







spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
C90H49	ARP3 YJR065C	actin-related protein	P47117	15	GEADTSLR VVDIGYER NFSLFNMV KVVDIGYER ERGEADTSLR IAQSELLSGTK STGVDVSVISHR DITLFIQSLLR FAQFVVENQEK DYEEYGPEIVR KDYEEYGPEIVR HGQVENWDHMER GLYNNIVLSGGSTMFK NAVWFGGSLLAQTAEFK TEPEDHFFLLTEPPLNPPENR	2.03 2.53 2.27 2.82 2.88 3.60 2.96 2.53 3.96 2.84 3.24 3.97 2.38 2.03 4.45	2 2 2 2 2 2 2 2 2 2 3 3 2 2 3	33%
B14I59	ARP5 YNL059C	actin-related protein	P53946	13	DIVELER LATVQSQR NYDEDIEK AVVIDDPLR NLASLAEDNVK YLHSLEQSLK EYEEYGPEYIK KEYEEYGPEYIK VLSVLQNAQFDDER AQM*VEAEDDSDLDEM*NEDKTAQK LLEHDPNFTEEDTLEAQYDWR EFTGFLPTGTNITVNM*SSDPSLDAWK QTPEPFDEQSAYNPQSPIAIDFGSSK	2.02 2.33 2.35 2.94 3.40 3.09 2.39 3.11 3.77 2.79 4.48 3.69 2.78	2 2 2 2 2 3 2 3 2 3 2 2 3	23%
C17H53	ASN2 YGR124W	asparagine synthetase 2	P49090	13	ALQLSK EAYWYR FDAQWFPQK STM*AWGLEAR ASTPM*FLLSR AIDAMFANPK ADWGDDIPTTK DPIGVVTLYM*GR ANADANEDNNVDEK RIPSTPVDYHAIR EQFSDGVGYSWIDGLR LHSFAIGLPNAPDLQAAR AFDTTDEPDVKPYLPEEILWR	1.61 1.53 2.39 3.75 2.27 3.11 1.58 3.33 4.29 3.88 3.35 2.45 5.18	1 1 2 2 2 2 1 2 2 3 2 2 3	27%
E12D01	BDH1 YAL060W	2,3-butanediol dehydrogenase	P39714	7	SIEILR IEDGWKEK IVVSEIAER GFQELMDHK KLGVEVFNPSK ILLTPNNHGEM*K PVPFQPM*DVTLQEK	1.53 2.34 3.33 2.71 2.81 2.59 2.63	1 2 2 2 2 2 2	18%
F23P39	CAP2 YIL034C	actin-capping protein 2	P13517	3	DAQAEVIR DLQDSPFPSAPLR SPWSNTYYPELSPK	2.72 3.87 3.54	2 2 2	12%
C59F37	CCT3 YJL014W	component of Chaperonin-containing T-complex	P39077	11	VDDIVSGVR NLQDAM*AVAR TLIQNAGGDPPIR GGSKDILNEIDR GVSDLAQHYLEK KGESQTNIEIEK HAQGNFTTGIDGDKGK VLKGVLLNKDVVHPK IVDM*VSYGIWEPEVIK M*LLDPM*GGLVLTNDGHAILR IVDM*VSYGIWEPEVIKQQSVK	2.69 2.53 2.78 2.52 3.08 3.25 4.67 4.02 4.53 3.08 3.76	2 2 2 2 2 2 3 2 2 3 3	26%
E42H59	CDC10 YCR002C	septin	P25342	4	SDTLTLDER ELIQNEFEK ISTHTLVEDR LTEIANVIPVIGK	2.61 2.64 2.21 4.60	2 2 2 2	13%

spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
B09L69	CDC48 YDL126C	ATPase of the AAA family (microsomal)	P25694	22	LSILNAQLR M*AGESESNLR GGSLGDAGGASDR GVLFYGPPTGK GVLM*YGPPGTGK FALGNSNPSALR RYEAYSQQM*K AVATEVSANFISVK TPLEPGLLELTAIAK VVSQLLTLM*DGM*K VEGEDVEM*TDEGAK KTPLEPGLLELTAIAK RVVSQLLTLM*DGM*K VVNQLLTEM*DGM*NAK AEQEPEVDPVPYITK ATQGFSGADLLYIVQR LDQLIYVPLDENAR AAAPTVVFLDELDSIAK ETVEYPVLHPDQYTK NAPAIIFIDEIDSIAPK SNVVVIAATNRPNSIDPALR ETVVESVNVTVDDVGGGLDEIKEELK	3.45 2.13 2.82 2.84 2.49 3.24 2.06 4.81 3.22 2.92 3.06 4.64 2.12 3.33 2.97 4.55 3.28 3.72 2.29 3.43 4.54 2.73	2 2 2 2 2 2 2 2 2 2 2 3 2 2 2 2 2 2 2 2 2 3 3	35%
D35B27	CIT1 YNR001C	mitochondrial citrate synthase	P00890	8	ALSADLAAR YLWDTLNAGR NLAQLLGYENK ITSTDPNADYGK AIGVLPQLIIDR ANQEVLEWLFK LVSTIYEVAPGVLTK TVIGEVLLSEQAYGGM*R	2.25 3.42 3.80 2.70 3.02 3.81 3.89 3.94	2 2 2 2 2 2 2 2	22%
E77R21	CLC1 YGR167W	clathrin light chain	P17891	4	SEVVDQWK EAEILGDEFK DEFFGQDNTTWDR ALQLINQDDADIIGGR	2.60 2.59 3.43 4.52	2 2 2 2	20%
J35B75	CPR1 YDR155C	cyclophilin	P14832	5	FPDENFKK GFGYAGSPFHR KVESLGSPSGATK HVVFGVVDGYDIVK HVVFGVVDGYDIVKK	2.83 2.94 4.05 5.39 4.62	2 2 2 2 3	29%
C07J99	CPS1 YJL172W	Gly-X carboxypeptidase yscS	P27614	9	IPTVVQDK YYWNLSK DVFVATPINA EK TTQAVDIINGGVK FVGSIIDIDLLK NPNPADDPDFYK LVEYISNQSHLR INLHSSVAEVFER HSVDTILHDP AFR	2.28 2.02 2.26 4.17 3.62 3.33 3.91 4.05 2.98	1 2 2 2 2 2 2 3 3	18%
C22G88	DED81 YHR019C	asparaginyl-tRNA synthetase	P38707	8	VIFVVL R FGDDIAEAAER TPAYALFASQQK IDDMDELMAGFK DAITWLNEHDIK IAEGSDPSLLDQR TEDNEYQEISASALK SVQYVLEDPIAGPLVK	2.35 4.78 4.51 4.34 3.39 4.29 4.70 5.01	2 2 2 2 2 2 2 2	18%
C89B83	DLD3 YEL071W	D-lactate dehydrogenase	P39976	8	LISEGMM*AK YDM*SLQLK DFDPVSGTFK LNAAGLIGDAPK GQSNLILLPNSTDK NHYPNGILNPYK SELSEILSAFEFM*DR ALNAVFFGIENFDTVQK	2.04 2.59 2.62 2.78 2.10 2.48 2.10 4.76	2 2 2 2 2 2 2 2	22%
D27H08	ENO2 YHR174W	enolase 2	P00925	5	GNPTVEVELTTEK LGANAILGVSM*AAAR AVDDFLLSLDGTANK SGETEDTFIADLVVGLR TAGIQIVADDLTVTNPAR	2.58 2.84 5.20 5.48 5.08	2 2 2 2 2	18%
E31H30	FBP1 YLR377C	fructose-1,6-bisphosphatase	P09201	2	FIIEHQK LLPDSSGTINDVLR	2.12 2.60	2 2	6%

spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
G15D72	FSH1 YHR049W	unknown	P38777	5	YLYDIYLK SKYLYDIYLK ISELVPDHPQFK MIFIYGASDQAVPSVR VSVVISGYSFTEPDPEHPGELR	3.01 2.51 2.56 2.94 2.63	2 3 3 2 3	25%
G65I02	FUR1 YHR128W	uracil phosphoribosyltransferase	P18562	3	IVTGALDR AGESMEQGLR LLVEEGLNHLFPVQK	2.11 2.55 3.71	2 2 2	15%
D31G39	GD11 YER136W	GDP dissociation inhibitor	P39958	10	FKQNPISK VTGHPLVLK DWNVDLIPK NTMDEVYVK FLEWISSYK FMGIAELFEPK DRDWNVDLIPK EDGSKDNIYSR APLVIADPTYFPEK SYDASSHFESM*TDDVK	2.38 2.27 2.56 2.24 2.53 3.46 2.78 2.15 3.99 2.87	2 2 2 2 2 2 2 2 2 3	22%
E32L89	GET3 YDL100C	ATPase involved in a general response to stress	Q12154	8	GLNNLTK WIFVGGK FGEITNK FSQFLNK VIYELEDK FLQLPNTLSK LGPM*LNSFM*GAGNVDISGK RQEQGEGETFDTVIFDTAPTGHGTLR	2.69 2.30 2.59 2.59 3.03 2.61 4.88 5.03	2 1 2 2 2 2 2 3	26%
E79J18	GLC7 YER133W	protein serine/threonine phosphatase PP1	P32598	4	DIVGWSENDR GVSFTFGPDVVNR AHQVVEDGYEFFSK GSKPGQQVDLENEIR	2.37 3.74 4.70 4.41	2 2 3 3	17%
D86C09	GLO1 YML004C	glyoxalase I	P50107	1	SLEFYQNVLMGK	3.65	2	4%
E48B19	GRE3 YHR104W	aldo/keto reductase with NADPH specificity	P38715	14	GIIVIPK AISEGLVSR KDIFVVS LLGNLEIEK KAISEGLVSR DISALNANIR FTLTEQELK LLGNLEIEKK FNDPWTWLDGK YPPGFYTGADDEK GHITEAHVPIIDTYR VSQNHPGSTTSQVLLR SIGVSNFQGSIIQDLLR KGHITEAHVPIIDTYR	2.06 2.48 2.26 2.16 2.72 3.27 2.11 2.63 3.52 2.46 3.99 3.47 4.25 2.72	2 2 2 2 2 2 2 2 2 2 3 3 2 3	39%
F79O88	GRX3 YDR098C	glutaredoxin	Q03835	4	FGFFDILR LVNAAPVM*LFM*K FGFFDILRDESVR ESLEEDPDFLQHALQS	3.12 3.30 3.07 2.96	2 2 3 2	14%
G47D83	GTT1 YIR038C	glutathione transferase	P40582	4	SPLLEVQDR ISQAYSSGEVK TITSEESYAASK NQDFDFVEGEISK	2.93 3.45 3.14 3.09	2 2 2 2	19%
D05N16	HAT2 YEL056W	histone acetyltransferase subunit	P39984	13	FAEINLPK SEGLQSTLK LM*M*WDLK ANNTTIDTVK YEHEEEITR DNGYALSFSTLVK DLFGTVSEDSLLK SNVPLMYDFVSETR TWNDLHSDIINDNK YM*PQDPNIVATINGQGTVFLYSR EILSNEDPQEEAGEEYQSSLPAPR LLSGSDDHTVALWEVGGGDPTKPVR QIGAEQTPDDAEDGVPELIM*VHAGHR	2.61 2.50 2.25 3.24 2.70 3.98 3.58 3.48 2.80 2.60 3.50 3.28 2.88	2 2 2 2 3 2 2 2 2 2 3 3 3	49%

spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
C72I52	HIS7 YBR248C	glutamine amidotransferase	P33734	18	DFNISGTSR GEFTVNDVK DLGVWELTR EYLLEHGLK STGLNYIDFK TNDQGDLVVTK AGLNVIENFLK TVFVPLTVGGGIK VSIGTDAVYAAEK YGSEEFIAAVNK IPALEVASLYFR AYGAQAVVISVDPK VFETEYPPNGEK QQSPPIPNYSAEK ELLMNDYSNYGLTR DGSNSGYDLELIEHVK YYFVHSFAAILNSEK IPVIASSGAGVPEHFEEAFLK	3.22 2.42 2.88 2.45 3.19 3.82 3.52 2.62 3.82 4.56 3.30 4.92 3.69 2.30 4.90 4.44 3.96 4.47	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3	41%
J93C60	HNT1 YDL125C	adenosine monophosphoramidase	Q04344	3	LDTYNVLQNNKG SGLIVGWPAQETDFDK YSYAFLDIQPTAEGHALIIPK	4,94 4,02 4,04	2 2 3	31%
E10C51	HOM2 YDR158W	aspartate-semialdehyde dehydrogenase	P13663	8	YVDAVNWK DSGYGVSVGR KYVDAVNWK NRPAPSVEQVK IREDPDLLDFK IAGVLGATGSVGQR EFM*EAGIAIVSNAK REQDVPLIVPVVNPEHLDIVAQK	2.54 3.13 2.32 2.88 2.65 4.24 3.77 4.90	2 2 2 2 3 2 2 3	25%
C66C98	HOM3 YER052C	aspartate kinase	P10869	6	VLGEVSSR LSIVSLVGK FILNPALQAK EVDGIFTADPR FPVQIVDDIVK TNTSNQFEHAIDER	2.39 2.19 2.71 2.90 3.13 2.56	2 2 2 2 2 2	12%
G04I11	HPT1 YDR399W	hypoxanthine phosphoribosyltransferase	Q04178	9	GIDTEKSPKM*K TNFGIFVLHDK KADLPAEM*LNDK NVLIVDEVDTR TTLHYALSELEK KADLPAEM*LNDKNR NFKPDLIIAIGGGGFIPAR M*AIEQGNDFIPEQEHK TTLHYALSELEKDAAEQAK	2.78 3.37 3.92 2.92 3.17 2.84 4.59 4.96 4.91	2 3 3 2 2 3 2 3 2	47%
F00J34	IPP1 YBR011C	inorganic pyrophosphatase	P00817	2	VIAIDINDPLAPK GIDLTNVTLPDPTPTYSK	4.46 3.16	2 2	11%
F10J16	IPP1 YBR011C	inorganic pyrophosphatase	P00817	3	VIAIDINDPLAPK EETLNPIIQDTK GIDLTNVTLPDPTPTYSK	4.86 2.76 4.74	2 2 2	15%
D65F15	LSC2 YGR244C	succinyl-CoA ligase, beta subunit	P53312	21	AVSNLYK VVELTQN FSIETSK YDLNFKV KVVELTQN KFSIETSK PVSAYVIVK QGFELILSNK VEEGRDIINK FGFDDNASFR EM*LNHNLITK DLSQEDPDEVK HEAYLSILMDR IYSFDELDPAAK SLGFSPDAQDEAAK DLSQEDPDEVKAK NVDAIFVNIFGGIVR VDTKHEAYLSILM*DR SGVHM*IESPQQAEDVAK KPM*IIASSQGGM*NIEEVAER DATQVEINPLSEIHDPTHK	1.54 2.22 1.75 2.12 2.87 2.18 2.96 2.78 2.52 2.87 2.28 3.53 3.06 3.48 1.68 3.58 5.41 3.33 3.01 4.94 4.11	1 1 1 2 2 2 2 2 2 2 2 2 2 2 1 2 2 3 2 3 2	48%

spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
D28J63	LYS9 YNR050C	saccharopine dehydrogenase	P38999	12	GVLLALR YGIYK FVLDTGK TSTLVYDGK TLANAQALAK EDLIASIDSK ATWKDEDRER TLANAQALAKPSGSK STSKEDLIASIDSK TDVVTSSYISPALR IETVSSSELM*ATAK TKTDVVTSSYISPALR	2.22 2.11 2.08 2.04 3.22 3.17 2.18 3.74 3.89 3.46 4.29 4.08	2 2 2 2 2 2 2 2 2 2 2 3	21%
A92J83	MET10 YFR030W	sulfite reductase	P39692	8	IGLINVR FNELTGLR FSEINIEK EQIPVSNIDSTK DLDLNSVESYVK LEDLVTPAGAVDLK LFIIDGETTNDISK TVLPLVESVPEASILAK	2.22 2.26 2.79 2.03 3.28 3.55 4.60 3.76	2 2 2 2 2 2 2 2	9%
A07K01	MLP1 YKR095W	myosin-like protein	Q02455	21	LNQLNLLR NLADKLESK IEDLSSQNK LLSNTLDLTK VAQGNNQLEAIR IM*VTQLQTLQK NVLENSLSEANAR DLESQVQDLQTR LVDLLESQNAVK SM*EQSGEIDVVLK ESLLEQLDLNSR SVNNVQNPPLLGLPR LNQPSNIM*EEIK LSQDSLTEQVNSLR SSSGGFNPFTSPSPNK TSVPNEDASYSNVTIK EQM*FNLNNELDLQK LSSITDEADEDNENLSAK KIEENSNSPFNPLLSGEK EYKDLYETTSQSLQQTNSK GLISSSSTLSTDTNDEELTSNNPAQK	3.03 2.22 2.15 2.38 2.31 2.42 4.08 2.56 3.85 3.59 3.40 3.12 2.64 3.91 2.84 3.06 2.44 3.50 3.85 2.76 3.04	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3 2	16%
G48N68	MRP8 YKL142W	mitochondrial ribosomal protein	P35719	18	LVNSLK QSLIISK YLGLSLR KQSLIISK VLELQLDK HDVTDVDFSK QVSELQDLVK QKHDVTDVDFSK DELDDAFNDVAR ELQGELNFIER EQEDFENFLEK FSKDELDDAFNDVAR VEAFHINETTDEEISK VEAFHINETTDEEISKELEK SGSATQFDATDFATNEDLVELVK KGSATQFDATDFATNEDLVELVK DDDDVIAPLPNADGDIPASDGVFPK KDDDDVIAPLPNADGDIPASDGVFPK	1.66 1.96 2.58 2.33 2.83 3.19 2.27 2.26 2.27 3.78 3.06 5.59 4.35 4.55 3.99 3.43 4.05 4.85	1 1 2 2 2 2 2 2 2 2 2 2 2 3 2 2 2 3	73%
F46L95	NNT1 YLR285W	putative methyltransferase involved in rDNA silencing	Q05874	6	DLLAEK DLEFFELAK VYAYLTHEK GQALVVFSPHRPK LLEKDLEFFELAK PM*FDEDEETIEVR	1.82 2.86 2.87 2.84 3.63 3.36	1 2 2 3 3 2	21%
D48C11	NPT1 YOR209C	nicotinate phosphoribosyltransferase	P39683	2	FTEEEIEYLK SFRPPYSDAYVGR	2,81 3,92	2 3	6%





spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
D81Q41	PEP4 YPL154C	protease A	P07267	12	AYWEVK KAYWEVK GDITWLPVR FAFYLGDTSK YDHEASSYK FKGDITWLPVR FDGILGLGYDTISVDK DTENGGEATFGGIDESK YYSIYDLGNNAVGLAK KYYSIYDLGNNAVGLAK QDFAEATSEPGLTFAFGK FAFYLGDTSKDTENGGEATFGGIDESK	1.81 2.69 3.11 3.18 2.86 3.20 5.11 5.35 4.59 4.52 5.33 5.20	1 2 2 2 2 2 2 2 2 2 2 2	26%
E14Q41	PEP4 YPL154C	protease A	P07267	11	KAYWEVK GDITWLPVR FAFYLGDTSK YDHEASSYK FKGDITWLPVR FDGILGLGYDTISVDK DTENGGEATFGGIDESK YYSIYDLGNNAVGLAK KYYSIYDLGNNAVGLAK QDFAEATSEPGLTFAFGK FAFYLGDTSKDTENGGEATFGGIDESK	2.46 3.36 2.93 2.59 2.90 4.76 4.46 4.39 4.23 5.42 4.15	2 2 2 2 2 2 2 2 2 2 2	26%
D65O10	PIL1 YGR086C	regulator of Pkh1p activity	P53252	7	IALIAGYGK SMELTANER DIEGVSQPSR SAAGAFGPESLR IEVLEQELVR AEAESLVAEAQLSNITR APTASQLQNPPPPSTTK	2.24 2.90 2.59 3.09 3.75 4.99 4.66	2 2 2 2 2 2 2	25%
A76J92	PIM1 YBL022C	serine protease	P36775	7	TYIGALPGR LEDIVVER TSDDIEALK IAEQYLVPSAK DYVGPPVYTTDR LSTLETSM*SEFGVIR SIDPTVAM*TGELTLTGK	2.49 3.24 2.72 3.28 2.41 3.46 2.00	2 2 2 2 2 2 2	8%
G17P93	POL30 YBR088C	polymerase 30	P15873	9	YLLDIK FEEASLFK FEEASLFKR LM* <sup>2</sup> DIDADFLK SGFLQFFLAPK EDGIIAQAVDDSR LSSEAPALFQFDLK LEM* <sup>2</sup> DQPVDLTFGAK DLSQLSDSINIM*ITK	2.42 2.74 2.02 3.38 3.92 4.32 4.27 4.38 4.60	1 2 2 2 2 2 2 2 2	36%
B93I62	PRD1 YCL057W	proteinase yscD (saccharolysin)	P25375	16	VWQDVQSK ELQVLQDMK ISVNSINFSK YPDIFPVMK HVNGALFTLR HDIFLQFAR GGLYDINDNLK IPESLINSLIK QIAVWNMDDPK NELINLSSHYYK QDISLISNGGTLK VPENEAILLDTLK YLLENFNVDLEK DYIHSGLELDEGNR LNQGADPNYYIWDHR KLNQGADPNYYIWDHR	2.04 2.14 2.72 2.58 2.11 2.47 3.32 2.16 2.05 2.42 2.78 3.31 3.40 3.39 2.97 2.72	2 2 2 2 2 2 2 2 2 2 2 2 2 3 2 3	24%
H13G69	PRE1 YER012W	beta-4 subunit of 20S proteasome	P22141	4	VQDSVILASSK RPYQVNVLIGGYDK NKPELYQIDYLGTK EDYELSPQAVSSFVR	3.41 4.51 3.41 3.49	2 2 2 2	27%
G96D53	PRE2 YPR103W	beta-5 subunit of 20S proteasome	P30656	4	FQGGIIVAVDSR VKEEEGSFNNVIG WDLSDVEDALYLGK EGPTIYYVDSGTR	3.36 2.22 4.28 2.23	2 1 2 2	18%

spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
H16I28	PRE3 YJL001W	beta-1 subunit of 20S proteasome	P38624	4	TTTGAYIANR LIFYPDEYEQL GEVYTIPLGGSVHK DNLTAGIIVAGYDDK	2.70 2.83 2.09 4.98	2 1 2 2	23%
G57E12	PRE4 YFR050C	beta-7 subunit of 20S proteasome	P30657	3	GYGTQKI NFSLAIDKNTGLTFK NFSLAIDKNTGLTFKK	1.70 3.77 4.12	1 2 2	9%
G83B52	PRE5 YMR314W	alpha-6 subunit of 20S proteasome	P40302	6	SNTHAVLVALK NADELSSYQK LFQVEYALEAIK DTPFTIYDGEAVAK NNYDGDVTVFSPTGR DESLTVDNLSIAIVGK	3.25 1.84 4.04 2.76 3.34 2.52	2 1 2 2 2 1	33%
G83B52	PRE5 YMR314W	alpha-6 subunit of 20S proteasome		5	TLDTFIK QGSVTVGLR IDGNPDELIK AGVEAISQLR SNTHAVLVALK	1.77 2.53 2.59 4.12 3.53	1 2 2 2 2	21%
F94A38	PRE6 YOL038W	alpha-4 subunit of 20S proteasome	P40303	3	SLLEVVQTGAK LTLEDPTVVEYLTR IDSHVVLFSGLNADSR	3.60 4.10 4.00	2 2 2	17%
G53D19	PRE7 YBL041W	beta-6 subunit of 20S proteasome	P23724	4	EFYELK DSFTSATER NITDYSINSR HIQVGDGLELIVTK	1.75 2.42 2.42 3.40	1 2 2 1	17%
B36H79	PRT1 YOR361C	translation initiation factor eIF3 subunit	P06103	17	FYAPETK DLILHQR KALTSLFSK PASILSNAER IFNIAGNLVK DFSFAPEGVK YVTAWSSSLK DQFVLQDDVK FVVVGALVGNM*R MVGDSLIVHDATK TFANTVSWSPAGR NINDNNDVSASLK YNSDDFDTEFR VRDQFVLQDDVK VVMMEFPIDEATGK DSVFEEFGWEPHGNR SDLQFYDMDYPGEK	1.68 2.05 2.50 2.63 3.26 2.35 2.00 2.53 2.07 3.34 3.42 2.84 2.50 2.61 3.42 3.37 3.78	1 2 2 2 2 2 2 2 2 2 2 2 2 3 2 2 2	24%
B36I35	PRT1 YOR361C	translation initiation factor eIF3 subunit	P06103	18	EDIAGFK SWLM*DDK NFM*PLEAK KALTSLFSK IFNIAGNLVK DFSFAPEGVK YVTAWSSSLK ENWSTNYVR DQFVLQDDVK M*VGDSLIVHDATK NINDNNDVSASLK VVM*EFPIDEATGK DSVFEEFGWEPHGNR SDLQFYDM*DYPGEK RSDLQFYDM*DYPGEK EWSAQFEEQDAM*EADTAM*R YLVTFSTEPPIVEEDNEFSPTK YNSDDFDTEFREPD*PTFVPSSSLK	1.90 1.77 2.16 2.81 3.05 2.57 2.58 2.43 2.32 2.87 3.96 3.59 3.36 3.49 2.75 4.03 2.23 4.71	1 1 2 2 2 2 2 2 2 3 2 2 2 2 2 2 2 3	28%
H25D85	PUP1 YOR157C	beta-2 subunit of 20S proteasome	P25043	1	STQGPIVADK	2.05	2	4%
H21L06	PUP3 YER094C	beta-3 subunit of 20S proteasome	P25451	2	LGSQSLGVSNKFEK FGPYFVGPVAGINSK	3.07 4.02	2 2	15%
C37E33	PUT2 YHR037W	delta-1-pyrroline-5-carboxylate dehydrogenase	P07275	2	AGGPNILSR IQSGVVEGK	2.92 2.17	2 2	3%

spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
E19D29	QCR2 YPR191W	ubiquinol cytochrome c reductase core protein 2	P07257	7	FFLGEENR DLSPAINYTK FNFQNTNTR DQDSAVVSSNIK GLGNPLLYDGVER FVDESLSTLPAGK FIGDSVAAIGIPVNK	2.24 2.16 2.96 3.47 4.07 3.51 4.17	2 2 2 2 2 2 2	22%
C71Q54	RAD23 YEL037C	nucleotide excision repair protein	P32628	6	AAFNNPDR IMEMGYQR TESASTPGFVVGTER VTEPPIAPESATTPGR VPLDLEPSNTILETK TKVTEPPIAPESATTPGR	2.24 2.98 2.88 3.31 3.67 3.42	2 2 2 2 2 3	16%
F37H97	RHR2 YIL053W	DL-glycerol-3-phosphatase	P41277	9	TYDAIAK LEGEIPEK WAVATSGTR YGEHSIEVPGAVK VVVFEDAPAGIAAGK RPEYFITANDVK NGLGFPINEQDPSK FAPDFADEEYVVK FAPDFADEEYVVKLEGEIPEK	2.27 2.57 2.43 3.44 4.21 3.68 3.13 3.39 3.47	2 2 2 2 2 3 2 2 2	37%
G60H56	RIB3 YDR487C	3,4-dihydroxy-2-butanone-4-phosphate synthase	Q99258	2	AADGGVLQR FVIVM*DDAGR	3.17 2.52	2 2	9%
H84C35	RIB4 YOL143C	6,7-dimethyl-8-ribityllumazine synthase	P50861	8	VIIDALVK PDQVYDGSK GLGKPDQVYDGSK PLDVVIPIGVLIK LGKPLDVVIPIGVLIK GSTM*HFEYISDSTTHALMNLQEK AGIDEAHSMHNHGEDWGAAAVEM*AVK MASLGVVEENNIITVPGSYELPWGK	2.66 2.22 3.31 3.34 3.36 4.80 5.08 3.98	2 1 2 2 2 3 3 2	67%
G88K88	RIB5 YBR256C	riboflavin synthase	P38145	9	DQEYFK HTQDNVIM*PLK QILLTLENQISK HTQDNVIM*PLKK IGDEVNIEVDLTGK DSTLNTM*ISNIIEEK VDPLSQGGAFYISM*IK SNVASWIQGTQVNLER FGGHVYQQGHVDTVANIVSR	1.97 3.12 2.93 2.81 4.17 3.90 4.10 4.94 3.80	1 2 2 3 2 2 2 2 3	46%
G77E50	RIP1 YEL024W	ubiquinol cytochrome c reductase iron-sulfur protein	P08067	4	TPNFDDVLK VEVNLAAIPLGK SYAYFM*VGAM*GLLSSAGAK TPNFDDVLKENNDADKGR	2.37 4.45 3.37 2.73	2 2 2 3	23%
B02I37	RIX7 YLL034C	putative ATPase that functions in rib. large subunit export	Q07844	13	ANFISIK IDGAIDFAK DTSLSESSSR NSLTSSLDNK IFQTYANIK SLFIELPNTEEK SGSVSESITETDDPK M*GLTEEM*KDAEEM*KQ IVAQLLTSM*DELTM*EK NYPEPLSGEQLSLLSIK GIFVIGATNRPDM*IDPAM*LR SGSVSESITETDDPKTEEVKK STPTTATDSSSEDNMEIDETANGDESSLK	2.05 2.27 2.64 2.95 2.94 2.63 3.15 2.08 4.88 3.87 2.74 2.71 4.04	2 2 2 2 2 2 2 2 2 3 3 3 2	21%
E18K94	RNR4 YGR180C	ribonucleotide reductase small subunit	P49723	6	WISNDDSLYAER NIPLFKEIANLPEVK YLIENFSAQLQNPEGK IITEAVEIEKEYYSNSLPVEK YYNAVNPFEFM*EDVATAGKTTFFEK IIEKIITEAVEIEKEYYSNSLPVEK	2.28 3.55 4.70 3.45 2.93 6.39	2 2 2 3 3 3	27%
D13F43	RPN6 YDL097C	proteasome subunit	Q12377	4	VVDQLFEK SLLDFNTALK IIGLDTQQVEGK LDDKPSLVDVHLLLESK	3.08 2.42 3.81 2.65	2 2 2 3	11%

spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
D06L18	RPT5 YOR117W	AAA component of 26S proteasome regulatory subunit	P33297	8	VDVLDPALLR STDEFNGAQLK HEDFVEGISEVQAR QTVFLPM*VGLVDPDK APTIIFIDELDAIGTK M*TTDDDDINWQELAR DSYLILDTLPEFDSR AM*EVDEKPTETYSVVGGLDK	3.50 3.06 4.07 2.87 4.67 3.70 4.34 2.77	2 2 3 2 2 2 2 3	27%
C03O52	RRB1 YMR131C	protein involved in ribosome assembly	Q04225	6	SIEDIQWSR SIEVNEEQDR KQEEAETLVQK ASNTDVNVISWSDK NYPQSILLTTATQSSR TESHSVPAIPASEEQDAPK	3.24 3.03 3.56 4.10 3.91 2.77	2 2 2 2 2 3	16%
B58I70	SEC23 YPR181C	involved in endoplasmic reticulum to Golgi transport	P15303	15	DEEGLYK FYNQIAQR M*AFNGNM*AVK LEAAELLVDR AETDDGADVIR FIDTEAGGSQAR FTWNVFPSTR LNPSDNYQDM*AR AGYQDDPQYADFK YADYNKDDPQSFR PTGPGGAASHLPNAM*NK KAGYQDDPQYADFK EYQLEALTEM*LTGQK KTDANNISEISEIGIGATSTWK LNQLLENLSPDQWSVPAGHRPLR	1.90 3.34 2.11 4.01 3.31 4.09 2.67 2.82 3.67 3.29 3.30 4.13 3.33 3.36 3.16	1 2 2 2 2 2 2 2 2 3 3 3 2 2 3	24%
D29I97	SER3 YER081W	3-phosphoglycerate dehydrogenase	P40054	4	QVSTLDELLNK SSLPEEELIEK GTVVDIPSLIQAVK SDFVTLHVPATPETEK	2.14 2.37 2.62 3.51	2 2 2 3	11%
D15G49	SER33 YIL074C	3-phosphoglycerate dehydrogenase	P40510	12	M*LSAPQFAAM*K DQQYQVEFHK QVSTLDELLNK SIELHTGTWVK GIAVFNPFNSNR GTVVDIPSLIQAVK TVNDILSDHNIEK IAGAALDVYPHEPAK SDFVTLHVPATPETEK ALKPFSTGDM*NILLLENVNATAIK AM*NFGSGSPGAVSTSPTQSFM*NTLPR QFSDSHGEIAYLM*ADISSVNQSEIK	2.60 3.13 2.75 2.95 3.91 3.15 2.92 3.74 3.76 4.41 3.17 4.65	2 2 2 2 2 2 2 2 2 3 2 3	40%
F79Q72	SKP1 YDR328C	component of Cbf3 kinetochore complex	P52286	7	VVAEMIR RENEWAEDR VTSNVVLVSGEGER DSNFPDEDDDDSR DSNFPDEDDDDSRK DNNNGDDDDDEDDDEIVMPVNVNR SKDNNNGDDDDDEDDDEIVMPVNVNR	2.13 2.89 3.81 2.47 2.95 2.05 3.83	2 2 2 2 2 2 3	36%
E72M67	SNF7 YLR025W	involved in glucose derepression	P39929	13	ELQAEM*GL TIEQLLSK EHINLLSK VSLPSVPSNK KTIEQLLSK LREHINLLSK TQITNQENEAR IVNNNVNAAPISENK DGEEDDEDEDEKALR TIHSGLDIDKVDETM*DEIR IVNNNVNAAPISENKVSLPSVPSNK QSENSVKDGEEDDEDEKALR VEGTM*ESM*EQQLFSIESANLNLETM*R	1.85 2.61 2.01 2.70 2.53 3.21 3.48 4.23 2.60 3.75 2.74 4.21 3.50	1 2 2 2 2 3 2 2 2 2 3 3 2	55%

spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
E73J02	SNZ2/SNZ3 YNL333W	putative pyridoxine (vitamin B6) biosynthetic enzyme	P53824	9	DLGEALR INEGAAM*IR IKAEIQQYK RINEGAAM*IR ENLKTESDFAAK AEIQQYKENLK TKGEAGTGDVSEAVK IKAEIQQYKENLK GGVIM*DVVTPEQAIIAER	2.19 2.71 2.27 2.72 2.52 2.97 3.77 3.31 4.10	2 2 2 3 2 2 2 2 2	24%
C04H18	SRV2 YNL138W	adenylate cyclase-associated protein	P17555	16	SAVFEHAG DESIFIGK RLEEATAR SDGGNIYLSK FLASFDNLK DAAQFWTNR KFLASFDNLK YTM*QGYNLVK GGFQSQLTFLR ESDPNAVEVVK DGMDFADAM*AQSTK KDGM*DFADAM*AQSTK FGIQVNHSLPQISIDK LEDVTIQEGYIQNK KPDYSSQTFADSLRPINENIIK NNKPSDSGADANTTNEPSAENAPEVEQDPK	1.56 2.30 3.60 3.29 2.50 3.46 2.56 3.00 3.79 3.09 4.07 2.48 3.60 4.91 4.01 2.37	1 2 2 2 2 2 3 2 2 2 2 2 3 2 3 2	34%
E52B41	TDH3 YGR192C	glyceraldehyde-3-phosphate dehydrogenase 3	P00359	8	VLPELQ GK VVDLVEHVAK YAGEVSHDDK VVDLVEHVAKA TASGNIIPSSTGAAK VPTVDVSVVDLTVK LVSWYDNEYGYSTR YAGEVSHDDKHIIVDGK	1.52 3.21 2.65 3.43 2.85 3.98 4.00 4.39	1 2 2 2 2 2 2 3	24%
C44E91	THI20 YOL055C	hydroxymethylpyrimidine phosphate kinase	Q08224	21	YFNDVSR DPDYFQK LKEVFGVK ELVIVGGVR DIVSLITEK LLQLGENRPK VNGLQDIFQIAK EVVFQTLESNLK GGHIPWNDEKEK KVNGLQDIFQIAK YITDVLFLGAEQK EVFGVKDPDYFQK TGM*LTA AAIEVLHEK LVVDPVLVATSGSSLAGK EKYITDVLFLGAEQK IPGGNFYEYLINHPK LKEVFGVKDPDYFQK VKPHWDSYINHEFVK DNGPINHVYAVEIPLEK SAADKIPGGNFYEYLINHPK ETVKDNGPINHVYAVEIPLEK	2.30 2.11 2.55 2.44 2.69 2.54 3.41 3.92 2.72 4.09 4.13 3.56 3.96 3.44 2.38 3.80 3.41 2.53 4.55 5.07 3.04	2 2 2 2 2 2 2 2 2 3 2 2 2 3 2 2 2 2 2 3 3 3	34%

spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
C43H14	THI22 YPR121W	hydroxymethylpyrimidine phosphate kinase	Q06490	20	DPDYLQK YLIDISR LREEFGVK DVVSLIEK RVADGTLER LQDVLEIAK SPTLEDLEK LLQLGENRPK HITDVLVLGAEQK EEFGVKDPDYLQK M*VSQLDANLQDM*K TGM*LTVDAIEVLHEK IPGGSFFNYLINHPK EKHITDVLVLGAEQK VGPINHVYAVEIPLEK LREEFGVKDPDYLQK VKPHWDAYVNHEFVK CYAMTC#VTTLTAQTPVK KPIEGSLDKIPGGSFFNYLINHPK LM*NHILETYPPDQLDSLVTIFAR	2.40 2.03 2.51 3.19 2.36 2.43 2.21 2.61 4.46 4.41 5.30 4.47 3.66 2.48 4.67 4.43 2.86 2.02 2.62 4.54	2 3 3	36%
E72E95	THI4 YGR144W	thiamine biosynthesis	P32318	10	VLQLPNVK EDWSDFK YFKDLDK KEDWSDFK RIVDIDQNQK HAALFISTVLSK MGPTFGAMALSGVHAAEQILK PAHLFLQLEIPIYEDEGDYVVVK DLDKFAVSDVIVGAGSSGLSAAAYVIAK KPAHLFLQLEIPIYEDEGDYVVVK	2.26 1.97 2.50 2.04 2.92 3.51 4.28 4.94 2.94 5.37	2 1 2 2 3 2 2 3 3 3	35%
E72F68	THI4 YGR144W	thiamine biosynthesis	P32318	2	HAALFISTVLSK M*GPTFGAM*ALSGVHAAEQILK	4.37 2.62	2 3	10%
E72F81	THI4 YGR144W	thiamine biosynthesis	P32318	4	IVDIDQNQK RIVDIDQNQK M*GPTFGAM*ALSGVHAAEQILK M*GPTFGAM*ALSGVHAAEQILKHFAA	2.56 2.98 3.85 2.54	2 2 3 3	11%
C35F69	THI6 YPL214C	thiamine-phosphate pyrophosphorylase/hydroxyethylthiazole kinase	P41835	11	TNIDTLVR NGVTLVQIR YNVPLIINDR KYNVPLIINDR LFDVAVGAVLLYK TVGIGGLHPDNIQR PITFDPVGYSATETR ILGWSVGKPEVETLAK WGPD*VDYIGVGTLPFTSTK IDVAM*AIDADGVHVGQDDM*PIPM*VR AAINAYNEVNRPIITFDPVGYSATETR	2.44 2.68 2.89 2.65 2.71 3.42 2.49 2.65 2.09 4.96 6.65	2 2 2 2 2 2 2 2 2 3 3	26%
E17I90	THR1 YHR025W	homoserine kinase	P17423	8	TALYVLR SDANLITR YQWNPAIK DLTPQEVER VHVSNIPLGR ESEGYSTVPLR LLEPAYDGASVEQQ AYPTQDLVFNLR	1.73 3.17 2.66 2.08 3.37 2.87 2.56 4.07	1 2 2 2 2 2 1 2	23%
H56M98	TIF11 YMR260C	translation initiation factor eIF1A	P38912	5	YNLDEAR NQGELPENAK EEGQEYAQITK VWM*GQGDIIIVLSLR ELIYKEEGQEYAQITK	2.31 2.48 2.29 4.99 4.81	2 2 2 2 2	26%
F16D03	TIF35 YDR429C	translation initiation factor eIF3, p33 subunit	Q04067	5	LGEEVELR GYMNLILR GSPAGPSAVTAR AGQVGGAGSIPGQYVPPSR TILSELVALEDPATNEGGVEAASEEK	2.63 3.08 2.14 3.21 3.56	2 2 2 2 2	27%
G40O65	TIF6 YPR016C	translation initiation factor eIF6	Q12522	7	NSLPDSVK DTLIETYS LQDAQPESISGNLR TQFENSNEIGVFSK ETEELISDVLGVEVFR GLLVPTQTTDQELQHLR RGLLVPTQTTDQELQHLR	1.64 1.82 4.14 4.58 4.04 3.28 4.46	1 1 2 2 2 2 3	32%

spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
B91I73	TOM70 YNL121C	protein-mitochondrial targeting	P07213	2	LAISLEHTGIFK NPTVENFIEATNLLK	2.12 2.40	2 2	5%
B62I80	TPA1 YER049W	unknown	P40032	17	YLYIDGK TFQDGLKK DFFGYVTK IISDASGNSR DESVLEFVK NILSFHEVK QISLEEDKIK EIETEIHFVK FRPGM*DFTLATK LVPQFNQIAFFK ISFILYLPDPDRK LFPSILPNVPHSDPSAK ENNFDAELALIDLAVFHK LSEAEFTYLSQYISPEHLSSK ADDSGDSVLINDPPAWNTFNLVLR EIEDSQPYNWGTIHELVDLLR NFQTEADILEALNNNDLPNFQFTK	2.03 2.49 2.23 3.28 2.69 2.64 2.38 2.66 3.53 2.27 3.06 3.18 2.53 3.98 3.46 3.12 4.64	2 2 2 2 2 2 2 2 3 2 3 2 3 2 2 2 2	36%
G59G74	TPI1 YDR050C	triose-phosphate isomerase	P00942	6	TLDVVER WVILGHSER QLNAVLEEVK ASGAFGTGENSVQIK ILYGGGANGSNAVTFK SYFHEDDKFIADK	2.37 2.91 2.07 4.21 3.95 2.55	2 2 2 2 2 3	28%
A03G28	URA2 YJL130C	multifunctional protein of pyrimidine biosynthesis pathway	P07259	8	TTAVNVIR FLDSNEVAIR IVNVNPLVSSVK SISGPVITDVASLK LAVDYSVPLVTNVK ELTSM*DEAESFAEK VLGTPIDTIITTEDR PSYVLSGAAM*NTVYSK	2.02 2.74 2.24 3.02 2.06 2.21 2.89 3.07	2 2 2 2 2 2 2 2	5%
E11D07	URA4 YLR420W	dihydroorotase	P20051	5	EQVIPQVISDGGK TTFLM*SFYLSK DLTPDLIHEAAQQHAIR PYFFFGSDSAPHPVQNK IRDGGVSIAYIM*PNLQPPITLDR	2.11 3.60 3.47 4.47 2.59	2 2 3 3 3	22%
B17J24	UTP13 YLR222C	component of the 80S U3 snoRNA complex	Q05946	9	FYGQLNSK DNTAIVWR LSEIPGM*VK IWSLDTFSVM*K ISNEDEQEITALK DDIINLWDFNMK GYPEFLLTASNDLTIK LQVEQEQLQNYM*SK VDNLVEQSYILDYALVEM*DK	2.45 2.69 2.48 3.55 4.26 4.18 4.44 4.67 5.47	2 2 2 2 2 2 2 2 3	14%
C70L17	VMA2 YBR127C	vacuolar H-ATPase regulatory subunit	P16140	21	LSLEFLEK ILDEFYDR IPVSEDMLGR TTVEFTGESLR AVEQGFNVKPR TFITQGAYEDR QDFEENGSLER DHGDVSNQLYAK AVVGEEALSIEDK KTTVEFTGESLR KDHGDVSNQLYAK DDADEDEEDPDTR GIYPPINVLPSLSR TVFESLDQAWSLLR YNEIVNLTLPDGTVR TSLFLNLANPTIER LALTTAEYLAYQTER ARDDADEDEEDPDTR HVLTLTDMSSYADALR LNYNTVSGVNGPLVILEK GYPGYM*YTDLSTIYER	2.36 2.07 2.89 3.11 2.47 3.01 2.71 3.37 3.95 2.85 3.80 2.20 2.17 4.45 4.53 3.71 5.05 3.51 4.89 4.47 2.80	2 2 2 2 2 2 2 2 2 2 3 2 2 2 2 2 2 3 2 2 2	46%
E63P35	VMA6 YLR447C	vacuolar H-ATPase subunit	P32366	1	AALANVYEYR	3.43	2	3%
F36F65	VMA8 YEL051W	vacuolar H-ATPase catalytic subunit	P32610	2	GANQGYSLLK VNAIEHVIIIPR	2.66 3.04	2 2	8%



spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
G33F18	XPT1 YJR133W	xanthine phosphoribosyl transferase	P47165	4	YIAAQTVPDK AGLPDSMMNSGR VLIVDEVDDTR KVLIVDEVDDTR	3.52 2.39 4.48 3.15	2 2 2 2	17%
G08P52	YAR1 YPL239W	involved in resistance to environmental stress and 40S ribosome biogenesis	P46683	4	AFVNEVNK YILETVSR EATEALREETEK KYDVEPEDDEEDTQTEGK	2.34 2.42 3.14 4.56	2 2 2 3	23%
F90D92	YBL036C YBL036C	unknown	P38197	4	ILLLVVSK DFATLVEWK IGTDIFGARPPK TQLIAQYESVR	2.00 3.10 2.92 3.82	2 2 2 2	16%
E69F13	YDL124W YDL124W	NAD(P)H-dependent reductase	Q07551	6	SEAQILR IPAIHIGTGTR NIGVSNFAVEDLQR M*SDSPADGLDLALKK LPGIIHIDAAEIYR NAIFLTDKYSPQIK	2.45 2.96 4.73 3.60 3.21 2.71	2 2 2 3 3 3	25%
E37E91	YGR043C YGR043C	putative transaldolase	P53228	6	FIDAAVEYGR ILVEFGTQILK IASTWEGIQAAR YVLNEDQMATEK DYTAETDPGVLSVK YEPQDSTTNPSLILAASK	3.80 2.19 4.42 3.80 4.26 4.20	2 2 2 2 2 2	23%
B56D37	YHR020W YHR020W	putative prolyl-tRNA synthetase	P38708	22	FSQYELK PPAESAVAVK LNQWNSVVR VVDFSQEVSK FLNMFEDSQK YVVSFDELEAR AGSSELEPIAIR AGTAAAAAAAALEDAK KYVVSFDELEAR VIGVM*VM*IHSDNK PTSETVM*YPYYAK VSQFQSVVIPVGITK AFGDYNDNYTPGWK IPEILEEM*QGDLFK ALDFPGWYQQILTK GIQGATSHHLGQNFSK EFLWQEGHTAHLTAK M*FNLSVENPLGSDHPK AIGVQNAYFPM*FVSSR KDDGEEFEEDDKAPSM*GAK SATPVPIVVVALQSTTTPSALIANATSSK AGSSELEPIAIRPTSETVM*YPYYAK	2,15 1,57 2,90 3,63 3,51 3,23 2,10 2,89 3,60 2,89 2,53 3,95 3,29 3,09 2,52 3,12 3,03 4,30 3,84 4,32 3,94 4,13	2 1 2 2 2 2 2 3 3 2 2 2 2 2 2 2 2 2 3 2 3	41%
B57D04	YHR020W YHR020W	putative prolyl-tRNA synthetase	P38708	26	NQVVVVR FSQYELK PPAESAVAVK QAFQSESAR LNQWNSVVR VVDFSQEVSK FLNMFEDSQK YVVSFDELEAR AGTAAAAAAAALEDAK VIGVM*VM*IHSDNK IFAYQNSWGLSTR VSQFQSVVIPVGITK AFGDYNDNYTPGWK IPEILEEMQGDLFK VIVNEWSGFVPALNK ALDFPGWYQQILTK GIQGATSHHLGQNFSK EFLWQEGHTAHLTAK AIGVQNAYFPMFVSSR M*FNLSVENPLGSDHPK VIVNEWSGFVPALNKK VVDFSQEVSKETATEGK EKDHVEGFAPEVAWVTR KDDGEEFEEDDKAPSMGAK LIGITVDKALDFPGWYQQILTK AGSSELEPIAIRPTSETVMYPYYAK	2.25 2.32 1.53 2.05 3.22 3.07 3.15 3.09 3.23 2.25 4.41 3.66 3.25 4.05 3.42 4.02 3.25 2.45 3.95 3.87 3.28 3.06 4.14 4.24 2.56 4.16	2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3	48%

spot #	gene ORF	protein	UniProt	nb pept	peptide sequence	score XC	charge z	coverage
G45H64	YKL033W-A YKL033W-A	similarity to holacid-halidohydrolase	Q86ZR7	1	LPITLDEYDER	2.74	2	5%
F36G04	YKR043C YKR043C	similarity to phosphoglycerate mutase	P36136	8	EIIELR PLSDEQR ERPWNIWR EWEYGDYEGM*LTR QTVDLVLKPLSDEQR NNQFLNPDNITYIFTSPR SGQYTGLTDLPLTPYGEGQM*LR VVVDDDLREWEYGDYEGM*LTR	1.51 1.64 2.44 2.63 2.34 4.17 2.54 5.68	1 1 2 2 2 3 2 3	33%
C49N01	ZPR1 YGR211W	unknown	P53303	18	WVEFFAK SIDEALYK KIDDFIQK FTTLEGLLR KSIDEALYK WSHTQYVR QVYEELESR LLLTSIPYFR FVELDIEIPAK TDEQNVQVGIIR IFTQTSDSMDEATK EQNEDLGLSDIK IFTQTSDSM*DEATK TKEQNEDLGLSDIK LTGAQDAM*GHPVQEIESLCM*NCGK EDLFKPVGEAAAEEVEDESIAEQNK GQLTTVEGLLSEM*IDDLSQDQEM*RK VGSANPQFLSDATDIENFNNEVQTFR	2.14 2.90 2.62 3.03 2.41 2.41 2.65 2.42 2.80 4.36 2.64 4.19 3.63 3.99 4.06 2.40 3.42 5.39	2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 2 3 2	43%