

Table 2. Putative Identifications of *Neurospora* cDNAs

Clone ID ^a	MatchAcc ^b	Identification ^c	P/E value ^d	Tissues ^e
I. Cell Division				
Apoptosis				
NP4B8	NP_035181.1	programmed cell death 6 protein (Mm)	4.0e-32	1P
Cell Cycle				
SC6F9	gi 762850	cell cycle regulator p21 protein (Sp)	2.0e-6	1C
NM3G1	pir S43279	cell division control protein 3 (Ca)	1.1e-80	1M
NP4C10	P36618	cell division control protein 16 (Sp)	7.0e-18	1P
SP6G3	gi 4097884	cell division control protein 42 (Gc)	2.0e-44	1P
NC2F1	pir S34027	cell division control protein 47 (Sc)	1.3e-50	1C
NM5H9	P41733	cell division control protein 91 (Sc)	3.2e-19	1M
SC2G4	pir S49206	G1 cyclin CLN1 (Ca)	5.0e-8	1C
SC2D8	P05453	G1 to S phase transition protein 1 homolog (Hs)	2.4e-9	1C
NP4C2	NP_010018	involved in cell cycle, cdc 50p (Sc)	1.0e-48	1P
NM1D8	NP_011747	mitochondrial protein, prohibitin (Sc)	2.0e-18	1M
SP6F11	P32334	MSB2 protein (Sc)	2.0e-6	1P
NC2A11	gi 2944404	serine/threonine protein phosphatase type 1 (Nc)	4.0e-49	2C, 1W
Chromosome Structure				
NC2A6	P46672	GU4 nucleic-binding protein 1 (Sc)	9.8e-12	1C
SC3B9	P08844	histone H2A (En)	1.6e-68	1C
NP4A11	P07041	histone H3 (Nc)	3.3e-87	2C, 1P, 2W
NC1B2	P04914	histone H4 (Nc)	1.9e-51	1C, 1M, 2W
SM2H6	Q09330	MLO3 protein (Sp)	2.0e-7	1M
SC5D8	P11633	nonhistone chromosomal protein 6B (Sc)	2.0e-29	1C
NP5B7	gi 172034	nucleosome assembly protein (Sc)	7.7e-48	1P
DNA Synthesis/Replication				
W08D11	NP_013968	DNA-binding protein, mtDNA stabilizing protein (Sc)	4.0e-40	1C, 1W
W09H12	CAA03898.1	MCM7-like protein (Sp)	9.7e-15	1W
SC3F6	Q03392	proliferating cell nuclear antigen, PCNA (Sp)	1.1e-50	1C
II. Cell Signalling/Cell Communication				
Channels/Transport Proteins				
SM1G3	P53386	aquaporin-like protein YPR192w (Sc)	5.3e-7	1M
NM4H11	P33970	halorhodopsin (light-induced chloride pump) (Hh)	8.3e-9	1M
NP2B6	gi 1063415	K ⁺ channel protein (At)	2.1e-67	1P
W01B10	gi 2654088	potassium transporter (At)	1.4e-12	1W
NM8G7	CAA73031.1	putative organic cation transporter (Dm)	9.8e-10	1M
Effectors/Modulators				
W17G8	Q01631	adenylate cyclase (Nc)	3.9e-88	1P, 1W
SC1B12	P26364	adenylate kinase 2 (Sc)	3.7e-15	1C
NP3C6	AAD42978.1	adenyl cyclase-associated protein (Ca)	4.0e-25	1P
NM5H5	CAA17814.2	beta-catenin family member (Sp)	2.0e-12	1M
W09C12	Q02052	calmodulin (Nc)	8.7e-86	1P, 2W
Hormones/Growth Factors				
W13B2	gi 2224892	gibberelin 7-oxidase (Cum)	4.0e-7	1W
Intracellular Transducers				
SM1B4	P2212624	kD ras-like protein (Nc)	1.1e-40	1M
NC4D7	pir S57839	CPC2 protein (Nc)	3.7e-27	1C
NC5F1	P39958	GDP-dissociation inhibitor (Sc)	3.9e-44	1C
NP3A7	Q05425	guanine nucleotide-binding protein alpha-2 subunit (Nc)	1.8e-108	1P
W10F8	Q01369	guanine nucleotide-binding protein, beta subunit-like protein (Nc)	3.7e-98	1W

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SC7C4	Q10107	multicopy suppressor of ras1 (Sp)	8.0e-18	1C
SM3A10	gi 1399532	nuc-2; nuclease-2 (Nc)	9.9e-68	1M
NP3E5	CAB05920	palA (En)	2.0e-52	1P
SM4D6	CAA22174.1	putative signal transduction protein (Sp)	5.0e-17	1M
SP6F6	Q09914	Rho1 protein (Sp)	5.0e-54	1P
SC2E3	P40319SUR4	protein (Sc)	1.0e-22	1C
NC2C11	NP_013741.1	Tap42p, physically associates with PP2A and SIT4 protein phosphatase catalytic subunits (Sc)	8.7e-19	2C
SM2H4	P35169TOR1,	phosphatidylinositol 3-kinase (Sc)	2.2e-45	1M
Metabolism				
NM6A6	P17296	metapyrocatechase 2 (catechol 2,3-dioxygenase II) (Ae)	6.7e-12	1M
NM4F4	P37297	phosphatidylinositol 4-kinase (Sc)	5.8e-72	1M, 2P
Protein Modification				
SC1C7	gi 806859	14-3-3 protein (Trh)	2.9e-93	3C, 1M, 2W
SM1H12	O14408	calcium/calmodulin-dependent protein kinase (Ma)	3.0e-45	2M NC2B3
	gi 516040	cAMP-dependent protein kinase catalytic subunit (Mg)	6.3e-46	1C
NC1F3	Q08466	casein kinase II, alpha catalytic subunit (At)	2.8e-47	1C
NM1F4	P46594	halotolerance protein HAL2 (Os)	2.7e-11	1M
NM5B1	CAB11500.1	MAP kinase kinase kinase (Sp)	1.0e-12	1M
SM2H12	gi 2832241	nonphototropic hypocotyl 1 (At)	2.7e-10	1M
W08A7	AAF09475	osmotic sensitivity MAP kinase (Pg)	1.0e-52	2W SM1D8
	gi 1322070	protein kinase, cAMP-dependent regulatory subunit (Nc)	1.5e-22	1M
SC2G1	CAA72731.1	protein kinase C homolog (Nc)	1.1e-69	2C
SP6F4	gi 2654106	protein kinase NRC-2 (Nc)	4.0e-50	1P
NM4G1	CAA22609.1	protein kinase skp1p (Sp)	1.0e-80	1M
W13A11	AAD15987.1	protein phosphatase 2A regulatory B subunit (Nc)	5.0e-5	1W
SC3A2	gi 458284	serine/threonine protein kinase (Trr)	3.7e-30	1C
NC5F10	P05323	serine/threonine protein phosphatase PP2A-alpha, catalytic subunit (Hs)	2.8e-87	1C
SP1F10	gi 1706961	Shk1 kinase-binding protein (Sp)	4.8e-18	1P
SP6D9	NP_014366	tyrosine phosphatase Siw14p (Sc)	2.0e-12	1P
Receptors				
W08E3	P30536	peripheral-type benzodiazepine receptor, mitochondrial (Hs)	8.8e-10	1W
SP6G1	gi 1655907	protein-tyrosine phosphatase CRYP-2 (Galg)	4.0e-12	1P
III. Cell Structure/Cytoskeleton				
Cell Wall				
SC5D3	Q12114	chitin biosynthesis protein CHS5 (Sc)	1.0e-23	1C
NC4G7	P29070	chitin-UDP acetyl-glucosaminyl transferase 3 (Nc)	4.6e-50	1C, 1W
SC7C2	gi 2613108	class V chitin synthase (Um)	2.0e-28	1C
SM3F10	AAB47060	exochitinase (Trh)	1.0e-53	2M
SM1F2	gi 3608406	GEL1 protein (Aspfu)	2.0e-76	2M
NP5B11	gi 1261823	glycine rich protein (Nc)	4.0e-31	1P
W01A6	P34226	skt5 protein (Sc)	3.8e-11	1W
NC5H6	NP_014035.1	soluble cell wall proteins Scw4p, Scw10p, Scw11p (Sc)	7e-13	3C, 1W
Cytoskeletal				
W17E2	gi 178045	actin, gamma (Hs)	8.0e-13	1W
NM4E10	CAB66436.1	actin-related protein (Sp)	6.0e-18	1M
NP4C4	P18091	alpha-actinin, sarcomeric (Dm)	2.4e-47	1P
NP5C11	P40234	casein kinase I, homolog Cki2 (Sp)	2.0e-64	1P
NM4B4	Q03048	cofilin (Sc)	1.2e-24	1M, 1W
W13D12	O13923	coronin-like protein (Sp)	2.1e-45	1W
W06D1	P14315	F-actin capping protein, beta subunit isoforms (Galg)	1.6e-19	1W
SC2E6	P32599	fimbrin (ABP67) (Sc)	1.3e-66	1C
NP5E9	AAF18567	myosin-related protein homolog MlpA (En)	8.0e-18	1P

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NC1G12	P78774	probable arp2/3 complex 41kD subunit (Sp)	1.0e-42	1C
NC3C2	P39825	profilin 1 (Sp)	5.5e-33	1C
NC3A1	CAB39803.1	putative actin polymerization complex protein (Sp)	4.0e-36	1C, 2M
SM2C5	P32368	recessive suppressor of secretory defect, SAC1 (Sc)	4.7e-23	1M
NP5B3	gi 6119698	tropomyosin, alpha & beta chains (Sp)	7.9e-30	1C, 2P
SC1G3	P38669	tubulin, alpha - B chain (Nc)	1.4e-64	1C, 1P
NC3D10	P05220	tubulin, beta (Nc)	7.4e-94	3C, 1P
SP3B12	pir S51342	verprolin (Sc)	1.8e-6	1P
Motility				
SM4C3	NP_001118.1	adaptin, beta subunit (Hs)	9.0e-29	1M
IV. Cell/Organism Defense				
Carrier Proteins/Membrane Transport				
SC5E7	BAA33011.1	flavohemoglobin (Fo)	4.0e-32	2C
Detoxification				
SM1E4	BAA08308.1	acr-2; acriflavine resistant (Nc)	6.7e-82	1M
NM9C10	P38918	aflatoxin B1 aldehyde reductase (AFB1-AR) (Rn)	3.7e-21	1M
SP7C3	Q02068	aliphatic nitrilase (Rhrh)	2.0e-30	1M, 2P
NP3D9	gi 603050	CAP20 (plays role in infection of host) (Gc)	7.6e-39	2M, 2P
NM2E10	P78574	catalase A (Aspfu)	9.0e-34	1M
NM6H12	CAA74698	catalase/oxidase (Strr)	4.0e-47	1M
NM3D4	CAA26793.1	copper metallothionein (Nc)	6.7e-45 ^f	1M
SM1G12	P38179	HM-1 killer toxin resistance protein (Sc)	4.6e-33	1M
SM3H12	pir S70702	maackiain detoxification protein 1 (Nh)	2.0e-10	1M
SM2D2	P35724	manganese resistance protein, MNR2 (Sc)	4.9e-29	1M
NC2D6	P38356	metal homeostasis protein Bsd2p (Sc)	1.5e-9	1C
NC4D11	gi 487426	pisatin demethylase (Nh)	1.6e-23	1C, 2M
SM2B10	Q39172	probable NADP-dependent oxidoreductase P1 (At)	3.1e-11	1M
SM4C9	NP_014140	putative copper binding/homeostasis protein Abx1 (Sc)	1.0e-6	1M
SC3A6	CAA21951	rehydrin-like protein (Ca)	8.0e-36	2C, 1P, 3W
SP7A9	gi 1117921	Rod1p, involved in drug resistance (Sc)	8.0e-26	1P
NM7A11	CAB66461.1	similarity to <i>S. cerevisiae</i> kti12 protein (Sp)	5.0e-5	1M
DNA Repair				
NM6F2	P40235	casein kinase I homolog (HHP1) (Sp)	1.4e-95	2M
NM1H10	P38632	DNA repair protein MMS21 (Sc)	4.0e-6	1M
NM4F3	gi 703466	exonuclease I (Sp)	2.6e-52	1M
Stress Response				
W01C2	CAA35682.1	cyclophilin A (Nc)	4.7e-104	4C, 2P, 4W
NC2C5	Q92249	Erp38 (Nc)	1.2e-15	1C
NC4A7	P20080	FK506-binding protein (Nc)	3.9e-76	2C, 2P, 2W
SM2F5	P40581	glutathione peroxidase (Sc)	1.0e-26	2M
NM2D3	CAA70214.1	grp78 homolog (endoplasmic reticulum Hsp70) (Nc)	2.0e-36	1M
NC2E9	P38523	GRPE protein homolog precursor (Sc)	2.4e-40	1C
W06B9	NP_010978	heat-regulated protein Hig1p (Sc)	7.0e-15	1W
SC6H9	CAA67431	heat shock protein 70 (En)	3.0e-72	1C, 1P
W01G6	AAF34607	heat stress protein 80-1 (Nc)	5.0e-61	1W
NM4A1	P12807	peroxisomal copper amine oxidase (Hp)	2.3e-71	1C, 1M
SC5D10	AAD42074.1	peroxisomal membrane protein (Pnci)	2.0e-34	2C, 1W
NC4F4	Q03178	pir1 protein precursor (Sc)	8.6e-9	1C
NP6H2	CAB50926.1	RIC1 protein (Phi)	4.0e-12	1P
W13G6	P80645	sulfate starvation-induced protein (Ec)	1.0e-5	1W
NM5H1	P39076	T-complex protein 1, beta subunit (Sc)	1.2e-82	2M
SC4A3	P39077	T-complex protein 1, gamma subunit (Sc)	7.9e-26	1C
NP3F8	P23618	thiazole biosynthetic enzyme (stress inducible protein sti35) (Fo)	8.6e-86	5C, 2M, 1P, 14W

V. Metabolism

Amino Acid

NC1H9	P25605	acetolactate synthase, small subunit homolog (Sc)	1.2e-50	5C, 1M, 2P
NC1G8	pir A53429	acetylglutamate kinase (arg-6) (Nc)	5.2e-6	1C
NC4E1	gi 1066330	adenosine-5'phosphosulfate kinase (Pnch)	2.7e-65	2C
W17B9	P50514	argininosuccinate lyase (Sp)	4.7e-32	2W
NC3G2	P22768	argininosuccinate synthase (Sc)	2.6e-16	1C
W07A10	P55325	aspergillopepsin A precursor (Aspn)	2.6e-13	1W
W01H2	Q99145	ATP phosphoribosyltransferase (his1) (Yl)	3.2e-23	1W
NP2D4	AAD10616.1	beta-isopropylmalate dehydrogenase (Nc)	6.4e-47	1P
SC5B10	P22572	carbamoyl phosphate synthase (arg-2) (Nc)	2.0e-58	3C
NC3A12	P03965	carbamoyl phosphate synthase, arginine-specific, large chain (Sc)	7.2e-28	1C
SM1F11	P08456	CDP-diacylglycerol-serine O-phosphatidyltransferase (Sc)	1.7e-48	1C, 1M
SP1E12	AAF11089.1	cephalosporin acylase (Dr)	2.0e-13	1P
SC5B3	Q12640	chorismate synthase (Nc)	4.0e-62	1C
NC5F6	P46794	cystathionine beta-synthase (Dd)	5.6e-6	1C NC3A10
	P31373	cystathionine gamma-lyase (Sc)	2.4e-59	1C, 1M
SC7G11	P78568	delta-1-pyrroline-5-carboxylate dehydrogenase (Ab)	5.0e-12	2C
NM6A1	P09624	dihydrolipoamide dehydrogenase (Sc)	4.8e-57	1M, 1W
SP1B12	BAA18999.1	farnesyl cysteine carboxyl methyltransferase (Sp)	2.1e-31	1P
NP2H3	CAA70219.1	fructosyl amino acid oxidase (Pnj)	3.6e-15	1P
NM2B7	P00369	glutamate dehydrogenase (Nc)	2.8e-52	1M, 1W
W09G5	NP_009807	glutamine amidotransferase (Sc)	1.0e-53	1M, 1W
SP1C9	NP_010110.1	glutamate synthase (NADH-dependent) (Sc)	9.0e-27	1P NC5G11
	gi 1322275	glutamine synthetase (Gc)	3.1e-73	4C, 1W
SM4H11	AAD35304.1	glycine cleavage system H protein (Tm)	4.0e-21	1M
W08H2	gi 2853023	histidine-3 protein (Nc)	3.7e-91	1W
SC6D3	CAA11503	homocitrate synthase (Pnch)	5.0e-19	2C, 2M
SC2C6	P31116	homoserine dehydrogenase (Sc)	1.2e-18	1C
NC3A9	pir S57097	indoleamine-pyrrole 2,3-dioxygenase homolog (Sc)	2.6e-13	1C
SC1H9	P38674	ketol-acid reductoisomerase precursor (Nc)	1.2e-65	3C
NM8H12	pir S40296	L-arginine:glycine amidinotransferase (Ssd)	1.3e-17	2M, 1P
NC1D10	P05694	methionine synthase (Sc)	9.4e-81	1C
SM4F2	Q92413	ornithine aminotransferase (En)	3.0e-37	1M
NC1F9	P27121	ornithine decarboxylase 1 (Nc)	1.4e-85	1C, 1P
SM4D5	P07547	pentafunctional arom polypeptide (En)	4.0e-28	1M
NM8D7	AAF04875.1	putative alanine aminotransferase (At)	7.0e-39	1M, 1P
SC5E11	Q10270	putative phosphoadenosine phosphosulfate reductase (Sp)	6.0e-5	1C
W10A5	P38999	saccharopine dehydrogenase (Sc)	9.7e-65	2W
W13G12	P48466	S-adenosylmethionine synthetase (Nc)	6.3e-40	1W
W10G12	P34898	serine hydroxymethyltransferase, cytosolic (Nc)	4.4e-70	2C, 1W
NM1H5	pir A53651	sulfate adenylyltransferase (Pnch)	2.7e-99	1M, 1P
NP3D4	gi 601846	T-cell reactive protein (Ci)	4.5e-31	2P
W07F11	P13228	tryptophan synthase (Nc)	4.4e-51	1W
W17A5	P07259	URA2 protein (Sc)	5.6e-38	1W
		Cofactors		
SP4F2	gi 1465774	cofactor C (Hs)	2.8e-7	1P
NC1B12	CAA87397	GTP cyclohydrolase I (Sc)	6.3e-64	1C
NM2H1	P10867	L-gulonolactone oxidase (Rn)	9.7e-27	1M
NC3F9	gi 2598964	molybdopterin cofactor biosynthetic protein (En)	2.0e-12	1C
W17D11	P38681	nitrite reductase (NAD(P)H) (Nc)	1.5e-56	3C, 2W
W01E6	P42882	nmt1 protein homolog, thiamine biosynthesis enzyme (Aspp)	2.6e-112	11C, 6M, 1P, 72W
SM3D2	CAB16409	pyridoxal reductase (Sp)	1.0e-26	1M SC7F11
	AAD49809.1	pyroa - pyridoxine biosynthesis protein (En)	2.0e-46	1C

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Energy/TCA Cycle				
SC3F7	P19414	aconitate hydratase (Sc)	5.8e-66	5C, 1M, 2P
W13E4	P11943	acyl carrier protein, mitochondrial precursor (Nc)	5.9e-58	1C, 1W
SC6F12	CAA12224	ATP citrate lyase (Som)	3.0e-29	1C, 1M, 1P
SC1H4	P37211	ATP synthase alpha chain, mitochondrial precursor (Nc)	3.9e-88	3C, 2M
SC3G5	P23704	ATP synthase beta chain, mitochondrial (Nc)	3.4e-103	3C, 1M, 1P
W13F5	P56525	ATP synthase delta chain, mitochondrial precursor (Nc)	1.8e-61	1W
SP1E7	P49377	ATP synthase gamma subunit, mitochondrial (Sc)	2.0e-34	3C, 2P, 5W
SC5G11	P05626	ATP synthase, subunit 4, mitochondrial precursor (Sc)	5.9e-8	1C
W17C6	P00842	ATP synthase, subunit 9, mitochondrial (Nc)	4.0e-62	2C, 5W
SC5D6	gi 3172115	beta-ketoadipate enol-lactone hydrolase (Acb)	3.0e-5	1C
SM1H6	CAB02709	C01G10.7 (similar to citrate lyase beta chain) (Ce)	3.1e-15	1M
NM6F5	P34085	citrate synthase, mitochondrial precursor (Nc)	1.1e-99	1M
NP6C12	P43635	citrate synthase 3 (Sc)	5.7e-27	1P
NP2A2	CAA20783	cytochrome c oxidase, subunit VIa (Sp)	1.0e-17	2P
SC7G9	P00427	cytochrome c oxidase polypeptide VI precursor (Sc)	4.0e-23	2C, 1M
NM1B3	gi 2443751	fumarase (At)	2.0e-60	2M, 1P
SM2H1	P27680	hexaprenyldihydroxybenzoate methyltransferase (Sc)	2.1e-5	1M
NP3E9	P28299	isocitrate lyase (Nc)	1.5e-49	1M, 1P
W08E4	P17505	malate dehydrogenase, mitochondrial precursor (Sc)	1.2e-38	1P, 2W
NM8D3	CAB41986.1	64kD mitochondrial NADH dehydrogenase (Nc)	7.0e-54	2M
W06E1	P11913	mitochondrial processing peptidase beta subunit precursor (Nc)	7.6e-48	1W
NP3A11	P36060	NADH-cytochrome B5 reductase precursor (Sc)	1.8e-14	1M, 1P
SC3A5	Q03015	NADH-ubiquinone oxidoreductase 12 kD subunit precursor (Nc)	1.3e-54	2C
SM1F6	P42116	NADH-ubiquinone oxidoreductase 17.8 kD subunit precursor (Nc)	2.2e-83	1M
SP6B10	P25711	NADH-ubiquinone oxidoreductase 21 kD subunit precursor (Nc)	7.0e-47	1P
SC6G8	P24917	NADH-ubiquinone oxidoreductase 51 kD subunit precursor (Nc)	2.0e-35	1C
SP4F8	O13931	putative ATP synthase J chain, mitochondrial (Sp)	3.0e-6	1P
NC3D2	P33287	pyruvate decarboxylase (cfp gene product) (Nc)	2.0e-107	10C, 1M, 2W
SC5F1	P37298	succinate dehydrogenase membrane anchor subunit precursor (Sc)	1.0e-5	1C
NC1F7	Q00711	succinate dehydrogenase (ubiquinone), flavoprotein subunit of complex II (Sc)	8.4e-57	1C
SC6G6	O42772	succinate dehydrogenase (ubiquinone), iron sulfur protein (Mg)	4.0e-48	1C, 1M
SC5H11	O13750	succinyl-CoA ligase, alpha chain precursor (Sp)	6.0e-18	1C, 1M
W13H10	P53312	succinyl-CoA synthetase, beta-chain precursor (Sc)	8.0e-25	2W
W01C7	pir S56285	sulfite reductase (Sc)	9.2e-36	1M, 2W
NM4C4	P00128	ubiquinol-cytochrome C reductase complex, 14 kD protein (complex III, subunit VII) (Sc)	1.3e-32	1M
NC2A1	P00127	ubiquinol-cytochrome C reductase complex, 17 kD protein (mitochondrial hinge protein) (Sc)	8.7e-13	1C, 1M
W10H7	P48503	ubiquinol-cytochrome C reductase complex subunit VIII (Nc)	2.7e-65	1C, 1W
SC7F10	P07056	ubiquinol-cytochrome C reductase Rieske iron-sulphur protein (Nc)	4.0e-50	1C, 1M
Lipid				
NC4G6	P15937	acetyl-CoA hydrolase (acu-8) (Nc)	2.5e-11	1C
SC1A4	Q04677	acetyl-Coenzyme A acetyltransferase (Ct)	3.9e-52	3C
SP6B1	CAA75926.1	acetyl-Coenzyme A carboxylase (En)	8.0e-78	1C, 1P

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W09H5	BAA13434	acetyltransferase (Aspa)	8.0e-67	1W NM4B3
	NP_005460.1	peroxisomal acyl-CoA thioesterase (Hs)	5e-15	1M
SC7E12	gi 3859560	acyl-protein thioesterase (Hs)	8.0e-8	1C
NM7A4	CAA96522.1	AMP-binding protein (Bn)	2.0e-27	1M
NP3D7	gi 2970667	beta-ketoacyl reductase (Psae)	3.5e-11	1P
NC1F6	gi 1161339	C-4 sterol methyl oxidase (Sc)	4.2e-38	2C
SP6F8	gi 1478048	cytochrome 450 monooxygenase (Dm)	4.0e-6	1P SP6G6
	BAA10929	cytochrome P450-like (Nt)	1.0e-7	1P
SC1E5	BAA11409	cytochrome P450 nor2 (Cl)	1.4e-49	1C
NM5B12	P25087delta (24)	sterol C-methyltransferase (Sc)	3.3e-38	1M
NM1B4	P19262	dihydrolipoamide succinyltransferase, mitochondrial (Sc)	8.3e-97	1M
NP3F2	NP_010580	dihydrosphingosine phosphate lyase (Sc)	2.0e-13	1P
SM3E6	CAB10453	enoyl-CoA hydratase (At)	2.0e-20	1M, 1P
NP4C6	P15368	fatty acid synthase, subunit alpha (Pnp)	2.2e-24	1P
SM1B1	P30839	fatty aldehyde dehydrogenase, microsomal, class 3 (Rn)	1.4e-13	1M
NM1C7	gi 348167	glycerol kinase (Hs)	8.4e-44	1M
NC5B9	pir A32937	glycerol-3-phosphate dehydrogenase (Dm)	4.9e-10	1C, 1P
NM3A1	P18900	hexaprenyl pyrophosphate synthetase (Sc)	1.1e-49	1M
NP3B8	P288113	hydroxyisobutyrate dehydrogenase (Psae)	8.1e-8	1P
SP7C9	Q10132	isopentyl-diphosphate delta isomerase (Sp)	3.0e-41	1P
NM5E11	Q05493	3-ketoacyl-CoA thiolase, peroxisomal (Yl)	1.0e-26	1M SP7D3
	AAD49559.1	linoleate diol synthase precursor (Gg)	7.0e-27	1P
SP1D3	P30624	long-chain fatty-acid-CoA ligase (Sc)	5.9e-65	3P
SP3B11	Q02253	methylmalonate semialdehyde dehydrogenase precursor (Rn)	9.3e-13	1P
NM4H8	pir S54786	multifunctional beta-oxidation protein (Nc)	2.7e-133	1M, 1P
SC5D5	gi 3152731	myo-inositol 1-phosphate synthase (Hv)	1.0e-5	1C
NC4H10	CAB10120.1	putative aldose reductase (Sp)	1.0e-15	1C
SP4C7	CAB11656.1	putative oxysterol binding protein (Sp)	9.0e-30	1P, 1W SC3C11
	CAA91416.1	similar to gamma-butyrobetaine, 2-oxoglutarate dioxygenase (Ce)	7.0e-9	1C
NP3H4	CAB52620.1	similar to phosphatidic acid phosphatase (Sp)	4.0e-13	1P SM4H12
	pir S52745	stearoyl-Coenzyme A desaturase (Ac)	9.0e-50	2C, 1M
SP3B10	CAA66277.1	sterol carrier protein x (Dm)	6.0e-21	1P
W10D7	P24640	triacylglycerol lipase (Mor)	1.6e-10	1W
NP4D5	pir S57337	trichodiene oxygenase 4 (Fs)	4.1e-34	1P
Nucleotide				
W07E5	P49435	adenine phosphoribosyltransferase (Sc)	4.0e-40	1M, 1W
W17C5	CAA75628	adenosine kinase (Pp)	9.2e-34	2W
SC2C3	P27604	adenosylhomocysteinase (Ce)	9.5e-49	1C, 1M, 1W
SM1G2	P32518	deoxyuridine 5'-triphosphate nucleotidohydrolase (Le)	1.4e-46	1M
SC1F7	gi 522302	endonuclease (Mg)	7.4e-21	1C
SM2E5	P38913	FAD synthetase (FMA adenylyltransferase) (Sc)	8.6e-25	1M
W07E2	CAA72985.1	GTPase (Sp)	3.0e-14	1W
SP6C3	P19117	inorganic pyrophosphatase (Sp)	6.0e-67	1C, 1P, 2W
SP4E4	P08466	mitochondrial nuclease (Sc)	2.8e-9	1P
NM2D1	Q05927	5' nucleotide precursor (ECTO-nucleotidase) (Bt)	2.0e-15	1P
SC6B6	Q99148	phosphoribosylamine-glycine ligase (GARS) (Yl)	2.0e-21	1C, 1P
SC2D12	P54113	phosphoribosylaminoimidazolecarboxamide formyltransferase (Sc)	2.4e-40	3C, 2W
SC5A4	Q01930	phosphoribosylaminoimidazole carboxylase (Pm)	2.6e-23	1C
NC2G7	P27602	phosphoribosylaminoimidazolesuccinocarboxamide synthase (Cm)	2.9e-35	1C
SC2A9	P38972	phosphoribosylformylglycinamide synthase (Sc)	9.8e-5	1C
W17G1	P04161	phosphoribosylglycinamide formyltransferase (Sp)	2.0e-18	2W

Clone ID ^a	MatchAcc ^b	Identification ^c	<i>P/E</i> value ^d	Tissues ^e
W07E10	P50095	probable inosine-5'-monophosphate dehydrogenase (Sc)		7.0e-35 1W NP5A12
	NP_010376	putative member of nontransport group of ATP-binding cassette (ABC) superfamily, Rli1 (Sc)		9.0e-65 1P
NC5G9	P23921	ribonucleoside-diphosphate reductase, M1 chain (Hs)		9.4e-45 1C
NC3E7	AAD40852.1	sirtuin, type 4 (Hs)		9.0e-9 1C
NP2C3	NP_003738	tankyrase, TRF-1-interacting ankyring-related ADP-ribose polymerase (Hs)		7.0e-11 1P
SC1G12	Q00511	uricase (Aspfl)		1.8e-41 1C
SM3A6	P27515	uridine kinase (Sc)		1.0e-47 1M
		Protein Modification		
SP7C6	P42158	casein kinase 1, delta isoform (At)		7.0e-21 1P
		Secondary Metabolism		
NP4F6	P32021	1-aminocyclopropane-1-carboxylate oxidase (Pss)		2.2e-10 1P
SP4A5	BAA12723	dihydroflavonol 4-reductase (Rh)		5.8e-13 1P
NP2G2	P16543	granaticin polyketide synthase (Strv)		3.8e-6 1P
NP4A9	P55441	hypothetical monooxygenase Y4FC (Rhz)		7.0e-32 1P
NP3C2	AAA33590	laccase (Nc)		2.2e-79 3P
SP4G5	pir S60224	melanin biosynthetic polyketide synthase PKS1 (Ctl)		2.1e-83 7M, 25P
NC3C12	AAD37457.1	NonF, nonactin biosynthesis (Strg)		3.0e-12 1C
NP5A6	P23262	salicylate hydroxylase (Pspt)		3.1e-7 1P
NP2G9	pir S41412	tetrahydroxynaphthalene reductase (Mg)		1.8e-88 2M, 7P
		Sugar/Glycolysis		
NC4C1	P41747	alcohol dehydrogenase 1 (Aspfl)		1.4e-66 7C, 2M, 2P, 1W
SC3H8	P38426	alpha, alpha-trehalose-phosphate synthase (Sc)		1.7e-28 1C
NM9B11	P21567	alpha-amylase precursor (Sf)		1.0e-23 1C, 1M
NC1E1	P327751.4	alpha-glucan branching enzyme (Sc)		9.7e-25 3C
NM1E6	Q12558	alpha-glucosidase precursor (maltase) (Aspo)		6.0e-73 1M, 1C
SM1G4	pir JC4836	alpha-glucuronidase (Trr)		1.7e-27 1M
SC2A7	Q00310	alpha-1,2-mannosyltransferase (Ca)		4.8e-14 1C
SM3H7	BAA29031	avicelase III (Aspac)		3.0e-48 1M
SP6F3	CAA05375.1	beta-1,3 exoglucanase (Trh)		3.0e-24 1C, 1P, 1W
SC5H10	gi 1491929	1,3-beta-D-glucan synthase catalytic subunit (En)		1.0e-50 1C
NP3B6	gi 493580	beta-D-glucoside glycohydrolase (Trr)		1.7e-92 5M, 1P
SP4D6	Q00023	cellulose-growth-specific protein precursor (Ab)		4.0e-15 1P
W01G4	gi 1154950	choline dehydrogenase (Rr)		5.3e-13 1W
NM2B6	CAB16581	dihydroxyacetone kinase (Sp)		5.0e-12 2M
NP4G12	P31382	dolichyl-phosphate-mannose--protein mannosyltransferase (Sc)		3.8e-58 1P
SC1H2	Q12560	enolase (Aspo)		8.0e-73 10C, 1P, 2W
NM1D6	Q07103	formate dehydrogenase, NAD-dependent (Nc)		1.0e-43 1M
W08E12	P53444	fructose 1,6 biphosphate aldolase (Nc)		4.3e-73 4C, 1M, 3W
NP3H2	P32604	fructose-2,6-bisphosphatase (Sc)		6.0e-90 2M, 1P
NP4D10	P08431	galactose-1-phosphate uridylyltransferase (Sc)		1.3e-8 1P
NM6H8	P49426	glucan 1,3-beta-glucosidase (Cc)		6.5e-37 1M, 3P
NM6B8	P14804	glucan 1,4-alpha-glucosidase (Nc)		3.0e-100 3M
W10H9	Q92407	glucokinase (Aspn)		1.5e-51 1W
W07H8	P53704	glucosamine-fructose-6-phosphate aminotransferase (Ca)		7.7e-8 1W
W07G12	pir S54720	glucose-6-phosphate dehydrogenase (Aspn)		4.0e-74 1C, 2W
NC2H9	gi 1532189	glyceraldehyde-3-phosphate dehydrogenase (Nc)		1.3e-120 25C, 2M, 1P, 47W
SM1F7	pir S61144	glycogen phosphorylase (Sc)		2.3e-75 2C, 5M, 4P
SC5B4	CAA08922.1	hexokinase (Aspn)		6.0e-38 2C, 1P
W01C8	P41734	isoamyl acetate-hydrolyzing esterase (Sc)		5.0e-8 4W
W01C1	gi 2266941	isocitrate dehydrogenase (NAD+ specific), mitochondrial subunit 1 precursor (Ac)		1.2e-20 1C, 1W

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NM1D7	gi 606352	maltodextrin phosphorylase (Ec)		7.6e-16 1M
SC5A11	Q02418	mannitol-1-phosphate 5-dehydrogenase (Sm)		3.0e-25 6C
SP1A12	BAA76558.1	Mok12, an alpha-glucan synthase (Sp)		1.0e-27 1P
W07A4	AAD43564.1	pectate lyase (Cg)		6.0e-24 1W
SM3H9	O43112	phosphoenolpyruvate carboxykinase (ATP) (Kl)		3.0e-68 1M
SC6G11	P387206	phosphogluconate dehydrogenase (Sc)		1.0e-48 1C, 1P
NC3D6	P38667	phosphoglycerate kinase (Nc)		2.2e-116 7C, 2W
NC2D12	gi 1673879	phosphoglycerate mutase (Mp)		2.3e-27 6C
W10B3	P31353	phosphomannomutase (Ca)		4.1e-52 1W
NM2H6	P29951	phosphomannose isomerase (En)		1.9e-35 1M
SC1C5	CAA19114	putative betaine-aldehyde dehydrogenase precursor (Sp)		2.0e-5 1C
SC5D9	CAA18655.1	putative mannose-1-phosphate guanyltransferase (Sp)		4.0e-41 1C
SC5C2	P16387	pyruvate dehydrogenase, E1 comp., alpha subunit (Sc)		2.2e-35 1C, 1M, 2W
SC5E2	P32473	pyruvate dehydrogenase, E1 comp., beta subunit (Sc)		2.0e-24 1C
NM6D2	gi 1016358	pyruvate formate lyase activating protein (Tl)		1.3e-12 1M
NC4C8	P31865	pyruvate kinase (Trr)		2.1e-51 3C, 1M, 1P
W13F7	P46969	ribulose-phosphate 3-epimerase (Sc)		2.6e-28 1W
SM1H9	P87218	sorbitol utilization protein, SOU1 and SOU2 (Ca)		9.5e-37 1M, 1W
NC3G5	P45055	transaldolase (Hi)		2.6e-65 1C, 1M, 2W
SC5C12	CAA21881.1	transketolase (Sp)		4.0e-69 3C, 1M, 2W
NC2D9	P04828	triosephosphate isomerase (En)		9.6e-68 8C, 1M, 1W
NC5C3	pir A54926	UDP glucose 6-dehydrogenase, 52 kD subunit (Bt)		1.2e-19 1C
Transport				
W09A5	P02723	ADP/ATP carrier protein (Nc)		1.9e-104 2C, 3M, 5P, 15W
W10D1	P40260	ammonium transporter MEP1 (Sc)		2.1e-17 2M, 1W
SP1A4	CAB06078	AmMst-1, monosaccharide transporter (Am)		8.0e-33 2P
NM1H8	AAC09237.1	annexin XIV (Nc)		1.0e-128 3M
NM8C11	CAA65259.1	canalicular multidrug resistance protein, cMrp (Hs)		4.3e-26 1M, 1P
NP4A3	CAB44434.1	carnitine/acyl carnitine carrier (En)		3.0e-55 1P
SM1B7	P53048	general alpha-glucoside permease (Sc)		6.2e-21 1M
SC7G7	P32836	GTP-binding nuclear protein GSP2/CNRs (Sc)		2.0e-28 1C
NM5F6	gi 1139591	H ⁺ /Ca ²⁺ exchange protein, vacuolar (Sc)		1.5e-26 1M
SM4A3	AAF26275.1	hexose transporter (Aspp)		1.0e-36 2M, 1P
SP3C1	O74713	high-affinity glucose transporter (Ca)		3.0e-6 1C, 1P
NM3A10	Q09887	hypothetical amino-acid permease (Sp)		2.2e-7 1M
NC3G12	Q02821	importin alpha subunit (Sc)		2.5e-13 1C
NM4E7	AAD53168.1	iron-transporter Fth1p (Sc)		8.0e-29 2M
NM7D6	AAA97590.1	Lpz1lp, hypothetical protein similar to mitochondrial carrier protein family (Sc)		2.9e-16 1M
NP5D11	P35848	mitochondrial import receptor subunit (Nc)		1.0e-84 1P
NP3E4	NP_012579	mitochondrial matrix protein involved in protein import; subunit of SceI endonuclease (Sc)		2.0e-63 2C, 1M, 1P
W06D9	P23641	mitochondrial phosphate carrier protein (Sc)		1.9e-8 1W
NM5B3	AAD44697.1	MUM2 (Hs)		9.0e-18 1M
NM7B1	CAA90827	nuclear transport protein Nip1 (Sc)		4.8e-21 1M
NC1D11	P07144	outer mitochondrial membrane protein porin (Nc)		1.6e-114 3C, 1M, 1W
SP2A11	P46030	peptide transporter PTR2 (Ca)		1.6e-18 1P
SP6E7	P07038	plasma membrane ATPase (proton pump) (Nc)		1.0e-81 2M, 2P
NC3E5	P40024	probable ATP-dependent transporter, ABC transporter protein (Sc)		1.7e-53 1C
NM6G6	O74431	probable cation-transporting ATPase (Sp)		1.0e-33 1M W17H1
	CAB65616.1	probable membrane transporter (Sp)		5.0e-14 1W
SP6A4	gi 2197050	putative 20 kD subunit of the V-ATPase (Nc)		2.0e-79 3M, 4P
SP6B8	gi 3885836	putative cercosporin transporter (Ck)		1.0e-12 1P

Clone ID ^a	MatchAcc ^b	Identification ^c	<i>P/E</i> value ^d	Tissues ^e
NP6E6	CAA21891.1	putative Golgi membrane protein-sorting protein (Sp)	7.0e-25	1P SP4F1
	CAA21303.1	putative Golgi uridine diphosphate-N-acetylglucosamine transporter (Sp)	2.0e-10	1P
SC5E1	P38988	putative mitochondrial carrier protein YHM1/SHM1 (Sc)	3.0e-25	1C, 1P
NM4A10	P38702	putative mitochondrial carrier protein YHR002W (Sc)	1.6e-28	1M NM4G4
	gi 805291	putative tartrate transporter (Av)	5.6e-30	1M
SC5A7	O13879	putative transporter C1B3.15C (Sp)	1.0e-5	1C
W17B2	CAA19115.1	RANBP7/importin-beta/Cse1p superfamily protein (Sp)	1.3e-43	1W
SP6C8	BAA13080.1	RAN/spi1 binding protein (Sp)	1.0e-41	1P, 1W
NM1C1	NP_015353	similar to human polyposis locus protein (YPD) (Sc)	4.0e-24	1C, 2M
NM7A7	gi 1066487	similar to mitochondrial ADP/ATP carrier protein (Sc)	6.0e-9	1M NM6B3
	CAB52718.1	similar to yeast component of COPII coat of ER-Golgi vesicles, SEC24 (Sp)	5.0e-33	1M
W01B12	P39111	vacuolar ATP synthase 14 kD subunit (Sc)	1.7e-25	1W
SM4C6	P31413	vacuolar ATP synthase 16 kD proteolipid subunit (Nc)	7.0e-40	1M, 1W
NM7G11	P11592	vacuolar ATP synthase catalytic subunit A (Nc)	2.5e-61	2C, 1M
NM7B4	P11593	vacuolar ATP synthase subunit B (Nc)	9.1e-79	1M, 1P
SC6H4	AAD45120.1	V-type ATPase subunit c' (Nc)	6.0e-40	1C
NC5G10	gi 1814380	V-type ATPase subunit G (Nc)	3.8e-43	1C
NM1E10	NP_013231	Zrt2p, low-affinity zinc transport protein (Sc)	3.0e-19	1M

VI. Protein Synthesis

Post-translational Modification/Targeting

NM4D4	P36581	calnexin homolog precursor (Sp)	8.6e-53	1C, 1M, 1W
SC1F12	P35605	coatamer beta subunit (Bt)	1.5e-43	1C
SP6B11	P87140	coatamer gamma subunit (Sp)	9.0e-49	1C, 1M, 1P
W07H12	BAA34384.1	cyclophilin (Trm)	5.0e-56	1C, 1W
NM6G8	P32469	diphthine synthase, DPH5 (Sc)	6.0e-47	1M
NC3C7	JC2291	disulfide-isomerase (Hui)	5.5e-59	2C, 1W
W13F2	P28748	GTP-binding nuclear protein SPII (Sp)	4.6e-7	3W
NM4C2	P36586	GTP-binding protein, YPT1-related protein 5, ypt5 (Sp)	3.6e-61	1C, 2M
NP2C4	P33723	GTP-binding protein, YPT1-related protein (Nc)	2.8e-95	1P
SM2A1	P36863	GTP-binding protein YPTV4 (Vc)	5.0e-36	1M
SC2D6	CAA17784.1	hypothetical ubiquitin system (Sp)	4.0e-7	1C
NP6C4	pir A23543	methylumbelliferyl-acetate deacetylase (Hs)	6.7e-61	2C, 1M, 2P
NC1F1	P33755	Np14 protein (Sp)	2.9e-39	1C
NP5F8	Q99144	peroxisomal targeting signal receptor (peroxisomal protein pay32) (YI)	4.3e-10	1P
NP4C9	NP_015173	similar to phosphotyrosyl phosphatase activator Rrd2p (Sc) SC3D1	2.0e-26	1P
gi 1723924		probable ubiquitin-protein ligase HUL5 (Sc)	3.0e-26	1C
SM4B11	P53024	protein transport protein SEC13 (Pip)	5.0e-40	2M
W09C6	Q10243	putative 35.8 kD vacuolar sorting protein C4G9.13C (Sp)	1.4e-21	1W
NP4F1	gi 1619843	rab2-like (Ce)	2.9e-10	1P
NM4H12	P46638	ras-related protein Rab11b (Mm)	3.0e-96	1M, 2W
SC5C11	Q40195	ras-related protein Rab11E (Lj)	5.0e-11	1C
SP4E3	AAD29715.1	ring-box protein 1 (Hs)	2.0e-45	1P
NC4H5	P39940	rsp5 protein (Sc)	2.0e-21	1C
W17F1	P45816	SEC14 cytosolic factor (YI)	7.3e-56	1W
NM4H10	P32916	signal recognition particle receptor (Sc)	8.6e-46	1M
W10B7	gi 2507637	SNARE protein Ykt6 (Hs)	4.3e-15	2W
SP6F9	CAA39056.1	ubiquitin-activating enzyme E1 (Sc)	3.0e-49	1P, 1W
NC2H3	CAB52608.1	ubiquitin carboxyl-terminal hydrolase-like protein (Sp)	2.0e-32	2C
NM1B5	P46595	ubiquitin conjugating enzyme (Sp)	1.2e-96	2C, 6M, 1P
NP3F9	pir UQNC	ubiquitin precursor (Nc)	1.2e-99	2C, 3M, 1P, 5W

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NC1C11	pir UQNCR	ubiquitin/ribosomal protein S27a (Nc)		9.8e-71 1C
NM8G8	gi 1244555	UDP-Glc:glycoprotein, glucosyltransferase (Sp)		7.8e-57 1M NM6H3
	gi 790621	Ufd1p (ubiquitin fusion degradation) (Sc)		7.3e-30 1M
NM1G1	gi 1477468	vacuolar protein sorting homolog r-vps33a (Rn)		3.3e-14 1M
Protein Turnover				
SM2A12	P37898	alanine/arginine aminopeptidase (Sc)		1.4e-45 1M
SM2A9	BAA00258.1	alkaline protease (Aspo)		1.3e-40 1M, 1P
SM3B3	P36774	ATP-dependent protease LA2 (Mx)		2.0e-23 1M
NM9C12	AAC96121	carboxypeptidase Y precursor (Pa)		7.0e-37 3M, 2P, 1W
SC3D10	gi 2408232	lysosomal pepstatin insensitive protease (Hs)		5.3e-5 1C
NC1B9	P23724	potential proteasome subunit C5 (Sc)		1.1e-46 1C
SC2B12	P21243	proteasome component C7-alpha (Sc)		2.6e-23 1C
W13F9	P40303	proteasome component PRE6 (Sc)		7.4e-8 1W
SM2E10	Q09841	proteasome component PUP1 precursor (Sp)		7.5e-68 1M
SM4E12	P32379	proteasome component PUP2 (Sc)		2.0e-25 1M
W06F9	P53616	proteasome component SUN4 (Sc)		5.2e-23 1C, 2W
NP6D4	P23639	proteasome component Y7 (macropain subunit Y7) (Sc)		9.1e-20 1P
NM7B2	P38886	26S proteasome regulatory component SUN1 (Sc)		9.3e-40 1M, 1P NM6F3
	P43122	putative protease QR17 (Sc)		1.1e-7 1M
SM3D1	Q09682	putative proteasome component C9/Y13 (Sp)		5.0e-49 1M SP1B11
	gi 1469396	secreted aspartic proteinase precursor (Gc)		5.9e-6 1P
NM5D6	P33295	subtilisin-like serine protease PEPC precursor (Aspn)		1.0e-78 1C, 3M, 6P
NM8F11	NP_015433	subunit of regulatory particle of proteasome Rpn7p (Sc)		3.0e-7 1M
NM4F2	NP_011981.1	vacuolar aminopeptidase (Sc)		3.5e-34 1C, 1M
Ribosomal Proteins^g				
NP2B1	Q01291	40S ribosomal proteins (assorted) (Nc)		1.7e-131 71C, 11M, 6P, 58W
NC5F7	P1412660S	ribosomal proteins (assorted) (Sc)		2.0e-98 73C, 13M, 1P, 53W
tRNA Synthesis/Metabolism				
SC2B2	P04802	aspartyl-tRNA synthetase (Sc)		7.3e-20 1C
NC1F12	gi 171768	isoleucyl-tRNA synthetase (Sc)		9.7e-95 1C
SM1D7	P10857	leucyl-tRNA synthetase, cytoplasmic (Nc)		3.1e-70 1M
NM7D3	CAA19575.1	tRNA splicing endonuclease subunit (Sp)		1.0e-9 1M
NC2B1	Q12109	tryptophanyl-tRNA synthetase (Sc)		9.7e-30 1C
Translation Factors				
NM7H7	Q64252	eukaryotic translation initiation factor EIF-3, P48 (Hs)		3.0e-9 1M
NP5G8	P46943	GTP-binding protein Guf1 (Sc)		3.0e-45 1P
SP6G12	Q10425	probable eukaryotic translation initiation factor EIF-3, P90 subunit (Sp)		3.0e-5 1P
SM4C5	Q09689	probable eukaryotic translation factor EIF-5 (Sp)		5.0e-8 1M
NM6E1	gi 961482	translation elongation factor 1, alpha (Nc)		1.9e-118 9C, 5M, 4P, 9W
NC1A10	P34826	translation elongation factor 1, beta (Oc)		2.3e-40 2C, 1M
NM6D9	pir S29345	translation elongation factor 1, gamma (Sc)		9.7e-36 3C, 1M
NM3E7	P32324	translation elongation factor 2 (Sc)		1.2e-92 8C, 3M, 3P
NP5E5	P47943	translation initiation factor 4A (Sp)		1.6e-105 2C, 2P, 3W
NM6C9	P23588	translation initiation factor 4B (Hs)		7.7e-6 1M, 1W
SP7B8	gi 3253159	translation initiation factor EIF-2C (Oc)		3.0e-9 1P SC6E9
	P79083	translation initiation factor EIF-3, P39 subunit (Sp)		2.0e-26 2C
NC5E11	gi 2351380	translation initiation factor EIF-3, P40 subunit (Hs)		3.6e-28 1C

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VII. RNA Synthesis				
RNA Polymerases				
NM5H4	P27999	DNA-directed RNA polymerase II, 14.2 kD (Sc)	4.8e-12	1M
SC6D4	P37382	DNA-directed RNA polymerase II, 33 kD (Sp)	3.0e-41	1C
RNA Processing				
SP7E5	NP_014287	ATP-dependent RNA helicase of DEAD box family (Sc)	3.0e-44	1P
W13A6	P15646	fibrillarin (nucleolar protein 1) (Sc)	4.7e-64	1W
W17F11	Q06975	GAR1 protein (Sp)	9.3e-33	1W
NM9H12	BAA25324.1	Moc2 RNA helicase (Sp)	4.0e-74	1M, 1P
NM6B12	gi 495128	nuclear poly(C)-binding protein (mCBP) (Mm)	6.1e-12	1M
NC3F12	gi 459650	poly(A) binding protein (Tc)	3.0e-8	1C, 1M W08D5
	Q07478	probable ATP-dependent RNA helicase P47 homolog (Sc)	1.9e-9	1W
SC1G4	P32843	RNA12 protein (Sc)	4.2e-8	1C
NM3H6	gi 172438	RNA-binding protein (Sc)	6.6e-10	1M NC2A10
	pir S31443	RNA-binding protein, glycine-rich (At)	9.1e-18	2C, 2P
NM3D5	Q00539	RNA-binding protein involved in mitochondrial RNA splicing, NAM8 (Sc)	5.4e-41	1M
SP4F4	CAA21234.1	RNA binding protein, putative pre mRNA splicing factor (Sp)	2e-21	2M, 1P
W08D9	P20449	RNA helicase Dbp5 (Sc)	2.0e-10	1W
Transcription Factors				
NM5E12	P07250	arginine metabolism regulation protein III (Sc)	1.2e-8	1M
SP4A1	gi 1517923	ascospore maturation 1 protein (Nc)	2.0e-70	1P, 2W
NM5F11	P36627	cellular nucleic acid binding protein (byr3) (Sp)	1.3e-33	1M
W01D5	P11115	cross-pathway control protein 1 (Nc)	6.1e-71	6C, 9M, 3P, 3W
SP1B4	Q04832	DNA-binding protein Hexbp (Lm)	2.0e-13	1P
W13E1	NP_009930	FMN-binding protein (Sc)	4.0e-11	1W
NM4D1	CAA19036.1	fungal Zn(2)-Cys(6) binuclear cluster zinc finger transcription factor (Sp)	4.0e-6	1M
NP3F1	gi 1176420	Hmp1 (Um)	7.2e-7	1P
W17H5	Q99160	homeobox protein HOY1 (YI)	1.2e-12	1W
W08G4	P43588	MPR1 protein (Sc)	7.8e-13	1W
NP3E6	P33181	probable sucrose utilization protein SUC1 (Ca)	9.8e-11	1P
NM5D7	Q09818	putative general negative regulator of transcription (Sp)	1.6e-29	1M
NC1B4	CAA22288	putative mitosis and maintenance of ploidy protein (Sp)	2.0e-7	1C
NM1F10	CAB11180.1	putative snf2 family helicase (Sp)	4.0e-62	1M
NC5D8	CAB10003.1	putative transcriptional activator (Sp)	4.0e-5	1C
NM7E9	gi 2367591	putative transcriptional regulator (Mg)	1.1e-34	1M, 1W
SC5A10	P78706	rco-1 gene product (Nc)	7.3e-52	1C, 1P
NC1H4	gi 1947129	similar to CCAAT/enhancer-binding protein (Ce)	3.8e-7	1C, 3M, 10P
W10A9	gi 2826519	STE12 alpha (Fn)	8.7e-21	1W
NP6F9	gi 1147800	Sug2p, putative transcriptional co-activator (Sc)	9.9e-94	1P
NM7H5	P47192	synaptobrevin-related protein (formerly called homeotic protein HAT24) (At)	1.4e-14	1M
SP4D5	NP_011967	Tra1p (ATM/Mec1/TOR1+2-related) (Sc)	1.0e-8	1P
W08B1	CAB11717.1	transcription factor BTF3 homolog (Sp)	7.4e-34	1M, 1W
W07H6	Q01371	white collar 1 protein (Nc)	4.6e-7	1W
NP5F3	CAA67549.1	zinc finger protein (Ai)	3.8e-67	1C, 2M, 1P
SP1E6	gi 498734	zinc finger protein HZF8, Krueppel-related (Hs)	7.1e-11	1P
Unclassified^h				
Clock-Controlled Genes				
SM4C4	Q01358	BLI-3 protein (Nc)	1.0e-44	1M
NP5G7	P22151	ccg-1, glucose-repressible gene protein (Nc)	2.2e-44	11M, 6P, 7W

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NC2C2	Q04571	ccg-2 (hydrophobin precursor; rodlet protein; blue light induced protein 7) (Nc)		2.3e-57 17C
NM9C1	gi 1184781	ccg-4, putative polypeptide 1 or 2 (Nc)		4.3e-59 1C, 18M, 5P
NM9D7	gi 1184784	ccg-6, putative polypeptide (Nc)		3.6e-23 5C, 2M, 2P, 13W
Related to Putative ORF in <i>S. cerevisiae</i>				
SM4B6	NP_009348	ORF YAL053w, hypothetical 87.5 kD protein		1.0e-18 1M
NM5F5	P38248ORF	YBR0727, hypothetical 48.3 kD protein homologous to Sps2p		6.0e-9 1M
NP5E3	P38286ORF	YBR159w		2.8e-19 1P
W13F11	P38297ORF	YBR179c, hypothetical ATP binding protein		5.3e-13 1C, 1W
SM4D11	P25618ORF	YCR017c, hypothetical 107.9 kD protein		4.0e-35 1M
SM3F3	CAA98605	ORF YDL045w-a		5.0e-8 1M
NM9A6	pir S51251	ORF YDR100w, probable membrane protein YD8557.09		1.1e-12 1M
NM6A12	gi 1078218	ORF YDR105c, hypothetical protein YD9727.01c		2.9e-29 1M
SC2E5	NP_010573	ORF YDR287w, hypothetical protein with similarity to inositol monophosphatases		1.6e-17 1C
NP2B7	NP_010617	ORF YDR330w		1.0e-38 1P
SM3G10	gi 1230675	ORF YDR348c, hypothetical protein		9.0e-12 1M
SM1D3	pir S69637	ORF YDR470c, hypothetical protein with similarity to chromosome segregation protein Cse1p		1.1e-70 1M
NM8G11	pir S56248	ORF YFL006w		8.7e-27 1M, 1P
SC2E9	P53173ORF	YGL054c, hypothetical 15.9 kD protein		1.2e-15 1C
SP1E11	P53134ORF	YGL114w, hypothetical 80.0 kD protein		1.4e-35 1P
NM6B4	CAA97021.1	ORF YGR033c		5.6e-13 1M
NM7F2	P32793ORF	YHR016c, SH3 domain containing protein		4.5e-13 1M
NM5G5	P38860ORF	YHR168w, hypothetical GTP-binding protein		3.8e-26 1M
NP4E4	P47111ORF	YJR044c, probable membrane protein		3.7e-32 1P SC1G9
	P47179ORF	YJR151c, hypothetical 118.4 kD protein		1.2e-18 1C
NM2E7	pir S37791	ORF YKL160w		4.4e-14 1M
NP3F11	CAA97471	ORF YLL023c		1.2e-13 2P
SM3G11	gi 609375	ORF YLR228c, probable membrane protein		4.0e-8 1M
SP6C2	pir S59397	ORF YLR251w, probable membrane protein		2.0e-18 1P
NP3A2	Q06063	ORF YLR405w, hypothetical 41.7 kD protein		8.1e-7 1P
SC7E5	NP_013755	ORF YMR041c, hypothetical 38.2 kD protein		2.0e-7 1C
NM3E5	pir S55125	ORF YMR178w, putative protein YM8010.08		1.3e-39 1M
SC2F7	Q04336	ORF YMR196w, hypothetical 126.6 kD protein		3.7e-77 2C
SM4A12	Q03655	ORF YMR215w, hypothetical 56.8 kD protein		4.0e-41 3M, 1P
W17A10	Q05016	ORF YMR226c, hypothetical oxidoreductase		7.0e-23 1M, 2W
NC2B4	P40157ORF	YNL212w, hypothetical 88.8 kD protein		1.8e-47 1C
W07G1	P40345ORF	YNR008w, hypothetical 75.4 kD protein		2.9e-26 1W
NP3F12	CAA99053.1	ORF YOL048c		5.1e-11 1P
W01C11	pir S66771	ORF YOL078w, hypothetical protein		5.0e-5 1W
NP2E2	gi 1420338	ORF YOR131c		7.9e-9 1P
SP1C8	pir S67089	ORF YOR197w		3.8e-26 1M, 1P
W17G6	pir S57544	ORF YPR011c, probable membrane protein		1.7e-20 1W
SP6D5	pir S54084	ORF YPR063c, probable membrane protein		1.0e-5 1P
NM6F11	NP_015480.1	ORF YPR154w, SH3 domain-containing protein		1.3e-7 3M
Related to Other Putative ORFs				
W08A4	BAA29511	440 a.a. long hypothetical protein (Pyh)		8.0e-14 1W
W06B9	Z99167.1	chromosome I cosmid C3G6 (Sp)		8.0e-12 ^f 4W
SC5F11	AAD35882.1	conserved hypothetical protein (AE001747) (Tm)		9.0e-11 1C, 2M
SM2D11	CAA22272.1	conserved hypothetical protein (AL034381) (Sp)		6.0e-14 1M
SC2E4	CAB53730.1	conserved hypothetical protein (AL110295) (Sp)		5.0e-9 1C
SC1A9	CAA21253.1	conserved hypothetical protein, Phd finger (Sp)		2.0e-17 1C
NM5D9	CAB16281.1	conserved hypothetical protein (Z99167) (Sp)		2.0e-27 1M

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NM1E1	gi 868225	F35D11.3 gene product (Ce)		1.4e-21 1M
SC6C6	gi 4226060	H04M03.4 protein (Ce)		3.0e-7 1C
SM3D3	Q22700	hypothetical 6.3 kD protein T23F2.3 (Ce)		8.0e-14 1M
W07A7	Q10167	hypothetical 8.2 kD protein C26A3.14C (Sp)		9.9e-12 1W
SM2E11	Q09896	hypothetical 13.5 kD protein C24B11.09 (Sp)		3.4e-41 1M W07C6
	P54607	hypothetical 24.7 kD protein, CSPB-GLPP intergenic (Bs)		3.1e-7 1W
SP4E5	O13725	hypothetical 26.5 kD protein C15A10.05c (Sp)		1.0e-23 1P
NP3B11	P53806	hypothetical 26.6 kD protein F54E7.7 (Ce)		2.0e-7 1P
W07E3	Q10010	hypothetical 26.6 kD protein T19C3.4 (Ce)		1.2e-5 1W
W13A9	Q10446	hypothetical 27.0 kD protein C12B10.13 (Sp)		4.1e-20 1W
NM2D12	Q09686	hypothetical 28.0 kD protein C13C5.04 (Sp)		5.5e-36 1M
SM2E3	P46218	hypothetical 31.5 kD protein (Sa)		6.0e-6 1M
W17E12	pir JC4256	hypothetical 32.0 kD protein (Nc)		1.4e-67 1W
SC5E3	Q10212	hypothetical 34.8 kD protein C4H3.04C (Sp)		3.0e-9 1C
SC2H7	Q10562	hypothetical 40.6 kD protein CY31.34 precursor (Mt)		1.7e-5 1C
SM4D8	Q09895	hypothetical 43.7 kD protein C24B11.08c (Sp)		3.0e-7 1M
NC1E7	Q09906	hypothetical 49.3 kD protein (Sp)		2.7e-29 1C
SC3G4	Q10478	hypothetical 51.8 kD protein C17C9.06 (Sp)		5.7e-14 1C
SM1G9	Q09744	hypothetical 63.9 kD protein C12C2.03C (Sp)		3.4e-36 1M
SP4A7	Q10211	hypothetical 74.5 kD protein (Sp)		6.2e-28 2P
NM5G4	Q09778	hypothetical 103.4 kD protein in C22F3.13 (Sp)		3.9e-5 1M
SP4C1	Q10064	hypothetical 420.8 kD protein C1F5.11C (Sp)		1.2e-12 1P
NP4D9	AAF01525.1	hypothetical protein (AC0009991) (At)		3.0e-24 1P
W01B2	CAA17792.1	hypothetical protein (AL022070) (Sp)		3.3e-13 1W
W17A11	CAA18310.1	hypothetical protein (AL022245) (Sp)		1.1e-37 2W
SM4A10	CAA20062	hypothetical protein (AL031154) (Sp)		3.0e-29 1M
SM3D8	CAB40177.1	hypothetical protein (AL049559) (Sp)		2.0e-19 1M, 1P
NP4G3	CAB60706.1	hypothetical protein (AL132798) (Sp)		1.0e-34 1P
SC7A11	CAB61580.1	hypothetical protein (AL133206) (Hs)		5.0e-13 1P
SC1F8	Q10342	hypothetical protein (C19G10.16) (Sp)		4.0e-9 1C
NC1H3	BAA18808	hypothetical protein (D90917) (Syn)		3.0e-33 1C
SC7H7	CAB11476.1	hypothetical protein (Z98762) (Sp)		1.0e-9 1C
NM8D1	CAB16230.1	hypothetical protein (Z99162) (Sp)		4.0e-12 1M
NM6D5	BAA34509.1	KIAA0789 protein (Hs)		4.0e-12 1M
W06E6	CAA20238	membrane protein with histidine rich charge clusters (Hs)		7.0e-13 1W
NM1A1	gi 1145409	ORF of unknown function (Sp)		1.8e-7 1M
SM2C6	CAB02772.1	predicted using Genefinder (Z81039) (Ce)		1.0e-7 1M
SP6C1	CAB05297.1	predicted using Genefinder (Z82285) (Ce)		8.0e-6 1P
NM3F5	O53426	proline-rich antigen homolog (Mt)		5.0e-6 1M
SM4F10	BAA12197	similar to pir:S52731 (Sp)		3.0e-26 1M
SC7G8	CAB02797.1	similar to yeast hypothetical protein YEY6 like (Ce)		5.0e-22 1C
SM2A6	gi 3676056	unknown ORF (En)		5.0e-18 1M
SM2A3	AAD32806.1	unknown protein (AC007660) (At)		1.0e-10 1M
NM6A11	AAF01586.1	unknown protein (AC009895) (At)		4.0e-13 1M
SP6D4	BAA19234.1	YNL157 homolog (Sp)		4.3e-7 1P
		Other genes, unclassified		
SC5A3	gi 2944191	acetyl xylan esterase II precursor (Pnpur)		6.0e-9 1C
NP3C8	gi 604427	AcoB protein (En)		2.2e-14 1P
NM2D11	CAA21790	carbonic anhydrase (Sp)		1.0e-24 1M
NP3C7	AAF13817.1	CARP (Oc)		8.0e-6 1P
NM3D8	P501972,5-dichloro-1,5-cyclohexadiene-1,4-diol	dehydrogenase (Spp)		1.0e-21 1M
NM6F12	gi 606960	lectin (Ab)		4.0e-13 7M, 1P
SC5B5	P53998	LET1 protein (Km)		4.0e-17 1C
SC1H6	P42058	minor allergen Alt A VII (Aa)		7.0e-64 2C, 1P
NC1F4	gi 2253310	myb-1 (Nc)		1.0e-28 1C, 1M

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SM2C11	gi 1353701	N33 protein (Hs)		2.5e-7 1M
NM9B2	P43076	pH responsive protein 1 precursor (Ca)		7.4e-42 2M
NM5C6	CAB45367.1	putative hydrolase (Strc)		2.0e-12 1M, 1W
W10D9	CAA04959	rAsp f4 (allergen) (Aspfu)		2.7e-11 1W
SM2B5	P40900	sexual differentiation process protein isp4 (Sp)		6.9e-29 1M SC2A3
	CAA10960.1	small glutamine-rich tetratricopeptide protein (SGT) (Rn)		9.9e-6 1C
W01H10	P35691	translationally controlled tumor protein homolog (Sc)		1.1e-44 1W
SP1E5	CAA73975	Vip1 protein (p53-related protein) (Sp)		1.1e-29 1P