=2	sp|Q12159	24956,3	42%	APPNAVAR-DIKQDAVR-EFFASQVGGVQR-FNGSPIDGGR-GQSTGMANITFK-LLDTTR-LNLIVDPNQRPVK-SLDEIIGSNK-VLLSYNER-VNVEGLPR		10	0	10
wt	Glucokinase-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GLK1 PE=1 SV=1	sp|P17709	55379,1	3%	SAYLAAVPLAAILIK		1	0	1
wt	RuvB-like protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RVB2 PE=1 SV=1	sp|Q12464	51613,1	10%	AVLVAGPPSTGK-AYLLFLDSAR-TEALTQAFR-TQGFLALFTGDTGEIR		4	0	4
wt	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MET6 PE=	sp|P05694	85862,4	6%	GTISAEEYEK-LDAEIK-VIQVDEPALR-VVVATSSSLLHTPVDLNNETK		4	1	3
wt	Chromatin structure-remodeling complex protein RSC58 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC58 PE=1 SV=1	sp|Q07979	57797	7%	IGIALTQTNNIK-INNVLPQTDIENEAPR-VPINNVR		3	0	3
wt	Peroxisomal-coenzyme A synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PCS60 PE=1 SV=1	sp|P38137	60489,9	35%	EFNFYLNDLK-FRVEYDIYSPEDNYK-FVNTNPVK-GENVTLGYANNPK-IDEAVAFGVPDDMYGQVVQAAIVLK-ISPIELDGIMLSHPK-LFWDQFVK-MTYEELVNFLK-QDTVAISMR-ScSSALAPATFHK-SSDVALILHTSGTTSTPK-		15	0	15
wt	Ribosome-interacting GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RBG1 PE=1 SV=1	sp|P39729	40702,5	44%	ATSFHLGQLK-ELEGVGIR-ELLTSASSGSGGGAGIGFDVAR-GGISITNTVPLTHLGNDEIR-GQIPDFTDPVVLR-IDSLSIEELELLYR-INSAEIAFR-LTGTESEAAEYEFTTLVTVPGVIR-NALVYGSSVK-QVIAVAR-TGVASVGFVGFPS		12	0	12
wt	40S ribosomal protein S3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS3 PE=1 SV=5	sp|P05750	26503	62%	AAYGVVR-ALPDAVTIIEPK-EEEPILAPSVK-ELAEEGYSGVEVR-FADGFLIHSGQPVNDFIDTATR-GcEVVVSGK-GLSAVAQAESMK-iNELTLLVQK-LLNGLAIR-QGVLGIK-RINELTLLVQK-TEVIIR-TQDVLGENGR-YAPGTIVLY		15	0	15
wt	Protein NRD1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NRD1 PE=1 SV=1	sp|P53617	63860,4	34%	AYLDETR-cFAMDISNNTANTASQQLSLDPK-DGALPLR-HEAENVLQNFNK-IISLIIDYSR-KLTTYALDHIDIESK-KSPPLNLNISLPTDLTSTDPAK-LGSLYIIDSIGR-LTTYALDHIDIESK-MLLDIWDR-mQQDDDFQNFVATLESFK-QI		19	0	19
wt	Protein NAM8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAM8 PE=1 SV=2	sp|Q00539	56972,5	15%	NNQGYcFVDFPSSTHAANALLK-QIWASLGEANINVR-QTTYYPSR-SSSSLNNENVDSR-VGPTSGQQQHVSGNNDYNR	c6: Carbamidome	5	0	5
wt	rRNA 2'-O-methyltransferase fibrillarin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOP1 PE=1 SV=1	sp|P15646	34465,5	43%	ANcIDSTVDAETVFAR-DHcIVVGR-GKEDLLVTK-HAGVYIAR-IIALNSHMFLK-IKPLEQLTLEPYER-ISVEEPSKEDGVPPTK-LAAGImGGLDELFIAPGK-MLIGMVDcVFADVAQPDQAR-NmAPGESVYGEK-VVI	c3: Carbamidome	11	0	11
wt	ISWI chromatin-remodeling complex ATPase ISW2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ISW2 PE=1 SV=1	sp|Q08773	130333,5	4%	FVFLLTTR-LLDILEDYcYFR-TLQTISFLGYLR-VLIFSQMSR		4	4	0
wt	Nucleolar protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NPL3 PE=1 SV=1	sp|Q01560	45407,3	19%	DDNPPPIR-ENSLETTFSSVNTR-GSVITVERDDNPPPIR-ILNGFAFVEFEEAESAAK-lNNIEFR-QEGELSNTR-SFANQPLEVVYSK		7	0	7
wt	ATP-dependent molecular chaperone HSC82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSC82 PE=1 SV=4	sp|P15108	80903,4	29%	AELINNLGTIAK-AILFIPK-APFDLFESK-ELISNASDALDK-GVVDSEDLPLNLSR-HSEFVAYPIQLLVTK-LFLKDDQLEYLEEK-LGVHEDTQNR-LLDAPAAIR-NIYYITGESLK-NPSDITQEEYNAFYK-QLETEPDLFIR-RAPFDLFES		20	19	1
wt	Potassium-activated aldehyde dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ALD4 PE=1 SV=2	sp|P46367	56725,2	14%	IAPALVTGNTVVLK-IVKEEIFGPVVTVTK-SPNIVFADAELKK-VAFTGSTATGR-YIPQAGIPPGVINIVSGFGK		5	0	5
wt	Protein SIS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SIS1 PE=1 SV=1	sp|P25294	37591,6	49%	DGDDLIYTLPLSFK-EISEAFEILNDPQK-EISEAFEILNDPQKR-EIYDQYGLEAAR-ESLLGFSK-FKEISEAFEILNDPQK-KTLQFVIQEK-LYDLLGVSPSANEQELK-LYDLLGVSPSANEQELKK-NQGDYNPQTGR-SASSSPTYPEEET		16	0	16
wt	Replication factor A protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RFA1 PE=1 SV=1	sp|P22336	70350,2	2%	VIIAEPAIVR		1	0	1
wt	Pre-mRNA-splicing factor PRP9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRP9 PE=1 SV=1	sp|P19736	63032,6	16%	DLDLNEIFTR-EGAEQVDGEQR-NMQGQSQLTSIAAVPPKPNPSQLK-QIILQQHEINIFLR-SYALLDAAAVENLIK-YALFSSSSDPSR		6	0	6
wt	Nucleoporin GLE2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GLE2 PE=1 SV=1	sp|P40066	40522,5	14%	HIAIINLANPTTIFK-LYDIASGQTQQIGMHSAPIK-SNTTSALGTSTAmANEK		3	0	3
wt	Keratin, type I cytoskeletal 14 - Homo sapiens	sp|P02533	51622,6	11%	EVATNSELVQSGK-GScGIGGGIGGGSSR-LAADDFR-LASYLDK-VTMQNLNDR		5	4	1
wt	DNA-directed RNA polymerase II subunit RPB3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPB3 PE=1 SV=2	sp|P16370	35297,7	6%	LGLIPLQSMDIEQLEYSR		1	0	1
wt	N-terminal acetyltransferase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAT2 PE=1 SV=2	sp|P37293	32805,8	5%	VPLTAVLTPSFVK		1	0	1
wt	Proteasome component C11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE1 PE=1 SV=2	sp|P22141	22517,4	6%	VQDSVILASSK		1	0	1
wt	26S protease regulatory subunit 7 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPT1 PE=1 SV=1	sp|P33299	51984,6	2%	FATLGIDPPK		1	0	1
wt	Mitochondrial protein import protein MAS5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDJ1 PE=1 SV=1	sp|P25491	44671,7	37%	EASAAYEILSDPEKR-FPENHFTSEENLK-FQTEcDVcHGTGDIIDPK-FYDILGVPVTATDVEIK-GEADQAPDVIPGDVVFIVSERPHK-HEISASLEELYK-ILEVHVEPGMK-IVPAIPK-KILEVHVEPGmK-QMGPMIQR-VGIVPGEVIAPG		12	0	12
wt	mRNA export factor MEX67 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MEX67 PE=1 SV=1	sp|Q99257	67353,5	25%	AEAESLMK-AYSTGAWK-DISAISTLAQTFPNLK-ELLMTNNPITTDK-FAGSNLK-GVFSSISTQSK-LQTVYSLPMK-LSIGQESINSIFK-LVVLDNVIVR-LVVLDNVIVRDEQK-NLcLANNQIFR-SLIVESVNLADNQLK-TWVIVPmNNS		13	0	13
wt	40S ribosomal protein S18-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS18A PE=1 SV=1	sp|P0CX55,sp|P0CX56	17037,9	64%	AGELTQEELER-DYHTLANNVESK-IPAWFLNR-IVQImQNPTHYK-IVYALTTIK-LLNTNVDGNIK-QNDITDGKDYHTLANNVESK-sLVVQEQGSFQHILR-YSNLVcK		9	0	9
wt	Malate dehydrogenase, peroxisomal OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MDH3 PE=1 SV=3	sp|P32419	37187,2	49%	AETFLVDYLMLK-EEQLVNTAVK-FKPGNVmGVTNLDLVR-ILVISNPVNSLVPIAVETLK-ILVISNPVNSLVPIAVETLKK-KVTVIGGHSGETIIPIITDK-LSPYVSELALYDIR-NGSVVSIDTSVLEK-QGAGSATLSmAFAGAK-SFILDSSK		14	0	14
wt	54S ribosomal protein L12, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MNP1 PE=1 SV=1	sp|P53163	20650,8	21%	GLLGLSLVEAK-IVQDISQLTLLETSSLINELK-TLEDLGAK		3	0	3
wt	U3 small nucleolar RNA-associated protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UTP10 PE=1 SV=1	sp|P42945	200093,1	4%	AIGALASNNSGVDEHNQILNK-GQGNVDQLPSK-LVINSLTSSLK-VLSLFTEAIGK-VTISPAAPTALK		5	0	5
wt	Nucleoporin POM34 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=POM34 PE=1 SV=1	sp|Q12445	34233,5	3%	LGNFESPVLK		1	0	1
wt	Cell division control protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC12 PE=1 SV=1	sp|P32468	46668,9	9%	QVIEAQEIR-SGSNPDSAAVEHAR-TTFINTLFQTVLK		3	0	3
wt	PAB1-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PBP1 PE=1 SV=1	sp|P53297	78783	13%	EIESQGTSGNIHIAEDR-NENAVSTDTSTPAAAGAPEGKPPQK-STFDEHLYTTK-TDVDISGSGR-TVSPTTQISAGK-VADSGVSDSVDDLAK		6	0	6
wt	Protein transport protein SEC13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SEC13 PE=1 SV=1	sp|Q04491	33042,6	18%	DVAWSPTVLLR-FGTILAScSYDGK-FPDVLWR-LIDTLTGHEGPVWR-VSVVEFK		5	0	5
wt	54S ribosomal protein L15, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRPL15 PE=1 SV=3	sp|P36523	28168,8	4%	LNLLGAQFLK		1	0	1
wt	Eukaryotic translation initiation factor 4E OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC33 PE=1 SV=1	sp|P07260	24254,6	45%	FALWTK-FEENVSVDDTTATPK-GADIDELWLR-KFEENVSVDDTTATPK-LTDDGHLEFFPHSSANGR-SDYHVFR-SEDKEPLLR-TVLSDSAHFDVK-WSFQLR-WTLWYTKPAVDK		10	0	10
wt	Altered inheritance of mitochondria protein 24, mitochondrial OS=Saccharomyces cerevisiae (strain RM11-1a) GN=AIM24 PE=3 SV=1	sp|B3LQG6,sp|C8ZBM7,sp|P47127	44429,4	5%	IIGSSVLEILAAPNFQTSR		1	0	1
wt	ATPase synthesis protein 25, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) GN=ATP25 PE=3 SV=1	sp|A6ZMF5,sp|B3LLY9,sp|B5VPM5,	70410,8	2%	IIQSSSGTETHNIR		1	0	1
wt	Eukaryotic translation initiation factor 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TIF6 PE=1 SV=1	sp|Q12522	26457,4	7%	GLLVPTQTTDQELQHLR		1	0	1
wt	Inorganic phosphate transport protein PHO88 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PHO88 PE=1 SV=1	sp|P38264	21138	26%	APSLFGGmGQTGPK-LQVTTVR-YTNPLFMQSISPVK-YVEPGNAMSGEGEK	m8: Oxidation (+	4	0	4
wt	GTP-binding nuclear protein GSP1/CNR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GSP1 PE=1 SV=1	sp|P32835	24810,6	23%	FDVWDTAGQEK-HLTGEFEK-HLTGEFEKK-LVLVGDGGTGK-SNYNFEKPFLWLAR-TITFHR		6	0	6
wt	Eukaryotic translation initiation factor 2A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YGR054W PE=1 SV=1	sp|P53235	71307,1	4%	FDATNTSVcK-VSLTTGPVHDFTWSPTSR	c9: Carbamidome	2	0	2
wt	Eukaryotic initiation factor 4F subunit p150 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TIF4631 PE=1 SV=2	sp|P39935	107103,8	37%	AcDEPHWSSMYAQLcGK-ADAEWVQSTASK-ASSEENISEAEK-AVIEQIFLK-DATPIEDVFSFNYPEGIEGPDIK-DSFITTR-EEVAPLVPSANR-ELNPDITDETNEGK-EQLEGSSGNNNIPmK-EVPVQEETK-FIGFLYR-	c2: Carbamidome	27	0	27
wt	Protein SCD6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SCD6 PE=1 SV=1	sp|P45978	39189,2	7%	STPQDTNVNSQSR-TISLISVTDNR		2	0	2
wt	THO complex subunit THP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=THP2 PE=1 SV=1	sp|O13539	30300,7	17%	DVAAGVQNPK-ELINSSIR-SISEYYSTFEHLNR-SSDDLLTESLK		4	0	4
wt	N-terminal acetyltransferase A complex subunit NAT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NAT1 PE=1 SV=2	sp|P12945	98912	1%	QQAINTLSQFEK		1	0	1
wt	Nascent polypeptide-associated complex subunit beta-1 OS=Saccharomyces cerevisiae (strain YJM789) GN=EGD1 PE=3 SV=1	sp|A6ZWL1,sp|Q02642	17020,5	24%	LHAVTIDNVAEANFFK-VGVQVAAQHNTSVFYGLPQEK		2	0	2
wt	ARS-binding factor 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ABF2 PE=1 SV=1	sp|Q02486	21563,3	23%	ENPTLRPAEISK-LYSEYQK-RPTSAYFLYLQDHR-WQNLEADIK		4	0	4
wt	Putative ribosomal RNA methyltransferase Nop2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NOP2 PE=1 SV=1	sp|P40991	69814,3	9%	DLAQTLVNR-GVNLQPIGSWTK-IGPSSFDDNQASAK-ILDmAAAPGGK-LVDTGLAIGK		5	0	5
wt	SWI5-dependent HO expression protein 2 OS=Saccharomyces cerevisiae (strain YJM789) GN=SHE2 PE=3 SV=1	sp|A6ZZJ0,sp|B3LQW9,sp|B5VM30,	28266,8	4%	FSQWmIESLR	m5: Oxidation (+	1	0	1
wt	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GFA1 PE=1 SV	sp|P14742	80048,7	3%	HGVLALVDENLPIIAFGTR		1	0	1
wt	Multiple RNA-binding domain-containing protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRD1 PE=1 SV=1	sp|Q06106	101123	2%	SQLIDAENSSSAVK		1	0	1
wt	60S ribosomal protein L9-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL9B PE=1 SV=1	sp|P51401	21657	36%	FIEVR-FLDGIYVSHK-HIDVTFTK-SLVDNmITGVTK-YIQTEQQIEIPEGVTVSIK-YVYAHFPINVNIVEK		6	5	1
wt	U2 small nuclear ribonucleoprotein B'' OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MSL1 PE=1 SV=1	sp|P40567	12830,3	24%	NTLYVSQLNEK-TIDQASLAQISLNGER		2	0	2
wt	Hexokinase-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HXK2 PE=1 SV=4	sp|P04807	53944,7	9%	GFDIPNIENHDVVPMLQK-IFTVPTETLQAVTK-mSSGYYLGEILR		3	0	3
wt	Transcription initiation factor TFIID subunit 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF12 PE=1 SV=1	sp|Q03761	61072,1	9%	FLQESTQQQR-IPGYSADEIR-LQSITSDK-QVYDALTLNR-TPAPVAYR		5	0	5
wt	Peroxiredoxin TSA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TSA1 PE=1 SV=3	sp|P34760	21590,1	45%	DYGVLIEEEGVALR-EGGLGPINIPLLADTNHSLSR-GLFIIDPK-HITINDLPVGR-KEGGLGPINIPLLADTNHSLSR-LVEAFQWTDK-NVDEALR-TAVVDGVFDEVSLDK-TAVVDGVFDEVSLDKYK		9	0	9
wt	60S ribosomal protein L11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL11A PE=1 SV=2	sp|P0C0W9,sp|Q3E757	19720	56%	AEEILER-DLKIEK-EDTVSWFK-IAVHVTVR-LVLNISVGESGDR-QKYDADVLDK-TTKEDTVSWFK-VKEYQLR-VLEQLSGQTPVQSK-YDADVLDK-YDPSIGIFGmDFYVVMNRPGAR		11	0	11
wt	Elongation factor 1-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TEF1 PE=1 SV=1	sp|P02994	50032,6	56%	EHALLAFTLGVR-eTSNFIK-FDELLEK-FDELLEKNDR-FQEIVK-FVPSKPMcVEAFSEYPPLGR-IGGIGTVPVGR-LPLQDVYK-NmITGTSQADcAILIIAGGVGEFEAGISK-QLIVAVNK-QTVAVGVIK-sGDAALVK-SHINVVVIGHVDS		19	0	19
wt	Eukaryotic peptide chain release factor GTP-binding subunit OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SUP35 PE=1 SV=1	sp|P05453	76550,7	7%	FVAQIAIVELK-IKGVEEEDISPGFVLTSPK-LVSSSGIK-YTILDAPGHK		4	0	4
wt	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TDH2 PE=1 SV=3	sp|P00358	35846,9	61%	eLDTAQK-ETTYDEIK-IATFQER-IVSNAScTTNcLAPLAK-KNVEVVALNDPFISNDYSAYmFK-KVVITAPSSTAPmFVmGVNEEK-LTGMAFR-lVSWYDNEYGYSTR-NVEVVALNDPFISNDYSAYmFK-TASGNIIPSS	n-term: Acetyl (+	18	14	4
wt	Chromatin structure-remodeling complex subunit RSC9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC9 PE=1 SV=1	sp|Q03124	65221,5	14%	ANEESAADNLDHK-APYmISLR-FPQELSDVSK-MEMALLSGIPEEIK-SIHYSLANFNVFQSLPK-TFILPLER-TLPDLLPLFK		7	0	7
wt	Vacuolar protein sorting-associated protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VPS1 PE=1 SV=2	sp|P21576	78740	42%	AEQTYINTAHPDLLK-DATIPTNEFVVDIIK-EAISNQFIQFLK-ELSSQELSGGAR-ENDITIQR-ETDKVTGANSGISSVPINLR-ETmETEVIK-EVDPEGTR-IYSPHVLTLTLVDLPGLTK-KLNSILLHHIR-LAALESPPPVLK-LQDALAPLG		23	0	23
wt	Histone H2A.Z OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HTZ1 PE=1 SV=3	sp|Q12692	14283,6	16%	ATIASGGVLPHINK-HLQLAIR		2	1	1
wt	Proteasome component C1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRE10 PE=1 SV=2	sp|P21242	31536,4	4%	TPIPIPAFADR		1	0	1
wt	60S ribosomal protein L14-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPL14B PE=1 SV=1	sp|P38754	15153,2	57%	AALTDFER-FQVMVLR-KVLIDGPK-KWAAAGVcEK-LAAIVEIIDQK-LVEVGR-QAINLGQVVLTPLTFALPR-RAALTDFER-VLIDGPK-WAAAGVcEK-WAASSWAK		11	0	11
wt	Translation machinery-associated protein 20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TMA20 PE=1 SV=1	sp|P89886	20278,3	7%	FPEAYPTVQVDR		1	0	1
wt	40S ribosomal protein S13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS13 PE=1 SV=3	sp|P05756	17029,8	58%	GISSSAIPYSR-GLTPSQIGVLLR-KGLTPSQIGVLLR-LILIESR-lSSESVIEQIVK-NAPAWFK-SNGLAPEIPEDLYYLIK-TVAVLPPNWK-YESATASALVN		9	0	9
wt	Partitioning protein REP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=REP1 PE=1 SV=1	sp|P03871	43231,6	3%	ELIQSQGTVK		1	0	1
wt	Spermidine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPE3 PE=1 SV=1	sp|Q12074	33324,4	4%	VLVIGGGDGGVLR		1	0	1
wt	Endosomal protein P24B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=EMP24 PE=1 SV=1	sp|P32803	23332,7	6%	EVKDEQSYIVIR		1	0	1
wt	Glucose-6-phosphate 1-epimerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YMR099C PE=1 SV=1	sp|Q03161	33956,4	11%	ENPPTVQFGLKPEIANPELTK-TAIEVENTSSSK		2	0	2
wt	Bud emergence protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BEM1 PE=1 SV=1	sp|P29366	61607,6	2%	QAPAQSTSGLK		1	0	1
wt	40S ribosomal protein S26-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPS26A PE=1 SV=1	sp|P39938,sp|P39939	13505	20%	DLSEASVYPEYALPK-NIVEAAAVR		2	0	2
wt	Protein disulfide-isomerase MPD1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MPD1 PE=1 SV=1	sp|Q12404	36410,3	15%	IDLSKPIDNAK-IDTLGSLLR-RLDGVVQVAAVNcDLNK-TLAPIVDFSLSR		4	0	4
wt	Nuclear protein STH1/NPS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STH1 PE=1 SV=1	sp|P32597	156750,6	4%	INSIIDFIK-ISADFNAK-QPSILVGGTLK-VIEKPMAIDIILK-VIVPQTVR		5	0	5
wt	ADP-ribosylation factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ARF2 PE=1 SV=3	sp|P19146	20658,2	16%	ILMVGLDGAGK-LFSNLFGNK-mLNEDELR		3	0	3
wt	Cystathionine beta-synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CYS4 PE=1 SV=1	sp|P32582	56024,8	7%	LSGLVTLSELLR-STLIEPTSGNTGIGLALIGAIK		2	0	2
wt	Inosine-5'-monophosphate dehydrogenase IMD2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=IMD2 PE=1 SV=1	sp|P38697	56531	25%	EQAANLIAAGADGLR-ESFPGLEVIAGNVVTR-GMGSIDAMQK-LLVVDEK-NPVTGAQGITLSEGNEILK-NPVTGAQGITLSEGNEILKK-NQNYPLASK-SLPRPDGLSVQELMDSK-TASAQLEGGVHNLHSYEK-YFSESDSVLVAQG		10	7	3
wt	37S ribosomal protein MRP17, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MRP17 PE=1 SV=1	sp|P28778	15021,7	8%	MLYELIGLVR		1	0	1
wt	Hsp90 co-chaperone HCH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HCH1 PE=1 SV=1	sp|P53834	17246,8	8%	LTSLSTVSSDGK		1	0	1
wt	NADPH dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=OYE2 PE=1 SV=3	sp|Q03558	45012	10%	FAYSIWK-FFISNPDLVDR-IGNNELLHR-TDEYGGSIENR		4	0	4
wt	Protein transport protein SSS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSS1 PE=1 SV=2	sp|P35179	8943,8	21%	LIHIPIR-LVEAPVEFVR		2	0	2
wt	Pyruvate kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC19 PE=1 SV=2	sp|P00549	54545,4	73%	AEVSDVGNAILDGADcVMLSGETAK-AGAGHSNTLQVSTV-AGLNIVR-AIIVLSTSGTTPR-AKEFGILK-EPVSDWTDDVEAR-EVLGEQGK-FSHLYR-GDLGIEIPAPEVLAVQK-GDTYVSIQGFK-GNYPINAVTTmA	c16: Carbamidon	32	0	32
wt	DNA-directed RNA polymerases I and III subunit RPAC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RPC40 PE=1 SV=1	sp|P07703	37687,6	30%	EANFDLINIDTSIANAFR-FSPVSTASYR-LLPQINILQPIK-LLPQINILQPIKGESAR-LRPGQEISLK-NHFIFNVESAGAmTPEEIFFK-sNIVGIEYNR-VTNTTSTDFPGFSK		8	0	8
wt	Transcription elongation factor SPT5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPT5 PE=1 SV=1	sp|P27692	115651,4	15%	AESTSNIPPLDGEEK-EGAVDLTSVSQSIK-EVTITANNLSK-FDEIDPTTQQR-FLLPSVDTATIWGVR-LDQANLYK-LLIPVQELPLLLKPNK-mGPSYVSAPR-SDDVALEEGSYVR-SIDTTATSSEYALHDIVELSAK-VSSVDANGNEIK-V		12	0	12
wt	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TDH1 PE=1 SV=3	sp|P00360	35750,2	65%	DIEVVAVNDPFISNDYAAYMVK-DPANLPWGSLK-EATYDQIKK-eLDTAQK-GTVSHDDKHIIIDGVK-HIIIDGVK-IATYQER-IATYQERDPANLPWGSLK-IDVAVDSTGVFK-IVSNAScTTNcLAPLAK-KDIEVVAVNDPFISNDYAAYM		20	0	20
wt	Chromatin structure-remodeling complex protein RSC8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RSC8 PE=1 SV=1	sp|P43609	63169,2	24%	EESATLGAEVAHK-FLSLPIEDNYIR-IHAFLEK-LQPQVYKPWSL-LSPYEYLTITAVR-NFIINTYR-NVAMDVASIVK-SLEELNVSK-SNPDFFNDSSR-VYIcHTcGNESINVR-WGLINYQIDPR-YIEESQAIIQELVK		12	0	12

Supplementary Table S5: Identification table referring to Figure 2b

sample name	Protein name	Protein accession numbers	Protein molecular weight (Da)	Percentage sequence coverage	Peptide sequence	Total number of peptide	Number of shared peptide	Number of discriminant peptide
WT	PRP42	sp|Q03776	65131,7	15%	IDDIMDLK-IDINYSGR-ILEIPLHSFSK-KSGQEILLNNLVQFYSK-SLAYWEK-SLLLWTSYLK-STEPQLLK-TFcQNSLYSSR	8	0	8
WT	PRP42	sp|Q03776	65131,7	19%	FcNNVISHQK-GLQAFNQR-IDDIMDLK-IDINYSGR-ILEIPLHSFSK-LIYFDTSR-NVLLMGLK-QLSQLTSKDELLK-SLLLWTSYLK-SYLDKR-TFcQNSLYSSR	11	0	11
WT	PRP42	sp|Q03776	65131,7	17%	GLQAFNQR-IDDIMDLK-IDINYSGR-ILEIPLHSFSK-LIYFDTSR-QLSQLTSKDELLK-SLLLWTSYLK-STEPQLLK-SYLDKR-TFcQNSLYSSR	10	0	10
WT	PRP39	sp|P39682	74734,2	22%	ANTFLPLDFK-FATIEYQLFGLK-FVTDPSK-GLDTQFLQDNTALVQAYR-IKQPFFNLGQVLNDDLENWSR-ILETSITNYINNQIDAK-INDLYTEEFLKEGK-IYEYIIEVPLHQYAR-SIAVLATSVK-SNNTLFNNIFNETVSR	10	0	10
WT	PRP39	sp|P39682	74734,2	18%	ANTFLPLDFK-GLDTQFLQDNTALVQAYR-INDLYTEEFLKEGK-IYEYIIEVPLHQYAR-PDETNFTIEDIEPRPDALR-SIAVLATSVK-SNNTLFNNIFNETVSR-YGNPNDSIK	8	0	8
WT	PRP39	sp|P39682	74734,2	22%	ANTFLPLDFK-FATIEYQLFGLK-FVTDPSK-GLDTQFLQDNTALVQAYR-IKQPFFNLGQVLNDDLENWSR-ILETSITNYINNQIDAK-INDLYTEEFLKEGK-IYEYIIEVPLHQYAR-SIAVLATSVK-SNNTLFNNIFNETVSR	10	0	10
WT	LUC7	sp|Q07508	30177,1	19%	IQQVTEELDVLDVR-LQELISK-NITENVGQSAQQK-TFPEFEREYLAILSR	4	0	4
WT	LUC7	sp|Q07508	30177,1	19%	IQQVTEELDVLDVR-NITENVGQSAQQK-TATTLPGR-TFPEFEREYLAILSR	4	0	4
WT	LUC7	sp|Q07508	30177,1	22%	IQQVTEELDVLDVR-LQELISK-NITENVGQSAQQK-TATTLPGR-TFPEFEREYLAILSR	5	0	5
WT	MUD1	sp|P32605	34361,8	43%	GNDETYNLDIKK-IVKEFETR-KVEEAEIDR-LQNNDVTIGFAK-MTNQAFLTFVTQEEADRFLEK-NLAFVEYETVADATK-NQLGSTYK-sALYFQNLPSRPANKENYTR-YAINPSLPLPHNK-YTTTALK-YTTTALKVQGR	11	0	11
WT	MUD1	sp|P32605	34361,8	33%	IVKEFETR-LQNNDVTIGFAK-MTNQAFLTFVTQEEADRFLEK-NLAFVEYETVADATK-NQLGSTYK-sALYFQNLPSRPANK-sALYFQNLPSRPANKENYTR-YAINPSLPLPHNK	8	0	8
WT	MUD1	sp|P32605	34361,8	44%	IVKEFETR-KVEEAEIDR-LQNNDVTIGFAK-MTNQAFLTFVTQEEADRFLEK-NLAFVEYETVADATK-NQLGSTYK-sALYFQNLPSRPANKENYTR-TNSLLGLSIEmQK-YAINPSLPLPHNK-YTTTALKVQGR	10	0	10
WT	NAM8	sp|Q00539	56954,5	6%	SSSSLNNENVDSR-VGPTSGQQQHVSGNNDYNR	2	0	2
WT	NAM8	sp|Q00539	56954,5	8%	QTTYYPSR-SSSSLNNENVDSR-VGPTSGQQQHVSGNNDYNR	3	0	3
WT	NAM8	sp|Q00539	56954,5	6%	SSSSLNNENVDSR-VGPTSGQQQHVSGNNDYNR	2	0	2

WT	SNU56	sp|Q03782	56482,3	11%	GQLSQGHYPTTSNDGQR-HAVNKPSNVLNSSNR-QNYIDIVYQNLNDLR-TRPIIETSK	4	0	4
WT	SNU56	sp|Q03782	56482,3	5%	GQLSQGHYPTTSNDGQR-GSLLILPMR	2	0	2
WT	SNU56	sp|Q03782	56482,3	9%	GQLSQGHYPTTSNDGQR-HAVNKPSNVLNSSNR-NINLTGSFYLPK	3	0	3
WT	SNU71	sp|A6ZV04,sp	71381,2	25%	AAAITLPEGTVK-ADIMSAENYEEHLEKNR-ASEFYSVFK-ELAPIQLSDGK-FSKVDEDEAFVNTLNYcK-NIEDQTDER-QALLNELRETFDEDGETIADR-SAAEDRLPFTADELNIR-SENYNADKNVSESSEHVK-SGFIPILK-TGTIPSVKPEK-VFDQIR	12	0	12
WT	SNU71	sp|A6ZV04,sp	71381,2	27%	AAAITLPEGTVK-ADIMSAENYEEHLEK-ADIMSAENYEEHLEKNR-ASEFYSVFK-ELAPIQLSDGK-EYVEDR-FSKVDEDEAFVNTLNYcK-NIEDQTDER-QFLPISLDQQIHTVSLQGVSSSFSR-SAAEDRLPFTADELNIR-SENYNADKNVSESSEHVK-SGFIPILK-TGTIPSVKPEK-VFDQIR	14	0	14
WT	SNU71	sp|A6ZV04,sp	71381,2	20%	ALFAFIR-ASEFYSVFK-ELAPIQLSDGK-NIEDQTDER-QFLPISLDQQIHTVSLQGVSSSFSR-SAAEDRLPFTADELNIR-SENYNADKNVSESSEHVK-SGFIPILK-TGTIPSVKPEK-VFDQIR-VFDQIRK	11	0	11
WT	YHC1	sp|Q05900	27027,8	15%	ELAQTSIDTLK-LLYDGSPGYSK-SRDETcESNPFPR	3	0	3
WT	YHC1	sp|Q05900	27027,8	10%	ELAQTSIDTLK-LLYDGSPGYSK	2	0	2
WT	YHC1	sp|Q05900	27027,8	5%	ELAQTSIDTLK	1	0	1
WT	LEA1	sp|Q08963	27176,2	30%	DLQLETDSESMPSSLK-LVPHLETLDFQNVTAEER-NNIVEVDGR-QADGDTLGPVNTAIR-QLAEATSLEEIAR	5	0	5
WT	LEA1	sp|Q08963	27176,2	30%	DLQLETDSESMPSSLK-LVPHLETLDFQNVTAEER-NNIVEVDGR-QADGDTLGPVNTAIR-QLAEATSLEEIAR	5	0	5
WT	LEA1	sp|Q08963	27176,2	30%	DLQLETDSESMPSSLK-LVPHLETLDFQNVTAEER-NNIVEVDGR-QADGDTLGPVNTAIR-QLAEATSLEEIAR	5	0	5
WT	PRP9	sp|P19736	63014,6	3%	DLDLNEIFTR-SSLIAENK	2	0	2
WT	PRP9	sp|P19736	63014,6	3%	TNILSDR-VFPDTKLPR	2	0	2
WT	PRP9	sp|P19736	63014,6	5%	DLDLNEIFTR-SSLIAENK-TNILSDR	3	0	3
WT	PRP21	sp|P32524	33035,8	14%	EIARPPDFLFSQYDTGISR-TILDNcFER-VYSFTGQEIKK	3	0	3
WT	PRP21	sp|P32524	33035,8	16%	EIARPPDFLFSQYDTGISR-IQFAAIPWDKFTQVAK-TILDNcFER	3	0	3
WT	PRP21	sp|P32524	33035,8	7%	EIARPPDFLFSQYDTGISR	1	0	1
WT	RSE1	sp|Q04693	153772,1	3%	SQIVSDSPLSIATK-SVQVEDIIQTINEVR-SVTQTPVSITK	3	0	3
WT	RSE1	sp|Q04693	153772,1	2%	SQIVSDSPLSIATK-SVTQTPVSITK	2	0	2
WT	RSE1	sp|Q04693	153772,1	4%	LSLNEQEFLAK-SQIVSDSPLSIATK-SVQVEDIIQTINEVR-TLVNQPLTR	4	0	4
WT	PRP11	sp|Q07350	29903,2	14%	GENVPYTFQDEKDDQVR-IVSGLELSDTKQK-VPPLIR	3	0	3

WT	PRP11	sp|Q07350	29903,2	20%	GENVPYTFQDEKDDQVR-IVSGLELSDTK-IVSGLELSDTKQK-KGGGGIASESQFNLQR-VPPLIR	5	0	5
WT	PRP11	sp|Q07350	29903,2	7%	IVSGLELSDTK-IVSGLELSDTKQK-VPPLIR	3	0	3
htb1K123	PRP42	sp|Q03776	65131,7	1%	LIYFDTSR	1	0	1
htb1K123	PRP42	sp|Q03776	65131,7	1%	LIYFDTSR	1	0	1
htb1K123	PRP42	sp|Q03776	65131,7	1%	LIYFDTSR	1	0	1
htb1K123	PRP39	sp|P39682	74734,2	7%	ANTFLPLDFK-IKQPFFNLGQVLNDDLENWSR-IYEYIIEVPLHQYAR	3	0	3
htb1K123	PRP39	sp|P39682	74734,2	6%	ANTFLPLDFK-IYEYIIEVPLHQYAR-SIAVLATSVK	3	0	3
htb1K123	PRP39	sp|P39682	74734,2	7%	ANTFLPLDFK-IKQPFFNLGQVLNDDLENWSR-IYEYIIEVPLHQYAR	3	0	3
htb1K123	LUC7	sp|Q07508	30177,1	3%	LQELISK	1	0	1
htb1K123	LUC7	sp|Q07508	30177,1	8%	LQELISK-NITENVGQSAQQK	2	0	2
htb1K123	LUC7	sp|Q07508	30177,1	8%	IQQVTEELDVLDVR-LQELISK	2	0	2
htb1K123	MUD1	sp|P32605	34361,8	11%	LQNNDVTIGFAK-sALYFQNLPSRPANKENYTR	2	0	2
htb1K123	MUD1	sp|P32605	34361,8	8%	LQNNDVTIGFAK-YAINPSLPLPHNK	2	0	2
htb1K123	MUD1	sp|P32605	34361,8	8%	LQNNDVTIGFAK-YAINPSLPLPHNK	2	0	2
htb1K123	NAM8	sp|Q00539	56954,5	4%	VGPTSGQQQHVSGNNDYNR	1	0	1
htb1K123	NAM8	sp|Q00539	56954,5	4%	VGPTSGQQQHVSGNNDYNR	1	0	1
htb1K123	SNU56	sp|Q03782	56482,3	7%	GQLSQGHYPTTSNDGQR-HAVNKPSNVLNSSNR	2	0	2
htb1K123	SNU56	sp|Q03782	56482,3	3%	GQLSQGHYPTTSNDGQR	1	0	1
htb1K123	SNU71	sp|A6ZV04,sp	71381,2	10%	AAAITLPEGTVK-ASEFYSVFK-ELAPIQLSDGK-SAAEDRLPFTADELNIR-TGTIPSVKPEK	5	0	5
htb1K123	SNU71	sp|A6ZV04,sp	71381,2	14%	AAAITLPEGTVK-ASEFYSVFK-ELAPIQLSDGK-NIEDQTDER-SAAEDRLPFTADELNIR-SENYNADKNVSESSEHVK-SGFIPILK	7	0	7
htb1K123	SNU71	sp|A6ZV04,sp	71381,2	13%	AAAITLPEGTVK-ADIMSAENYEEHLEK-ELAPIQLSDGK-NIEDQTDER-SAAEDRLPFTADELNIR-SGFIPILK-TGTIPSVKPEK	7	0	7
htb1K123	YHC1	sp|Q05900	27027,8	5%	ELAQTSIDTLK	1	0	1
htb1K123	YHC1	sp|Q05900	27027,8	5%	ELAQTSIDTLK	1	0	1
htb1K123	YHC1	sp|Q05900	27027,8	5%	ELAQTSIDTLK	1	0	1
htb1K123	PRP21	sp|P32524	33035,8	3%	TILDNcFER	1	0	1
htb1K123	RSE1	sp|Q04693	153772,1	1%	LSLNEQEFLAK	1	0	1
htb1K123	RSE1	sp|Q04693	153772,1	1%	SVQVEDIIQTINEVR	1	0	1

Supplementary Table S6: Complete spectral count table referring to Figure 2b

			NO TAG	**NO TAG**	**NO TAG**	**WT**	**WT**	**WT**	***htb1K123R***	***htb1K123R***	***htb1K123R***
Identified Proteins	Accession Number	Molecular Weight	Injection 1 number of spectrum	Injection 2 number of spectrum	Injection 3 number of spectrum	Injection 1 number of spectrum	Injection 2 number of spectrum	Injection 3 number of spectrum	Injection 1 number of spectrum	Injection 2 number of spectrum	Injection 3 number of spectrum
STO1	sp|P34160	100 kDa	7	3	4	429	429	429	429	429	429
CBC2	sp|Q08920	24 kDa	7	3	4	152	127	142	157	155	159
PRP42	sp|Q03776	65 kDa	0	0	0	11	9	14	2	2	2
PRP39	sp|P39682	75 kDa	0	0	0	9	13	15	5	5	5
LUC7	sp|Q07508	30 kDa	0	0	0	4	5	7	2	5	3
MUD1	sp|P32605	34 kDa	0	0	0	10	14	15	3	3	5
NAM8	sp|Q00539	57 kDa	0	0	0	3	3	3	2	0	2
SNU56	sp|Q03782	57 kDa	0	0	0	3	6	5	3	0	2
SNU71	sp|A6ZV04 (+	71 kDa	0	0	0	16	16	13	9	11	11
YHC1	sp|Q05900	27 kDa	0	0	0	3	4	2	2	2	2
LEA1	sp|Q08963	27 kDa	0	0	0	5	5	6	0	0	0
PRP9	sp|P19736	63 kDa	0	0	0	2	2	3	0	0	0
PRP21	sp|P32524	33 kDa	0	0	0	3	3	1	2	0	0
RSE1	sp|Q04693	154 kDa	0	0	0	3	3	6	2	0	2
PRP11	sp|Q07350	30 kDa	0	0	0	5	3	3	0	0	0