

Supplementary Table 2. List of proteins identified on the yeast protein map^a

Spot			Gene		Protein					
Number	Apparent pI	Apparent M _r	Name ^{b)}	CBI	Name	Calculated pI	Calculated M _r	SWISS P.	Acetylation ^{c)}	Identification method ^{d)}
E44J62	4.97	37000	AAH1*	0.21	adenine deaminase	5.01	39635	P53909	0	Gi
B42M92	4.37	86400	ABP1*	0.30	actin binding protein	4.33	65575	P15891		MS
B60N10	4.33	79900	ABP1*	0.30	actin binding protein	4.33	65575	P15891		MS
C27C07	6.35	62200	ACH1	0.33	acetyl-CoA hydrolase	6.30	58580	P32316	0	MS, sq
C28C39	6.27	62000	ACH1	0.33	acetyl-CoA hydrolase	6.30	58580	P32316		
B38A18	6.86	87900	ACO1	0.58	aconitase	6.85	82774	P19414		Ga
B39A63	6.73	87500	ACO1	0.58	aconitase	6.85	82774	P19414		Ga
B41C54	6.24	86800	ACO2	0.25	aconitase	6.00	83592	P39533	0	MS, Gi, Ga
B41D03	6.13	86800	ACO2	0.25	aconitase	6.00	83592	P39533	0	Gi, Ga
B65C56	6.24	78300	ACS1	0.36	acetyl-CoA synthetase	6.14	79139	Q01574		MS
B65C95	6.15	78300	ACS1	0.36	acetyl-CoA synthetase	6.14	79139	Q01574		
B68C24	6.31	77300	ACS2	0.47	acetyl-CoA synthetase	6.20	75490	P52910	0	MS
D83I60	5.13	41600	ACT1	0.83	actin	5.19	41731	P02579		anti, int, aac, MS
E97G97	5.40	32800	ADE1	0.31	SAICAR synthetase	5.38	34513	P27616	A	aac
C87D90	6.00	51800	ADE13	0.42	adenylosuccinate lyase	5.97	54510	Q05911	0	aac, MS
C88D64	5.95	52000	ADE13*	0.42	adenylosuccinate lyase	5.97	54510	Q05911	0	MS
C16C94	6.15	64500	ADE16	0.19	AICAR transformylase/IMP synthetase	6.09	65281	P54113	0	MS
C19D37	6.06	63900	ADE17	0.45	AICAR transformylase/IMP cyclohydrolase	6.09	65262	P38009	0	aac
C20C80	6.18	63700	ADE17	0.45	AICAR transformylase/IMP cyclohydrolase	6.09	65262	P38009		aac, MS
C33A23	6.84	61000	ADE2	0.22	phosphoribosylaminoimidazole carboxylase	6.98	62338	P21264		Ga
C33A93	6.64	61000	ADE2	0.22	phosphoribosylaminoimidazole carboxylase	6.98	62338	P21264		Ga
A98B46	6.50	109700	ADE3	0.42	C1-tetrahydrofolate synthase (trifunctional enzyme)	6.37	102072	P07245	0	aac
A99B81	6.41	108700	ADE3	0.42	C1-tetrahydrofolate synthase (trifunctional enzyme)	6.37	102072	P07245	0	aac
C47E48	5.83	58300	ADE4	0.28	amidophosphoribosyltransferase	5.84	56718	P04046	0	Ga
C47E95	5.75	58300	ADE4	0.28	amidophosphoribosyltransferase	5.84	56718	P04046		Ga
B54K19	4.87	82000	ADE5,7	0.28	GARSase + AIRSase	4.84	86067	P07244	0	Ga, sq, aac
B53K43	4.83	82300	ADE5,7*	0.39	GARSase + AIRSase	4.84	86067	P04046	0	MS
A62J96	4.91	146500	ADE6	0.39	5'-phosphoribosylformyl glycinamide synthetase	4.90	148814	P38972	A	MS
A60K23	4.86	148600	ADE6*	0.39	5'-phosphoribosylformyl glycinamide synthetase	4.90	148814	P38972	A	MS
D97D29	6.07	40400	ADH1	0.91	alcohol dehydrogenase I	6.06	36760	P00330	A	anti, co, Gi
D99B91	6.39	40300	ADH1	0.91	alcohol dehydrogenase I	6.21	36849	P00330	0	anti, co, aac, Gi
D99C53	6.24	40300	ADH1	0.91	alcohol dehydrogenase I	6.06	36760	P00330	A	anti, co, aac, MS, Gi
E09C51	6.25	39500	ADH1*	0.91	alcohol dehydrogenase I	6.06	36760	P00330	A	MS
D86B82	6.41	41300	ADH2	0.71	alcohol dehydrogenase II	6.27	36600	P00331	0	anti
D86C41	6.27	41300	ADH2	0.71	alcohol dehydrogenase II	6.12	36642	P00331	A	anti
D86D07	6.12	41300	ADH2	0.71	alcohol dehydrogenase II	6.12	36642	P00331	A	anti
E18E85	5.76	38800	ADH4	0.66	alcohol dehydrogenase IV	5.70	40881	P10127	0	ace
E18F56	5.64	38800	ADH4	0.66	alcohol dehydrogenase IV	5.58	40923	P10127	A	MS
G53F81	5.59	24500	ADK1	0.66	adenylate kinase	5.68	24078	P07170	A	aac
E67K97	4.74	34700	ADO1	0.52	adenosine kinase	4.74	36240	P47143	0	aac, MS
E68L49	4.64	34600	ADO1	0.52	adenosine kinase	4.66	36282	P47143	A	aac, MS
E04L90	4.57	39900	AHP1	0.68	alkyl hydroperoxide reductase	4.61	19025	P38013	0	MS
H71L94	4.56	19800	AHP1	0.68	alkyl hydroperoxide reductase	4.61	19025	P38013	A	aac, MS
H72L07	4.72	19800	AHP1	0.68	alkyl hydroperoxide reductase	4.76	18983	P38013	0	ace

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Number	Apparent pI	Apparent M _r	Name ^{b)}	CBI	Name	Calculated pI	Calculated M _r	SWISS P.	Acetylation ^{c)}	Identification method ^{d)}
A98I03	5.22	109700	ALA1	0.47	alanyl-tRNA synthetase	5.15	107276	P40825	0	aac, MS
A98I27	5.19	109700	ALA1*	0.47	alanyl-tRNA synthetase	5.15	107276	P40825	0	MS
C96G63	5.45	50700	ALD3	0.16	aldehyde dehydrogenase	5.36	55384	P54114		aac, Gi
C96H01	5.39	50700	ALD3	0.16	aldehyde dehydrogenase	5.36	55384	P54114		aac, Gi
C54E97	5.74	57100	ALD4	0.42	aldehyde dehydrogenase	5.66	53974	P46367		MS
C38I52	5.14	60000	ALD6	0.66	aldehyde dehydrogenase	5.09	54413	P54115	0	aac
C39H93	5.24	59800	ALD6	0.66	aldehyde dehydrogenase	5.09	54413	P54115	0	aac, MS
E24L63	4.62	38400	APA1	0.43	ATP adenyltransferase 1	4.63	36402	P16550	A	MS
G99L11	4.71	22500	APT1*	0.39	adenine phosphoribosyltransferase	4.81	20629	P49435		Ga
G99L60	4.62	22500	APT1*	0.39	adenine phosphoribosyltransferase	4.69	20587	P49435		Ga, MS
E40G98	5.39	37300	ARA1	0.27	D-arabinose dehydrogenase	5.43	38776	P38115	A	MS
B69C66	6.21	77000	ARB1	0.49	ATPase of the ATP-binding cassette (ABC) family	6.05	68376	P40024	0	MS
F15L68	4.61	31800	ARD1*	0.15	N-acetyltransferase subunit	4.51	27603	P07347		MS, Gi
D10H20	5.36	48900	ARG1	0.58	argininosuccinate synthase	5.33	46808	P22768	0	ace, MS
D10I00	5.23	48900	ARG1	0.58	argininosuccinate synthase	5.21	46850	P22768	A	aac, MS
D11I73	5.11	48800	ARG1*	0.58	argininosuccinate synthase	5.05	46850	P22768	A	MS
E32F21	5.70	37800	ARG3	0.18	ornithine carbamoyltransferase	5.68	37755	P05150	A	Ga, MS
D14I42	5.16	48500	ARG4	0.32	argininosuccinate lyase	5.23	51899	P04076	A	MS, Gi
D06D62	6.00	49400	ARG5*	0.22	N-acetylglutamate kinase	6.28	52364	Q01217	0	Gi
E44A84	6.67	37000	ARG6*	0.22	N-acetylglutamylphosphate reductase	6.22	36320	Q01217		MS
F65O84	4.24	28900	ARG7*	0.16	ornithine acetyltransferase	4.21	24977	Q04728		Gi, MS
D63C06	6.35	43300	ARG8	0.22	acetylornithine aminotransferase	6.34	45080	P18544		MS
A33E02	5.92	176200	ARO1	0.25	arom pentafunctional enzyme	5.83	174753	P08566	0	MS
C02C93	6.15	67800	ARO10	0.11	putative indole-3-pyruvate decarboxylase	6.07	71383	Q06408	0	MS
D70B50	6.49	42700	ARO4	0.69	2-Dehydro-3-deoxyphosphoheptonate aldolase	6.50	39617	P32449	0	ace
D70C44	6.26	42700	ARO4	0.69	2-Dehydro-3-deoxyphosphoheptonate aldolase	6.27	39659	P32449	A	aac, MS
C72G17	5.53	54200	ARO8	0.32	aromatic amino acid aminotransferase I	5.57	56045	P53090	0	ace
C73G96	5.40	54000	ARO8	0.32	aromatic amino acid aminotransferase I	5.46	56088	P53090	A	MS
C50H95	5.24	57800	ARO9	0.16	aromatic amino acid aminotransferase II	5.11	58526	P38840	0	MS
D95H86	5.25	40600	ARP2	0.27	actin-related protein	5.26	44115	P32381		Ga, anti, int
C90H49	5.31	51500	ARP3*	0.26	actin-related protein	5.28	49452	P47117	A	MS
B14I59	5.13	93300	ARP5*	0.14	actin-related protein	5.07	87470	P53946	A	MS
F36G70	5.44	30500	ASC1	0.88	ribosomal protein of the 40S ribosomal subunit	5.53	34715	P38011	A	MS, int, aac
C08F67	5.62	66400	ASN1	0.49	asparagine synthetase 1	5.65	64469	P49089	0	MS
C17H17	5.36	64300	ASN2	0.40	asparagine synthetase 2	5.41	64592	P49090	0	MS
C17H53	5.30	64300	ASN2*	0.40	asparagine synthetase 2	5.41	64592	P49090	0	MS
D24K11	4.88	47300	ATP2	0.57	F1-beta ATP synthase	4.89	51125	P00830	0	aac, MS, sq
E12D01	6.13	39300	BDH1*	0.31	2,3-butanediol dehydrogenase	6.18	41538	P39714		MS
F48Q83	3.96	29900	BGL2*	0.60	endo-beta-1,3-glucanase of the cell wall	3.95	31743	P15703		MS
F40M92	4.37	30300	BMH1	0.45	signal transduction during pseudohyphal growth	4.54	30001	P29311	A	MS
F16M93	4.36	31700	BMH2	0.47	signal transduction during pseudohyphal growth	4.54	30971	P34730	A	aac
H04G92	5.40	22300	BNA1	0.14	3-hydroxyanthranilate 3,4-dioxygenase	5.38	20234	P47096	0	MS
F23P39	4.18	31300	CAP2*	0.15	actin-capping protein 2	4.17	32539	P13517		MS
B76J56	4.98	74900	CAPSID		capsid protein of virus L-A	4.92	78225		A	MS
E28I64	5.13	38100	CAR1	0.34	arginase	5.23	35661	P00812	0	Ga
D65C04	6.36	43100	CAR2*	0.50	ornithine aminotransferase	6.38	45996	P07991	A	Gi

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F66K81	4.76	28900	CCP1	0.26	cytochrome-c peroxidase	4.78	33430	P00431	0	aac, MS
F97C06	6.35	27200	CCS1	0.18	superoxide dismutase 1 copper chaperone	5.95	27240	P40202	A	Ga
C32C90	6.16	61200	CCT1	0.31	component of Chaperonin-containing T-complex	6.04	60348	P12612	0	ace
C32D60	6.01	61200	CCT1	0.31	component of Chaperonin-containing T-complex	5.90	60390	P12612	A	MS
C49F12	5.71	58000	CCT2	0.25	component of Chaperonin-containing T-complex	5.56	57113	P39076	A	MS
C59F37	5.67	56200	CCT3*	0.27	component of Chaperonin-containing T-complex	5.70	58814	P39077	0	MS
C38J05	5.06	60000	CCT5	0.24	component of Chaperonin-containing T-complex	5.05	61824	P40413	A	MS
C05G87	5.41	67100	CCT6	0.28	component of Chaperonin-containing T-complex	5.33	59833	P39079	A	MS
C67I48	5.15	54900	CCT7	0.19	component of Chaperonin-containing T-complex	5.22	59734	P42943	0	MS
C30G81	5.42	61600	CCT8	0.27	component of Chaperonin-containing T-complex	5.36	61530	P47079	0	ace
C31H34	5.34	61400	CCT8	0.27	component of Chaperonin-containing T-complex	5.27	61572	P47079	A	MS
C31H79	5.26	61400	CCT8	0.27	component of Chaperonin-containing T-complex	5.27	61572	P47079	A	ace
E42H59	5.30	37100	CDC10*	0.14	septin	5.35	37024	P25342	0	MS
C15L41	4.66	64800	CDC37	0.11	Hsp90 co-chaperone	4.69	58384	P06101	0	MS
B09L54	4.63	98400	CDC48	0.41	ATPase of the AAA family (microsomal)	4.56	91995	P25694	0	aac, MS
B09L69	4.61	98400	CDC48*	0.41	ATPase of the AAA family (microsomal)	4.56	91995	P25694	0	MS
A68G21	5.52	140400	CDC60	0.36	leucyl-tRNA synthetase	5.43	124050	P26637	A	MS
D35B27	6.55	46100	CIT1*	0.31	mitochondrial citrate synthase	6.52	49216	P00890	0	Gi, MS
D42D71	5.99	45400	CIT2	0.16	peroxisomal citrate synthase	5.91	51412	P08679	0	MS
D43E24	5.88	45300	CIT2	0.16	peroxisomal citrate synthase	5.91	51412	P08679		
E77R21	3.88	34100	CLC1*	0.20	clathrin light chain	3.97	26442	P17891		MS
J16K51	4.82	15800	COF1	0.67	cofilin	4.64	15811	Q03048	A	aac, int, MS
F52J01	5.07	29600	COQ5*	0.17	mitochondrial C-methyltransferase	5.05	31461	P49017	0	Gi
D40D07	6.12	45600	COR1	0.42	ubiquinol cytochrome-c reductase core protein 1	5.85	47408	P07256	0	aac, MS
D78A39	6.80	42000	CPA1*	0.28	carbamoylphosphate synthetase subunit	6.68	45272	P07258	A	Gi
D79B22	6.57	41900	CPA1*	0.28	carbamoylphosphate synthetase subunit	6.68	45272	P07258	A	Gi
A82J41	5.00	126100	CPA2	0.30	carbamoylphosphate synthetase subunit	4.96	123782	P03965	0	ace
A83J74	4.95	125000	CPA2	0.30	carbamoylphosphate synthetase subunit	4.93	123824	P03965	A	MS
A84J58	4.97	124000	CPA2	0.30	carbamoylphosphate synthetase subunit	4.93	123824	P03965	A	ace
J35B75	6.43	15500	CPR1*	0.77	cyclophilin	6.49	17301	P14832	A	MS
G67I94	5.08	23900	CPR5*	0.35	cyclophilin	5.05	22783	P35176	0	Gi
C07J99	4.90	66600	CPS1*	0.31	Gly-X carboxypeptidase yscS	4.91	60162	P27614		MS
C17D88	5.95	64300	CTT1	0.31	catalase T	6.16	64520	P06115		MS
E24E12	5.90	38400	CYS3	0.62	cystathionine gamma-lyase	5.94	42452	P31373	A	ace
E25D56	6.02	38300	CYS3	0.62	cystathionine gamma-lyase	6.05	42410	P31373	0	aac, MS
C73B70	6.44	54000	CYS4	0.44	cystathionine beta-synthase	6.23	55890	P32582	0	aac
C74C16	6.33	53900	CYS4	0.44	cystathionine beta-synthase	6.03	55932	P32582	A	ace
C38I91	5.08	60000	DAK1	0.27	dihydroxyacetone kinase	5.03	62074	P54838	0	ace
C40J40	5.00	59600	DAK1	0.27	dihydroxyacetone kinase	4.97	62116	P54838	A	MS
C37D91	5.95	60200	DAL7	0.23	malate synthase 2	6.02	62793	P21826		MS
C22G88	5.41	63200	DED81*	0.54	asparaginyl-tRNA synthetase	5.36	62117	P38707	A	MS
C30F74	5.60	61600	DLD1	0.27	mitochondrial D-lactate dehydrogenase	5.63	62169	P32891	0	MS
C84I38	5.17	52400	DLD2*	0.20	D-lactate dehydrogenase	5.07	54801	P46681	0	Gi
C89B41	6.52	51700	DLD3	0.24	D-lactate dehydrogenase	6.42	55224	P39976	0	aac, MS
C89B83	6.41	51700	DLD3*	0.24	D-lactate dehydrogenase	6.42	55224	P39976		MS
E64L60	4.62	34900	DPH5*	0.24	diphthamide methyltransferase	4.58	33847	P32469	0	Gi

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C11C80	6.18	65700	DPS1	0.50	aspartyl-tRNA synthetase	6.01	63425	P04802	A	MS
D92N04	4.34	40800	DSK2	0.23	involved in ubiquitin-dependent proteolysis	4.42	39256	P48510	A	MS
D56H87	5.25	44000	DYS1	0.52	deoxyhypusine synthase	5.22	42802	P38791	A	MS
A46I58	5.14	162900	ECM17	0.30	sulfite reductase	5.11	161217	P47169	0	MS
F48Q40	4.04	29900	EFB1	0.88	translation elongation factor EF-1beta	3.99	22626	P32471	A	aac, MS
B16D54	6.02	91300	EFT1	0.89	translation elongation factor EF-2	5.85	93288	P32324	0	aac, MS
I02C79	6.18	18800	EGD1	0.78	beta subunit of the NAC complex	6.09	17020	Q02642	0	aac
G12L43	4.65	26500	EGD2	0.72	alpha subunit of the NAC complex	4.49	18619	P38879	A	aac
C87G27	5.51	52000	EMI2*	0.21	similarity to Glk1p	5.72	55831	Q04409	A	Gi
C92F51	5.64	51300	EMI2*	0.21	similarity to Glk1p	5.72	55831	Q04409	A	Gi
D15C39	6.27	48300	ENO1	0.93	enolase 1	6.14	46670	P00924	0	anti, co, MS
D27E54	5.82	47000	ENO2	0.96	enolase 2	5.56	46782	P00925	0	aac
D29F95	5.57	46700	ENO2	0.96	enolase 2	5.56	46782	P00925	0	aac, MS
D30F26	5.69	46600	ENO2	0.96	enolase 2	5.56	46782	P00925	0	anti, aac, MS
D47H00	5.39	44800	ENO2 f		enolase 2 fragment			P00925	0	MS
D27H08	5.38	47000	ENO2*	0.96	enolase 2	5.56	46782	P00925		MS
D72G68	5.44	42500	ERG19	0.24	mevalonate pyrophosphate decarboxylase	5.37	44115	P32377	0	MS
D69H23	5.35	42800	ERG6	0.41	S-adenosyl-methionine delta-24-sterol-C-methyltransferase	5.29	43341	P25087	A	MS
A18I56	5.14	191600	FAS2*	0.55	fatty acid synthase subunit alpha	5.12	206946	P19097		MS
D97G47	5.48	40400	FBA1	0.94	fructose-bisphosphate aldolase	5.39	39489	P14540	0	Ga, aac
D98F80	5.59	40300	FBA1	0.94	fructose-bisphosphate aldolase	5.39	39489	P14540	0	Ga, aac, MS
E31G11	5.54	37900	FBP1	0.26	fructose-1,6-bisphosphatase	5.54	38130	P09201		MS
E31G44	5.48	37900	FBP1	0.26	fructose-1,6-bisphosphatase	5.54	38130	P09201		
E31H30	5.34	37900	FBP1*	0.26	fructose-1,6-bisphosphatase	5.54	38131	P09201		MS
C89E74	5.78	51700	FRDS1*	0.39	fumarate reductase	5.74	50754	P32614	A	Gi
B86G53	5.47	72000	FRS1	0.43	phenylalanyl-tRNA synthetase, alpha subunit	5.38	67232	P15624	0	MS
C54H80	5.26	57100	FRS2	0.45	phenylalanyl-tRNA synthetase, beta subunit	5.29	57408	P15625	A	aac
G15D72	5.98	26300	FSH1*	0.52	unknown	5.89	27339	P38777	0	MS
G65I02	5.23	24000	FUR1*	0.53	uracil phosphoribosyltransferase	5.19	24505	P18562	A	MS
B54H76	5.27	82000	GAG		major coat protein of virus L-A	5.39	75993			MS
B40E69	5.79	87200	GCN20	0.36	required for activation of Gcn2 protein kinase	5.72	84937	P43535	A	MS
E20G51	5.47	38700	GCS1*	0.12	GTPase-activating protein	5.52	39165	P35197		Gi
C93H96	5.24	51100	GDH1	0.74	NADP-glutamate dehydrogenase 1	5.26	49462	P07262	A	aac, MS, Gi
D38J36	5.01	45800	GDH3	0.19	NADP-glutamate dehydrogenase 2	5.14	49626	P39708		MS
D31G39	5.49	46500	GDI1*	0.25	GDP dissociation inhibitor	5.55	51206	P39958	0	MS
E32L89	4.57	37800	GET3*	0.40	ATPase involved in a general response to stress	4.60	39353	Q12154	0	MS
E79J18	5.04	33900	GLC7*	0.24	protein serine/threonine phosphatase PP1	5.08	35907	P32598	0	MS
C77F88	5.58	53400	GLK1	0.24	glucokinase	5.74	55245	P17709	0	ace, Gi
C78G12	5.54	53300	GLK1	0.24	glucokinase	5.64	55287	P17709	A	MS, Gi
C83F43	5.66	52500	GLK1	0.24	glucokinase	5.64	55287	P17709	A	MS, Gi
C79G62	5.45	53100	GLK1*	0.24	glucokinase	5.64	55287	P17709		Gi
D77E39	5.85	42100	GLN1	0.68	glutamine synthetase	5.88	41574	P32288	0	ace
D78F14	5.71	42000	GLN1	0.68	glutamine synthetase	5.75	41616	P32288	A	aac, MS
D78F87	5.58	42000	GLN1	0.68	glutamine synthetase	5.75	41616	P32288	A	ace
D86C09	6.35	41300	GLO1*	0.18	glyoxalase I	6.38	37077	P50107		MS, Gi
D71G34	5.50	42600	GLY1	0.52	threonine aldolase	5.70	42725	P37303	A	ace

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Number	Apparent pI	Apparent M _r	Name ^{b)}	CBI	Name	Calculated pI	Calculated M _r	SWISS P.	Acetylation ^{c)}	Identification method ^{d)}
D72F66	5.62	42500	GLY1	0.52	threonine aldolase	5.82	42683	P37303	0	MS
D31C33	6.29	46500	GND1	0.76	6-Phosphogluconate dehydrogenase	6.17	53411	P38720	0	ace
D31D06	6.12	46500	GND1	0.76	6-Phosphogluconate dehydrogenase	6.01	53453	P38720	A	aac, MS
D47174	5.11	44800	GPD1	0.62	glycerol-3-phosphate dehydrogenase	5.05	42737	Q00055	A	Ga
D49J40	5.00	44700	GPD1	0.62	glycerol-3-phosphate dehydrogenase	5.05	42737	Q00055	A	Ga
D49J98	4.91	44700	GPD1	0.62	glycerol-3-phosphate dehydrogenase	5.05	42737	Q00055	A	Ga
E42F84	5.59	37100	GRE2*	0.30	alpha-acetoxy ketone reductase	5.56	38080	Q12068		Gi
E48B19	6.57	36800	GRE3*	0.26	aldo/keto reductase with NADPH specificity	6.65	36987	P38715		MS
B73G05	5.55	75800	GRS1	0.50	glycyl-tRNA synthase	5.59	75278	P38088	0	ace
B74G45	5.48	75400	GRS1	0.50	glycyl-tRNA synthase	5.52	75320	P38088	A	aac
F79O88	4.23	28200	GRX3*	0.13	glutaredoxin	4.29	32481	Q03835		MS
G10D22	6.09	26600	GSP1	0.74	GTP-binding protein of the ras superfamily	6.10	24678	P32835	0	ace
G11E53	5.82	26500	GSP1	0.74	GTP-binding protein of the ras superfamily	5.78	24720	P32835	A	aac
G09D61	6.01	27500	GSP2*	0.28	GTP-binding protein of the ras superfamily	5.94	24901	P32836		Gi
G47D83	5.96	24800	GTT1*	0.29	glutathione transferase	6.18	26663	P40582	0	MS
C65D68	5.99	55300	GUA1	0.60	GMP synthetase	6.02	58350	P38625	0	Ga, sq, aac
C66E20	5.89	55100	GUA1	0.60	GMP synthetase	6.02	58350	P38625	0	Ga
H31C48	6.25	21300	GUK1*	0.42	guanylate kinase	5.86	20548	P15454	A	Ga
E17L50	4.64	38900	GVP36	0.36	golgi vesicle protein of unknown function	4.64	36580	P40531	A	aac, MS
H13I48	5.15	22000	HAM1*	0.19	protein controlling 6-N-hydroxylaminopurine sensitivity	5.08	22004	P47119	A	Gi
D05N16	4.32	49600	HAT2*	0.08	histone acetyltransferase subunit	4.46	45060	P39984	0	MS
E67K59	4.80	34700	HCR1	0.37	putative component of translation initiation factor eIF3	4.71	29474	Q05775	A	MS
E86F98	5.56	33500	HIS1	0.23	ATP phosphoribosyltransferase	5.74	32265	P00498	0	MS
G39D44	6.04	25200	HIS3	0.02	imidazoleglycerol-phosphate dehydratase	5.92	23789	P06633		Gi
B23J58	4.97	94300	HIS4	0.37	trifunctional enzyme of histidine biosynthesis	4.96	87720	P00815	0	Gi, aac
B24J35	5.01	93800	HIS4	0.37	trifunctional enzyme of histidine biosynthesis	4.96	87720	P00815	0	Gi, MS
D59C87	6.17	43700	HIS5*	0.26	histidinol-phosphate aminotransferase	5.99	46646	P07172	0	MS, Gi
C72I52	5.14	54200	HIS7*	0.17	glutamine amidotransferase	5.13	61067	P33734	0	MS
E25J06	5.06	38300	HMT1*	0.31	HnRNP methyltransferase 1	4.98	39697	P38074	A	Gi
J93C60	6.23	14500	HNT1*	0.31	adenosine monophosphoramidase	6.49	17679	Q04344		MS
E05B89	6.39	39800	HOM2	0.59	aspartate-semialdehyde dehydrogenase	6.27	39543	P13663	0	Ga, MS, Gi
E10C51	6.25	39400	HOM2*	0.59	aspartate-semialdehyde dehydrogenase	6.27	39543	P13663	0	MS, Gi
C66C98	6.14	55100	HOM3*	0.31	aspartate kinase	6.20	57978	P10869	0	MS
E44A28	6.83	37000	HOM6	0.61	homoserine dehydrogenase	7.67	38502	P31116		MS
F64E51	5.83	29000	HOR2	0.38	DL-glycerol-3-phosphatase	5.72	27682	P40106	0	aac, MS
G04I11	5.21	26900	HPT1*	0.36	hypoxanthine phosphoribosyltransferase	5.13	25101	Q04178	A	MS
B49M21	4.51	83700	HSC82	0.69	chaperonin	4.52	80740	P15108	0	Ga
B50M07	4.53	83400	HSC82	0.69	chaperonin	4.52	80740	P15108	0	Ga, sq, aac
B00H39	5.33	107600	HSP104	0.40	heat shock protein	5.06	102075	P31539		aac
G37J53	4.98	25300	HSP26	0.43	heat shock protein	5.08	23748	P15992		Ga, MS
C28K91	4.75	62000	HSP60	0.55	mitochondrial chaperonin	4.73	58266	P19882	0	Ga, aac, MS
C28L13	4.71	62000	HSP60	0.55	mitochondrial chaperonin	4.73	58266	P19882	0	Ga
B64E70	5.79	78600	HSP78	0.22	mitochondrial protease	5.89	85119	P33416	0	aac
B43L54	4.63	86000	HSP82	0.66	heat-inducible chaperonin	4.58	81274	P02829	0	gm
B43L70	4.60	86000	HSP82	0.66	heat-inducible chaperonin	4.58	81274	P02829	0	gm
C56D25	6.08	56700	HTS1	0.39	histidinyl-tRNA synthetase	5.97	57661	P07263	A	MS

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C79J19	5.04	53100	HXK1	0.61	hexokinase I	5.07	53606	P04806	0	Ga, Gi
C80I57	5.14	53000	HXK1	0.61	hexokinase I	5.07	53606	P04806	0	Ga, Gi
C80J46	4.99	53000	HXK1*	0.61	hexokinase I	5.07	53606	P04806		Gi
C78J84	4.93	53300	HXK2	0.75	hexokinase II	4.92	53837	P04807	0	Ga, Gi, aac
C79J29	5.02	53100	HXK2	0.75	hexokinase II	4.92	53837	P04807	0	Ga, Gi, aac, MS
C26D67	5.99	62400	ICL1	0.33	isocitrate lyase	5.94	62276	P28240		Ga, sq
C26D85	5.96	62400	ICL1	0.33	isocitrate lyase	5.94	62276	P28240		Ga
C26E04	5.92	62400	ICL1	0.33	isocitrate lyase	5.94	62276	P28240		Ga
C26E23	5.88	62400	ICL1	0.33	isocitrate lyase	5.94	62276	P28240		Ga
C26E41	5.85	62400	ICL1	0.33	isocitrate lyase	5.94	62276	P28240		Ga
E40L54	4.63	37300	IDI1	0.27	isopentenyl-diphosphate isomerase	4.62	33219	P15496	0	MS
D75F20	5.70	42200	IDP2	0.20	isocitrate dehydrogenase	5.74	46561	P41939		MS
D75F93	5.57	42200	IDP2	0.20	isocitrate dehydrogenase	5.74	46561	P41939		
C01B68	6.45	68100	ILV2	0.36	acetolactate synthase	6.63	64761	P07342	0	aac
E18B67	6.45	38800	ILV5	0.89	ketol-acid reductoisomerase	6.28	39176	P06168	0	aac, MS
F00H54	5.30	32700	ILV6	0.40	acetolactate synthase regulatory subunit	5.39	31360	P25605	0	Gi, sq, MS
C73C02	6.36	54000	IMD2	0.44	inosine-5'-monophosphate dehydrogenase	8.62	56529	P38697		MS
C48G20	5.53	58100	INO1	0.20	inositol-1-phosphate synthase	5.40	62016	P11986	0	Gi, MS
C48G88	5.41	58100	INO1	0.20	inositol-1-phosphate synthase	5.40	62016	P11986		Gi, ace
F08I30	5.18	32200	IPP1	0.75	inorganic pyrophosphatase	5.17	32168	P00817	0	aac, MS
F00J34	5.01	32700	IPP1*	0.75	inorganic pyrophosphatase	5.17	32168	P00817		MS
F10J16	5.04	32100	IPP1*	0.75	inorganic pyrophosphatase	5.17	32168	P00817		MS
B85M24	4.50	72300	KAR2	0.59	heat shock protein	4.43	69824	P16474	0	aac, MS
D19F86	5.58	47900	KES1	0.34	protein implicated in ergosterol biosynthesis	5.63	49491	P35844	A	MS
A92C28	6.30	115800	KGD1	0.29	2-oxoglutarate dehydrogenase	6.36	111057	P20967	0	MS
A93C51	6.25	114800	KGD1	0.29	2-oxoglutarate dehydrogenase	6.36	111057	P20967		
D15H48	5.31	48300	KGD2	0.33	dihydrolipoamide succinyltransferase	5.47	45784	P19262		MS
D19I06	5.22	47900	KGD2	0.33	dihydrolipoamide succinyltransferase	5.47	45784	P19262	0	MS
B90F24	5.69	70900	KRS1	0.54	lysyl-tRNA synthetase	5.69	67826	P15180	0	ace
B90F70	5.61	70900	KRS1	0.54	lysyl-tRNA synthetase	5.62	67868	P15180	A	MS
C70H06	5.38	54500	LAT1	0.38	dihydrolipoamide S-acetyltransferase	5.40	48540	P12695	0	MS
B20F30	5.68	95600	LEU1	0.44	3-Isopropylmalate dehydratase	5.47	85793	P07264	0	MS
B20F69	5.61	95600	LEU1	0.44	3-Isopropylmalate dehydratase	5.47	85793	P07264	0	aac
D78H99	5.23	42000	LEU2	0.59	3-Isopropylmalate dehydrogenase	5.36	38849	P04173		Gi, Ga, aac
C10F94	5.57	65900	LEU4	0.41	2-Isopropylmalate synthase	5.59	68407	P06208	0	MS
E52M99	4.35	35700	LIA1	0.59	deoxyhypusine hydroxylase	4.50	36075	P47120	A	MS
C73A76	6.69	54000	LPD1	0.35	dihydrolipoamide dehydrogenase	6.58	51550	P09624	0	MS
D65F15	5.71	43100	LSC2*	0.24	succinyl-CoA ligase, beta subunit	5.69	43530	P53312	0	MS
D78N30	4.29	42000	LSP1	0.34	regulator of Pkh1p activity	4.36	38070	Q12230	0	MS
E11B03	6.62	39300	LYS12	0.48	homocitrate dehydrogenase	6.53	38588	P40495	0	MS
A53G59	5.46	155700	LYS2	0.24	aminoadipate reductase	5.50	155344	P07702	0	Gi
A53G87	5.41	155700	LYS2	0.24	aminoadipate reductase	5.50	155344	P07702	0	Gi
D22B43	6.51	47500	LYS20	0.48	homocitrate synthase	6.90	47098	P48570	0	MS, Gi
D22A14	6.87	47500	LYS20*	0.48	homocitrate synthase	6.90	47098	P48570		Gi
D05F62	5.63	49600	LYS21	0.47	homocitrate synthase	5.71	48504	Q12122	A	MS, Gi
D05G48	5.48	49600	LYS21	0.47	homocitrate synthase	5.71	48504	Q12122	A	MS, Gi

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B64B38	6.52	78600	LYS4	0.27	homoacnitase	6.47	73353	P49367	0	MS
D29K01	4.90	46700	LYS9	0.46	saccharopine dehydrogenase	4.84	48917	P38999	0	aac, MS, Gi
D28J63	4.96	46800	LYS9*	0.46	saccharopine dehydrogenase	4.84	48917	P38999	0	MS, Gi
B95C52	6.24	69600	MAE1*	0.35	mitochondrial malate dehydrogenase	6.27	68967	P36013		Gi
D10E82	5.77	48900	MAP2*	0.25	methionine aminopeptidase isoform 2	5.87	47371	P38174	0	Gi
E72A38	6.80	34400	MDH1	0.45	mitochondrial malate dehydrogenase	6.86	33832	P17505	0	aac
D78B62	6.46	42000	MDH2*	0.28	cytosolic malate dehydrogenase	6.44	39634	P22133		Gi
D78C30	6.30	42000	MDH2*	0.28	cytosolic malate dehydrogenase	6.44	39634	P22133		Gi
B55E69	5.69	81600	MEF1	0.22	mitochondrial elongation factor G	5.63	79682	P25039	0	MS
B56D21	6.09	81300	MES1	0.32	methionyl-tRNA synthetase	6.07	85587	P00958	A	MS
A92J83	4.93	115800	MET10*	0.32	sulfite reductase	4.93	114827	P39692	0	MS
C14H41	5.32	65000	MET13	0.32	methylenetetrahydrofolate reductase	5.43	68471	P53128	0	MS
F95G23	5.52	27300	MET16	0.13	3'-phosphoadenylylsulfate reductase	5.50	30380	P18408	0	Ga
D36E12	5.90	46000	MET17	0.58	O-acetylhomoserine sulfhydrylase	5.96	48540	P06106	0	Ga, aac, MS
D36E62	5.81	46000	MET17	0.58	O-acetylhomoserine sulfhydrylase	5.96	48540	P06106		MS
C62H38	5.33	55700	MET3	0.39	sulfate adenylyltransferase	5.39	57723	P08536	0	Ga
B45D45	6.04	85200	MET6	0.77	homocysteine methyltransferase	6.01	85727	P05694	0	aac
B48C95	6.15	84100	MET6	0.77	homocysteine methyltransferase	6.01	85727	P05694	0	sq, aac, MS
G71J55	4.98	23700	MGE1	0.29	folding of mitochondrial proteins	5.08	20810	P38523	0	MS
A07K01	4.90	202800	MLP1*	0.11	myosin-like protein	4.91	218365	Q02455		MS
C36A55	6.75	60400	MLS1	0.30	malate synthase 1	6.77	62790	P30952		MS
C36B10	6.60	60400	MLS1	0.30	malate synthase 1	6.77	62790	P30952		MS
G48N68	4.20	24800	MRP8*	0.24	mitochondrial ribosomal protein	4.39	25097	P35719		MS, Gi
D11F90	5.58	48800	MTF2	0.09	mitochondrial mRNA splicing	5.52	48587	P10849		Ga
A91G15	5.53	116900	NMA111	0.16	putative serine protease	5.52	110879	P53920	0	MS
F46L95	4.56	30000	NNT1*	0.08	putative methyltransferase involved in rDNA silencing	4.71	29543	Q05874	A	MS
C65I96	5.07	55300	NPL3	0.55	protein involved in pre-rRNA processing	5.14	45317	Q01560	A	MS
D48C11	6.34	44800	NPT1*	0.19	nicotinate phosphoribosyltransferase	6.30	48929	P39683	A	MS
K70Q31	4.05	13800	NTF2	0.42	nuclear transport factor	4.17	14453	P33331		aac
D84C98	6.14	41500	OYE2	0.53	NADPH dehydrogenase	6.11	44879	Q03558	0	gm
H00H92	5.24	22500	PAA1*	0.29	polyamine acetyltransferase	5.30	21858	Q12447	A	Gi
C08F11	5.72	66400	PAB1	0.62	poly(A)-binding protein	5.58	64343	P04147	0	ace
C08F76	5.60	66400	PAB1	0.62	poly(A)-binding protein	5.49	64254	P04147	A	MS
C36D79	5.97	60400	PCK1	0.42	phosphoenolpyruvate carboxykinase	5.88	60982	P10963		MS
C36E01	5.93	60400	PCK1	0.42	phosphoenolpyruvate carboxykinase	5.88	60982	P10963		MS
C36E20	5.89	60400	PCK1	0.42	phosphoenolpyruvate carboxykinase	5.88	60982	P10963		MS
C36E43	5.84	60400	PCK1	0.42	phosphoenolpyruvate carboxykinase	5.88	60982	P10963		MS
D51E28	5.87	44500	PDA1	0.40	pyruvate dehydrogenase complex E1-alpha subunit	5.85	42711	P16387	0	MS, Gi
D49D06	6.12	44700	PDA1*	0.40	pyruvate dehydrogenase complex E1-alpha subunit	6.20	42711	P16387		MS, Gi
D50E30	5.87	44600	PDA1*	0.40	pyruvate dehydrogenase complex E1-alpha subunit	5.85	42711	P16387		Gi
D52C96	6.15	44400	PDA1*	0.40	pyruvate dehydrogenase complex E1-alpha subunit	6.20	42711	P16387	0	Gi, MS
F05L41	4.66	32400	PDB1	0.49	pyruvate dehydrogenase complex E1-beta subunit	4.59	36480	P32473	0	aac
C54F32	5.68	57100	PDC1	0.95	pyruvate decarboxylase 1	5.73	61363	P06169	0	Ga, Gi, aac
C55G66	5.45	56900	PDC1	0.95	pyruvate decarboxylase 1	5.62	61405	P06169	A	Ga, Gi
C58G01	5.56	56400	PDC1	0.95	pyruvate decarboxylase 1	5.62	61405	P06169	A	Ga, Gi, aac, MS
C80E68	5.80	53000	PDC1 f		pyruvate decarboxylase 1 fragment			P06169		MS

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C89E73	5.79	51700	PDC1 f		pyruvate decarboxylase 1 fragment			P06169		MS
C93E70	5.79	51100	PDC1 f		pyruvate decarboxylase 1 fragment			P06169		MS
D86E68	5.80	41300	PDC1 f*		pyruvate decarboxylase 1 fragment			P06169	0	MS
C47E78	5.78	58300	PDC5	0.83	pyruvate decarboxylase 2	5.86	61822	P16467		Gi of PDC1
C47E46	5.84	58300	PDC5*	0.83	pyruvate decarboxylase 2	5.86	61822	P16467		MS
C07Q13	4.08	66600	PDI1*	0.59	protein disulfide isomerase	4.08	55345	P17967		MS
C18Q13	4.08	64100	PDI1*	0.59	protein disulfide isomerase	4.08	55345	P17967		MS
C16L24	4.69	64500	PDR13	0.60	Hsp70 protein	4.66	58148	P38788		aac, MS
D81Q41	4.03	41700	PEP4*	0.47	protease A	4.04	35749	P07267		MS
E14Q41	4.03	39100	PEP4*	0.47	protease A	4.04	35749	P07267		MS
B00D92	5.94	107600	PFK1	0.61	phosphofructokinase alpha subunit	5.93	107968	P16861	0	Ga, Gi
B00E24	5.88	107600	PFK1	0.61	phosphofructokinase alpha subunit	5.93	107968	P16861	0	Ga, Gi, aac
B08D26	6.08	99400	PFK2	0.66	phosphofructokinase beta subunit	6.21	104485	P16862	0	Ga, Gi
B09D80	5.97	98400	PFK2	0.66	phosphofructokinase beta subunit	6.06	104485	P16862	0	Ga, Gi
C59D55	6.02	56200	PGI1	0.79	glucose-6-phosphate isomerase	5.98	61167	P12709	0	ace
C59E48	5.83	56200	PGI1	0.79	glucose-6-phosphate isomerase	5.75	61209	P12709	A	ace
C61E00	5.93	55900	PGI1	0.79	glucose-6-phosphate isomerase	5.89	61209	P12709	A	Ga, aac, MS
E53D97	5.93	35600	PGK1 f		3-phosphoglycerate kinase fragment			P00560	0	MS
C14E12	5.90	65000	PGM2	0.40	phosphoglucomutase	6.03	62999	P37012		MS
F01D82	5.96	32600	PHO13*	0.25	4-nitrophenylphosphatase	5.94	34493	P19881	0	Gi
D89N61	4.22	41100	PIL1	0.49	regulator of Pkh1p activity	4.28	38348	P53252		MS, Gi
D65N94	4.15	43100	PIL1*	0.49	regulator of Pkh1p activity	4.28	38348	P53252		MS, Gi
D65O29	4.29	43100	PIL1*	0.49	regulator of Pkh1p activity	4.28	38348	P53252		Gi
A76J92	4.92	132200	PIM1*	0.21	serine protease	4.86	115774	P36775	0	MS
D43G31	5.51	45300	PMI40	0.34	mannose-6-phosphate isomerase	5.44	48099	P29952	A	MS
G72F35	5.67	23700	PNC1	0.40	pyrazinamidase and nicotinamidase	5.64	24904	P53184	0	aac
G17P93	4.11	26200	POL30*	0.30	polymerase 30	4.11	28916	P15873		MS
F59E77	5.78	29300	PRB1	0.45	protease B (cerevisin)	6.13	30017	P09232	0	MS
B93I62	5.13	70100	PRD1*	0.17	proteinase yscD (saccharolysin)	5.17	78747	P25375	0	MS
H13G69	5.44	22000	PRE1*	0.23	beta-4 subunit of 20S proteasome	5.46	22516	P22141	0	MS
G96D53	6.02	22700	PRE2*	0.26	beta-5 subunit of 20S proteasome	5.93	23300	P30656	0	MS
H16I28	5.18	21800	PRE3*	0.17	beta-1 subunit of 20S proteasome	5.18	21493	P38624		MS
G57E12	5.90	24300	PRE4*	0.16	beta-7 subunit of 20S proteasome	5.63	25919	P30657	0	MS
G83B52	6.49	23200	PRE5*	0.15	alpha-6 subunit of 20S proteasome	6.50	25646	P40302		MS
F94A38	6.80	27400	PRE6*	0.24	alpha-4 subunit of 20S proteasome	7.18	28308	P40303		MS
G53D19	6.10	24500	PRE7*	0.14	beta-6 subunit of 20S proteasome	6.23	24851	P23724		MS
G36H58	5.30	25300	PRE8	0.13	alpha-2 subunit of 20S proteasome	5.14	27072	P23639	A	aac, MS
G26K72	4.78	25800	PRE9	0.22	alpha-3 subunit of 20S proteasome	4.71	28624	P23638	A	aac, MS
D17I13	5.21	48100	PRO2	0.30	phosphoglutamate dehydrogenase	5.09	49650	P54885	A	MS
E79H82	5.26	33900	PRO3	0.30	pyrroline-5-carboxylate reductase	5.19	30131	P32263	0	Ga, MS
B36I08	5.22	88700	PRT1	0.38	translation initiation factor eIF3 subunit	5.18	83307	P06103		MS
B36H79	5.26	88700	PRT1*	0.38	translation initiation factor eIF3 subunit	5.18	83307	P06103	0	MS
B36I35	5.17	88700	PRT1*	0.38	translation initiation factor eIF3 subunit	5.13	83349	P06103	A	MS
E08E03	5.92	39600	PSA1	0.72	mannose-1-phosphate guanyltransferase	5.90	39525	P41940	0	aac, MS
H24H56	5.30	21500	PST2	0.57	similarity to S. pombe brefeldin resistance protein	5.35	20965	Q12335	0	MS
C75L33	4.67	53700	PUB1	0.39	major poly-adenylated RNA binding protein	4.63	50673	P32588	A	aac, MS

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Number	Apparent pI	Apparent M _r	Name ^{b)}	CBI	Name	Calculated pI	Calculated M _r	SWISS P.	Acetylation ^{c)}	Identification method ^{d)}
H25D85	5.96	21500	PUP1*	0.23	beta-2 subunit of 20S proteasome	6.05	25085	P25043		MS
F88N68	4.20	27700	PUP2	0.15	alpha-5 subunit of 20S proteasome	4.38	28659	P32379		MS
H21L06	4.72	21600	PUP3*	0.22	beta-3 subunit of 20S proteasome	4.66	22515	P25451	A	MS
C37E33	5.86	60200	PUT2*	0.17	delta-1-pyrroline-5-carboxylate dehydrogenase	5.88	62778	P07275		MS
A74F15	5.71	134300	PYC1	0.36	pyruvate carboxylase 1	5.77	129966	P11154	0	Ga, Gi
A74F42	5.66	134300	PYC1	0.36	pyruvate carboxylase 1	5.72	130008	P11154	A	Ga, Gi
A74F68	5.61	134300	PYC1	0.36	pyruvate carboxylase 1	5.64	130009	P11154	A	Ga, Gi
A72D55	6.02	136300	PYC2	0.43	pyruvate carboxylase 2	6.03	130033	P32327	0	Ga, Gi
A72D78	5.97	136300	PYC2	0.43	pyruvate carboxylase 2	5.98	130075	P32327	A	Ga, Gi
A72E01	5.93	136300	PYC2	0.43	pyruvate carboxylase 2	5.89	130076	P32327	A	Ga, Gi
D55H13	5.37	44100	PYK1 f		pyruvate kinase fragment			P00549	0	MS
E19D29	6.07	38700	QCR2*	0.33	ubiquinol cytochrome c reductase core protein 2	5.99	38747	P07257		MS
C71Q54	4.01	54300	RAD23*	0.24	nucleotide excision repair protein	3.98	42366	P32628		MS
E46J23	5.03	36900	RBK1	0.19	ribokinase	4.95	36923	P25332	0	Gi
F37H63	5.29	30500	RHR2	0.70	DL-glycerol-3-phosphatase	5.15	27815	P41277	0	MS
F37H97	5.23	30500	RHR2*	0.70	DL-glycerol-3-phosphatase	5.15	27815	P41277	0	MS
G60H56	5.30	24200	RIB3*	0.27	3,4-dihydroxy-2-butanone-4-phosphate synthase	5.32	22567	Q99258	0	MS
H84C35	6.28	19400	RIB4*	0.27	6,7-dimethyl-8-ribityllumazine synthase	6.06	18555	P50861		MS
G88K88	4.75	23000	RIB5*	0.20	riboflavin synthase	4.80	26196	P38145	0	MS
G77E50	5.83	23500	RIP1*	0.43	ubiquinol cytochrome c reductase iron-sulfur protein	5.91	20099	P08067	0	MS
B02I37	5.17	105600	RIX7*	0.18	putative ATPase that functions in rib. large subunit export	5.04	93068	Q07844	0	MS
D89E07	5.91	41100	RNQ1	0.29	may be required for resistance to certain drugs	6.16	42579	P25367	0	Gi
B03E77	5.78	104600	RNR1*	0.39	ribonucleotide reductase large subunit	5.75	99602	P21524	0	Gi
E21K55	4.81	38600	RNR4	0.62	ribonucleotide reductase small subunit	4.82	40096	P49723		MS
E18K94	4.74	38800	RNR4*	0.62	ribonucleotide reductase small subunit	4.82	40096	P49723	0	MS
E80B07	6.61	33900	RPL1	0.89	ribosomal protein	6.38	33611	P26321	0	aac, MS
F03M98	4.35	32500	RPN10	0.07	proteasome subunit	4.48	29616	P38886	0	MS
F70M38	4.47	28700	RPN12	0.16	proteasome subunit	4.55	31788	P32496	0	MS
D13F43	5.66	48600	RPN6*	0.13	proteasome subunit	5.71	49684	Q12377	A	MS
F12H07	5.38	31900	RPP0	0.89	ribosomal protein	4.48	33765	P05317		aac
K49R97	3.70	14000	RPP2A	0.89	ribosomal protein	3.63	10746	P05319		aac
K47R55	3.81	14000	RPP2B	0.88	ribosomal protein	3.78	11050	P02400		aac
F46M98	4.35	30000	RPS0A	0.81	ribosomal protein	4.35	27934	P32905	A	int, MS
F57M59	4.43	29400	RPS0B	0.85	ribosomal protein	4.39	27872	P46654	A	int, MS
J35N07	4.40	15500	RPS12*	0.92	ribosomal protein	4.36	15382	P48589		MS
J39O85	4.24	15400	RPS12*	0.92	ribosomal protein	4.36	15382	P48589		MS
G25B08	6.60	25800	RPS5	0.90	ribosomal protein	8.78	24949	P26783	A	MS
C69I03	5.22	54600	RPT1	0.26	AAA component of 26S proteasome regulatory subunit	5.08	51982	P33299	0	Ga
D12J06	5.06	48700	RPT3	0.27	AAA component of 26S proteasome regulatory subunit	5.16	47969	P33298	0	MS
D07H42	5.32	49300	RPT4	0.26	AAA component of 26S proteasome regulatory subunit	5.37	49407	P53549	A	MS
D06L18	4.70	49400	RPT5*	0.25	AAA component of 26S proteasome regulatory subunit	4.63	48166	P33297	A	MS
C03O52	4.27	67600	RRB1*	0.23	protein involved in ribosome assembly	4.17	57171	Q04225		MS
C97F70	5.61	50600	RVB1	0.23	DNA helicase	5.52	50452	Q03940	0	MS
C89J69	4.95	51700	RVB2	0.23	DNA helicase	4.92	51521	Q12464	A	MS
C63G87	5.41	55600	RVS167	0.22	protein involved in actin distribution	5.49	52684	P39743	A	Ga
D45E75	5.78	45100	SAH1	0.76	adenosylhomocysteinase	5.69	49035	P39954	A	MS

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Number	Apparent pI	Apparent M _r	Name ^{b)}	CBI	Name	Calculated pI	Calculated M _r	SWISS P.	Acetylation ^{c)}	Identification method ^{d)}
D45F32	5.68	45100	SAH1	0.76	adenosylhomocysteinase	5.69	49035	P39954	A	ace
D30K32	4.85	46600	SAM1	0.67	S-adenosylmethionine synthetase 1	4.79	41686	P10659	0	Ga, MS
D30K79	4.77	46600	SAM1	0.67	S-adenosylmethionine synthetase 1	4.79	41686	P10659		Ga
D39K32	4.85	45700	SAM1	0.67	S-adenosylmethionine synthetase 1	4.79	41686	P10659		MS
D57J44	5.00	43900	SAM2	0.64	S-adenosylmethionine synthetase 2	4.93	42124	P19358	0	Ga
D58K00	4.90	43800	SAM2	0.64	S-adenosylmethionine synthetase 2	4.85	42166	P19358	A	Ga
E80J84	4.93	33900	SAM4*	0.23	S-adenosylmethionine homocysteine methyltransferase	4.89	36668	Q08985	0	Gi
H41J56	4.98	20900	SAR1	0.46	GTP-binding protein of the ras superfamily	4.99	21450	P20606	0	aac, int
G05P04	4.22	26800	SBA1	0.34	Ste5p-associated protein	4.13	23992	P28707		aac, MS
D80H73	5.27	41800	SBP1	0.50	single-stranded nucleic acid-binding protein	5.19	32900	P10080	A	MS
G31E73	5.79	25600	SCL1	0.17	alpha-1 subunit of 20S proteasome	5.55	27911	P21243	A	MS
A50F98	5.56	158800	SCP160	0.41	control of mitotic chromosomal transmission	5.45	134718	P06105	A	MS
C02C10	6.34	67800	SDH1	0.36	succinate dehydrogenase subunit	6.45	67109	Q00711		MS
C02C38	6.28	67800	SDH1	0.36	succinate dehydrogenase subunit	6.45	67109	Q00711		
E89I20	5.20	33300	SEC14	0.37	phosphatidylinositol/phosphatidylcholine transfer protein	5.17	34769	P24280	0	MS
F43L38	4.66	30100	SEC17	0.06	vesicular-fusion protein	4.64	32668	P32602	A	MS
B58I70	5.12	80600	SEC23*	0.35	involved in endoplasmic reticulum to Golgi transport	5.22	85384	P15303	0	MS
G39K92	4.75	25200	SEC53	0.66	phosphomannomutase	4.83	28973	P07283	A	aac
G41K31	4.85	25100	SEC53	0.66	phosphomannomutase	4.91	28931	P07283	0	ace
D63D77	5.97	43300	SER1	0.29	phosphoserine aminotransferase	5.95	43325	P33330	A	aac, MS
E52K32	4.85	35700	SER2*	0.22	phosphoserine phosphatase	4.81	34076	P42941	0	Gi
E53K86	4.76	35600	SER2*	0.22	phosphoserine phosphatase	4.74	34118	P42941	A	Gi
D29I97	5.07	46700	SER3*	0.42	3-phosphoglycerate dehydrogenase	5.20	51193	P40054		MS, Gi
D29J63	4.96	46700	SER3*	0.42	3-phosphoglycerate dehydrogenase	5.20	51193	P40054		Gi
D29K18	4.87	46700	SER3*	0.42	3-phosphoglycerate dehydrogenase	5.20	51193	P40054		Gi
D11E14	5.90	48800	SER33*	0.29	3-phosphoglycerate dehydrogenase	5.83	51098	P40510	A	Gi
D15G49	5.48	48300	SER33*	0.29	3-phosphoglycerate dehydrogenase	5.95	51188	P40510		MS, Gi
C72E65	5.80	54200	SES1	0.48	seryl-tRNA synthetase	5.69	53309	P07284	0	MS
D58C19	6.32	43800	SFA1	0.32	glutathione-dependent formaldehyde dehydrogenase	6.15	40952	P32771	A	MS
E14N67	4.21	39100	SGT2	0.23	unknown	4.38	37128	Q12118	A	MS
E15N45	4.25	39000	SGT2	0.23	unknown	4.42	37086	Q12118	0	MS
C96M58	4.44	50700	SHP1	0.13	potential regulatory subunit for Glc7p	4.63	46986	P34223		MS
C97M23	4.50	50600	SHP1	0.13	potential regulatory subunit for Glc7p	4.63	46986	P34223		MS
C98L88	4.57	50500	SHP1	0.13	potential regulatory subunit for Glc7p	4.63	46986	P34223		MS
F79Q72	3.98	28200	SKP1*	0.21	component of Cbf3 kinetochore complex	4.04	22330	P52286		MS
B72O11	4.31	76100	SMI1*	0.14	involved in beta-1,3-glucan synthesis	4.33	57079	P32566		Gi
B72O30	4.29	76100	SMI1*	0.14	involved in beta-1,3-glucan synthesis	4.33	57079	P32566		Gi
B72O50	4.27	76100	SMI1*	0.14	involved in beta-1,3-glucan synthesis	4.33	57079	P32566		Gi
E72M67	4.42	34400	SNF7*	-0.01	involved in glucose derepression	4.42	26987	P39929	0	MS
E73H87	5.25	34300	SNZ1	0.24	putative pyridoxine (vitamin B6) biosynthetic enzyme	5.22	31816	Q03148	0	MS
E73J02	5.06	34300	SNZ2-3*	0.29	putative pyridoxine (vitamin B6) biosynthetic enzyme	5.11	31944	P53824		MS
I01G27	5.51	18800	SOD1	0.56	copper-zinc superoxide dismutase	5.55	15723	P00445	0	Ga, aac
H12D38	6.06	22000	SOD2	0.35	manganese superoxide dismutase	6.06	23082	P00447	0	aac
C95I99	5.07	50900	SPE1*	0.17	ornithine decarboxylase	5.07	52195	P08432		Gi
E73K17	4.87	34300	SPE2a*	0.20	S-adenosylmethionine decarboxylase	5.02	36065	P21182	0	Gi
F29I45	5.16	30900	SPE3	0.47	spermidine synthase	5.17	33323	Q12074	0	ace

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F31J16	5.04	30800	SPE3	0.47	spermidine synthase	5.07	33234	Q12074	A	MS
F44K66	4.79	30100	SPE4*	0.10	spermine synthase	4.75	34090	Q12455		Gi
C29M60	4.43	61800	SRP1	0.35	karyopherin-alpha subunit	4.54	60440	Q02821	0	gm
C04H18	5.36	67300	SRV2*	0.26	adenylate cyclase-associated protein	5.28	57390	P17555	0	Gi, MS
C04H41	5.32	67300	SRV2*	0.26	adenylate cyclase-associated protein	5.28	57390	P17555	0	Gi
B95L23	4.69	69600	SSA1	0.83	cytoplasmic chaperone	4.70	69677	P10591	A	aac
G88L98	4.55	23000	SSA1 f*		cytoplasmic chaperone fragment			P10591	A	MS
B95L70	4.60	69600	SSA2	0.89	cytoplasmic chaperone	4.62	69380	P10592	A	ace
B97L49	4.64	69100	SSA2	0.89	cytoplasmic chaperone	4.66	69380	P10592	A	aac, MS
B82K88	4.75	73100	SSA3	0.20	cytoplasmic chaperone	4.76	70457	P09435		aac
B90L12	4.71	70900	SSA4	0.24	cytoplasmic chaperone	4.74	69561	P22202		gm
B90L36	4.67	70900	SSA4	0.24	cytoplasmic chaperone	4.74	69561	P22202		gm
C01J52	4.98	68100	SSB1	0.91	cytoplasmic chaperone	5.04	66511	P11484	A	ace
C02J18	5.04	67800	SSB1	0.91	cytoplasmic chaperone	5.04	66511	P11484	A	Ga, Gi, aac, MS
C02I80	5.10	67800	SSB2	0.88	cytoplasmic chaperone	5.09	66504	P40150	A	aac
B91J07	5.06	70600	SSC1	0.68	chaperonin for mitochondrial proteins	5.01	68095	P12398	0	aac
B91J48	4.99	70600	SSC1	0.68	chaperonin for mitochondrial proteins	5.01	68095	P12398	0	aac
B53J51	4.98	82300	SSE1	0.64	cytoplasmic chaperone	4.89	77277	P32589	0	ace
B54J69	4.95	82000	SSE1	0.64	cytoplasmic chaperone	4.86	77276	P32589	A	aac, MS
B54J89	4.92	82000	SSE1	0.64	cytoplasmic chaperone	4.86	77319	P32589	A	ace
B79H23	5.35	74000	STI1	0.31	heat shock protein	5.26	66133	P15705	0	aac
B79H74	5.27	74000	STI1	0.31	stress-induced protein	5.19	66175	P15705	A	aac
C97I85	5.09	50600	SUB2	0.45	pre-mRNA splicing factor	5.09	50219	Q07478	A	MS
D06L29	4.68	49400	SUP45	0.38	translational release factor eRF1	4.64	48916	P12385	A	MS
E48E64	5.80	36800	TAL1	0.70	transaldolase	5.73	36964	P15019	A	Ga, aac
E62B94	6.38	35000	TDH2	0.98	glyceraldehyde-3-phosphate dehydrogenase 2	6.50	35715	P00358	0	anti, Ga, aac, MS, Gi
E65B04	6.61	34800	TDH2	0.98	glyceraldehyde-3-phosphate dehydrogenase 2	6.50	35715	P00358	0	anti, Ga, Gi
E63B51	6.49	35800	TDH2*	0.98	glyceraldehyde-3-phosphate dehydrogenase 2	6.50	35715	P00358	0	Gi
E52B78	6.42	35700	TDH3	0.99	glyceraldehyde-3-phosphate dehydrogenase 3	6.50	35600	P00359	0	anti, Ga, aac, Gi
E56A89	6.66	35400	TDH3	0.99	glyceraldehyde-3-phosphate dehydrogenase 3	6.50	35600	P00359	0	anti, Ga, aac, MS, Gi
E52B41	6.52	35700	TDH3*	0.99	glyceraldehyde-3-phosphate dehydrogenase 3	6.50	35600	P00359		MS, Gi
G11D89	5.95	26500	TFS1*	0.15	nutrient- and ammonia-response cell cycle regulator	5.82	24399	P14306		Gi
C44E91	5.75	58900	THI20*	0.32	hydroxymethylpyrimidine phosphate kinase	5.73	61137	Q08224		MS
C43H14	5.37	59100	THI22*	0.22	hydroxymethylpyrimidine phosphate kinase	5.55	63306	Q06490		MS
E72E28	5.87	34400	THI4*	0.55	thiamine biosynthesis	5.79	34859	P32318		Gi
E72E95	5.75	34400	THI4*	0.55	thiamine biosynthesis	5.79	34859	P32318		Gi, MS
E72F68	5.61	34400	THI4*	0.55	thiamine biosynthesis	5.79	34859	P32318		Gi, MS
E72F81	5.59	34400	THI4*	0.55	thiamine biosynthesis	5.79	34859	P32318		Gi, MS
E72G46	5.48	34400	THI4*	0.55	thiamine biosynthesis	5.79	34859	P32318		Gi
C35F69	5.61	60600	THI6*	0.18	thiamine-phosphate pyrophosphorylase/hydroxyethylthiazole kinase	5.53	58058	P41835		MS
E17I90	5.08	38900	THR1*	0.41	homoserine kinase	5.05	38712	P17423		MS
C66H43	5.32	55100	THR4	0.51	threonine synthase	5.26	57473	P16120	0	aac
B49B25	6.56	83700	THS1	0.51	threonyl-tRNA synthetase	6.48	84430	P04801	A	MS
D66L18	4.70	43000	TIF1	0.83	translation initiation factor eIF4A	4.72	44607	P10081	A	Ga, Gi
D67K55	4.81	42900	TIF1	0.83	translation initiation factor eIF4A	4.77	44565	P10081	0	Ga, Gi
D67K86	4.76	42900	TIF1	0.83	translation initiation factor eIF4A	4.72	44607	P10081	A	Ga, Gi, aac, MS

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H56M98	4.35	20300	TIF11*	0.49	translation initiation factor eIF1A	4.36	17435	P38912		MS
C87J08	5.05	52000	TIF3	0.50	translation initiation factor eIF4B	4.92	48521	P34167	0	MS
E15I07	5.22	39000	TIF34	0.38	translation initiation factor eIF3, p39 subunit	5.26	38755	P40217	0	MS
F15B90	6.39	31800	TIF35*	0.33	translation initiation factor eIF3, p33 subunit	6.43	30370	Q04067	0	ace
F16D03	6.13	31700	TIF35*	0.33	translation initiation factor eIF3, p33 subunit	6.03	30412	Q04067	A	MS
G11J14	5.04	26500	TIF45	0.45	translation initiation factor eIF4E	4.98	24164	P07260	A	Ga, MS
C97K56	4.81	50600	TIF5	0.38	translation initiation factor eIF5	4.65	45171	P38431	A	MS
H88N39	4.27	19200	TIF51A	0.91	translation initiation factor eIF5A	4.34	17025	P23301	A	ace
H91M73	4.41	19100	TIF51A	0.91	translation initiation factor eIF5A	4.42	17024	P23301	A	aac
H94M10	4.53	19000	TIF51A	0.91	translation initiation factor eIF5A	4.51	16982	P23301	0	ace
G40O65	4.26	25100	TIF6*	0.43	translation initiation factor eIF6	4.27	26457	Q12522		MS
B83B65	6.45	72800	TKL1	0.66	transketolase 1	6.54	73673	P23254	0	aac
B84B23	6.56	72500	TKL1	0.66	transketolase 1	6.54	73673	P23254	0	aac
B79F01	5.73	74000	TKL2	0.23	transketolase 2	5.68	75028	P33315		MS
B79F51	5.64	74000	TKL2	0.23	transketolase 2	5.68	75028	P33315		aac
G76O99	4.22	23500	TMA19*	0.83	translationally-controlled tumor protein homolog	4.11	18740	P35691	0	aac, MS, Gi
D82J89	4.92	41600	TOM40	0.38	protein of the mitochondrial import channel	4.98	41948	P23644	A	MS
B91I73	5.11	70600	TOM70*	0.31	protein-mitochondrial targeting	5.00	70104	P07213	0	MS
B62I80	5.10	79200	TPA1*	0.30	unknown	5.01	74041	P40032	0	MS
G57E89	5.76	24300	TPI1	0.90	triose-phosphate isomerase	5.61	26663	P00942	0	co, aac, MS
G59G74	5.43	24300	TPI1*	0.90	triose-phosphate isomerase	5.61	26663	P00942	0	MS
F23O21	4.30	31300	TPM1	0.49	tropomyosine	4.32	23583	P17536		aac
C90F62	5.63	51500	TPS1	0.27	trehalose-6-phosphate synthase	5.64	56016	Q00764	0	Ga
C90G23	5.52	51500	TPS1	0.27	trehalose-6-phosphate synthase	5.55	56058	Q00764	A	Ga
H30J76	4.94	21300	TRP1	0.05	phosphoribosylanthranilate isomerase	5.03	24144	P00912		Ga
C61H10	5.37	55900	TRP2	0.24	anthranilate synthase component I	5.43	56635	P00899	0	Ga, sq
C61H72	5.27	55900	TRP2	0.24	anthranilate synthase component I	5.34	56677	P00899	A	Ga
C90C13	6.34	51500	TRP3	0.22	anthranilate synthase component II	6.33	53399	P00937	A	Ga
E13D38	6.06	39200	TRP4	0.15	anthranilate phosphoribosyltransferase	6.09	41284	P07285	A	Ga, Gi
B84D52	6.03	72500	TRP5	0.45	tryptophan synthase	6.03	76494	P00931	0	Ga
B85D91	5.95	72300	TRP5	0.45	tryptophan synthase	5.95	76536	P00931	A	Ga, aac, MS
B85E32	5.86	72300	TRP5	0.45	tryptophan synthase	5.95	76536	P00931	A	Ga
E82G26	5.51	33800	TRR1	0.36	thioredoxin-dependent peroxide reductase	5.55	34106	P29509	0	MS
H12L19	4.70	22000	TSA1	0.85	thioredoxin peroxidase	4.79	21458	P34760	0	aac
H14K44	4.83	21900	TSA1	0.85	thioredoxin peroxidase	4.79	21458	P34760	0	aac, MS
C70K77	4.77	54500	TUB1	0.39	tubulin alpha-1 chain	4.73	49799	P09733	0	int, MS
C82M72	4.41	52700	TUB2	0.40	tubulin beta chain	4.37	50922	P022557	0	gm
C76K23	4.86	53500	TUB3	0.35	tubulin alpha-3 chain	4.84	49693	P09734	0	int, Gi
D51F45	5.66	44500	TUF1	0.41	mitochondrial translation elongation factor Tu	5.57	43785	P02992	0	MS
D51G20	5.53	44500	TUF1	0.41	mitochondrial translation elongation factor Tu	5.57	43785	P02992	0	MS
A87K81	4.76	120900	UBA1	0.25	ubiquitin-activating enzyme	4.71	114133	P22515	0	ace
A87K93	4.74	120900	UBA1	0.25	ubiquitin-activating enzyme	4.69	114175	P22515	A	aac
A87L06	4.72	120900	UBA1	0.25	ubiquitin-activating enzyme	4.69	114175	P22515	A	ace
J68F35	5.67	14900	UBC4	0.42	ubiquitin-conjugating enzyme	5.68	16366	P15731	A	aac
C69A16	6.86	54600	UGP1	0.46	UDP-glucose pyrophosphorylase	6.84	55898	P32861		Ga
C70A64	6.72	54500	UGP1	0.46	UDP-glucose pyrophosphorylase	6.65	55898	P32861		Ga

Spot			Gene		Protein					
Number	Apparent pI	Apparent M _r	Name ^{b)}	CBI	Name	Calculated pI	Calculated M _r	SWISS P.	Acetylation ^{c)}	Identification method ^{d)}
E91E63	5.81	33200	URA1	0.24	dihydroorotate dehydrogenase	5.68	34800	P28272	0	Gi
E94G07	5.55	33000	URA1	0.24	dihydroorotate dehydrogenase	5.44	34711	P28272	A	Gi
A03G28	5.51	206900	URA2*	0.36	multifunctional protein of pyrimidine biosynthesis pathway	5.45	244992	P07259		MS
G13A71	6.71	26400	URA3	0.21	orotidine-5'-phosphate decarboxylase	6.51	29150	P03962	A	Ga
E11D07	6.12	39300	URA4*	0.04	dihydroorotase	6.06	40313	P20051	0	MS, Gi
G75E74	5.78	23500	URA5*	0.36	orotate phosphoribosyltransferase 1	5.68	24533	P13298	0	Gi
G75F68	5.61	23500	URA5*	0.36	orotate phosphoribosyltransferase 1	5.68	24533	P13298		Gi
B90F86	5.58	70900	URA7	0.39	CTP synthase	5.58	64710	P28274	0	MS
D66D65	6.00	43000	URE2*	0.03	regulator of nitrogen catabolite repression	5.99	40270	P23202		Ga
D66E07	5.91	43000	URE2*	0.03	regulator of nitrogen catabolite repression	5.99	40270	P23202		Ga
D62E41	5.85	43400	URE2*	0.03	regulator of nitrogen catabolite repression	5.99	40270	P23202		Ga
D62E88	5.76	43400	URE2*	0.03	regulator of nitrogen catabolite repression	5.99	40270	P23202		Ga
B17J24	5.03	97000	UTP13*	0.13	component of the 80S U3 snoRNA complex	5.01	91031	Q05946		MS
B90J90	4.92	70900	VMA1	0.41	vacuolar H-ATPase catalytic subunit	4.94	67591	P17255	0	ace
B90K45	4.83	70900	VMA1	0.41	vacuolar H-ATPase catalytic subunit	4.89	67633	P17255	A	ace
B91K17	4.87	70600	VMA1	0.41	vacuolar H-ATPase catalytic subunit	4.89	67633	P17255	A	aac
C75K95	4.74	53700	VMA2	0.55	vacuolar H-ATPase regulatory subunit	4.71	57617	P16140	0	aac, MS
C70L17	4.70	54500	VMA2*	0.55	vacuolar H-ATPase regulatory subunit	4.71	57617	P16140	0	MS
G25I53	5.14	25800	VMA4	0.42	vacuolar H-ATPase hydrophilic subunit	5.09	26339	P22203	0	ace
G30J40	5.00	25600	VMA4	0.42	vacuolar H-ATPase hydrophilic subunit	4.98	26381	P22203	A	MS
E63P35	4.18	35000	VMA6*	0.31	vacuolar H-ATPase subunit	4.20	39659	P32366		MS
F36F65	5.62	30500	VMA8*	0.44	vacuolar H-ATPase catalytic subunit	5.37	29236	P32610	A	MS
D18C90	6.16	48000	WRS1	0.35	tryptophanyl-tRNA synthetase	6.17	49260	Q12109	A	MS
C38J50	4.99	60000	WTM1	0.37	transcriptional modulator	4.95	48382	Q12363	0	MS
G33F18	5.70	25500	XPT1*	0.36	xanthine phosphoribosyl transferase	5.57	23582	P47165	A	MS, Gi
G08P52	4.16	26700	YAR1*	0.08	involved in resistance to environmental stress and 40S ribosome biogenesis	4.10	22355	P46683		MS
F90D92	5.94	27600	YBL036C*	0.24	unknown	5.75	29123	P38197	A	MS
D33E37	5.86	46300	YDJ1	0.49	protein folding	5.87	44670	P25491	0	Ga
E69F13	5.71	34600	YDL124W*	0.21	NAD(P)H-dependent reductase	5.76	35429	Q07551		MS
C20C20	6.32	63700	YDR341C	0.34	arginyl-tRNA synthetase	6.20	69435	Q05506	A	MS
A82G48	5.48	126100	YEF3	0.86	translation elongation factor EF-3A	5.63	115334	P16521	A	ace
A85G22	5.52	123000	YEF3	0.86	translation elongation factor EF-3A	5.68	115334	P16521	A	aac, MS
H22E95	5.75	21600	YER067W	0.12	unknown	5.71	18989	P40043		MS
C96I08	5.22	50700	YFR044C	0.44	protease	5.15	52781	P43616	A	MS
E37E91	5.75	37500	YGR043C	0.16	putative transaldolase	5.79	37164	P53228		MS
D97E31	5.87	40400	YHB1	0.32	flavoheмоprotein	5.82	44645	P39676	0	MS
B56D37	6.06	81300	YHR020W*	0.47	putative prolyl-tRNA synthetase	5.96	77254	P38708	0	MS
B57D04	6.13	80900	YHR020W*	0.47	putative prolyl-tRNA synthetase	5.96	77254	P38708	0	MS
G24D73	5.98	26700	YIR035C*	0.35	putative oxidoreductase	5.90	27522	P40579		Gi
G45H64	5.29	24900	YKL033W-A*	0.17	similarity to holacid-halidohydrolyase	5.27	26081	Q86ZR7	A	MS
F36G04	5.55	30500	YKR043C*	0.28	similarity to phosphoglycerate mutase	5.54	31022	P36136	A	MS
G69M69	4.41	23800	YLR179C	0.32	unknown	4.49	22019	Q06252	0	ace
G71N49	4.25	23700	YLR179C	0.32	unknown	4.39	22061	Q06252	A	aac
G08K13	4.88	26700	YLR301W	0.41	unknown	4.88	27500	Q05905	A	aac
G20J00	5.07	26100	YNL010W	0.42	unknown	5.06	27480	P53981	0	MS
E03F63	5.62	39900	YNL134C	0.32	alcohol dehydrogenase activity	5.60	41074	P53912	A	MS

Spot			Gene		Protein					
Number	Apparent pI	Apparent M _r	Name ^{b)}	CBI	Name	Calculated pI	Calculated M _r	SWISS P.	Acetylation ^{c)}	Identification method ^{d)}
G60L54	4.63	24200	YOR021C	0.21	unknown	4.67	24743	Q12314	0	MS
E58G37	5.50	35300	YPR127W	0.33	unknown	5.57	38600	Q06494		MS
F29F35	5.67	30900	YRB1	0.62	Ran-specific GTPase-activating protein	5.50	22863	P41920	A	MS
C49N01	4.35	58000	ZPR1*	0.33	unknown	4.48	54982	P53303	A	MS
E26N44	4.26	38200	ZPS1	0.43	surface protein	4.60	27566	Q12512		MS
C66E62	5.81	55100	ZWF1	0.22	glucose-6-phosphate dehydrogenase	5.73	57431	P11412	A	Ga, aac, MS

^a The spot apparent pI and M_r, the corresponding gene name and its CBI, the calculated pI and M_r of the protein, its SWISS PROT access number and its N-terminal acetylation status

(0, no acetylation; A, acetylation), and the methods of identification are reported.

^b Asterisks indicate newly identified spots.

^c Deduced from the comparison of the protein pattern of the *nat1* mutant strain and a wild type strain.

^d The methods of identification are: aac, amino acids composition; ace, acetylation; anti, antibody; co, comigration; Ga, gene amplification; Gi, gene inactivation;

gm, gel matching; int, intron; MS, mass spectrometry; sq, sequencing.