

Special Papers

Neurospora proteome 2000

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The filamentous fungus, *Neurospora crassa*, has an eminent history as a central organism in the elucidation of the tenets of classical and biochemical genetics. Of particular significance are the experiments of George Beadle and Edward Tatum in the 1940s with *N. crassa* that led to the "one gene-one enzyme" hypothesis (Beadle and Tatum 1941 Proc. Natl. Acad. Sci. USA 27:499-506). In six decades, over 1,000 genes have been mapped and characterized (Perkins, Radford and Sachs 2000 *The Neurospora Compendium: Chromosomal Loci*. Academic Press; Perkins 2000 Fungal Genet. Newsl., this volume), but that leaves perhaps 10,000 or more genes not yet identified by classical genetics. High-throughput, automated partial sequencing of cDNA libraries to generate expressed sequence tags (ESTs) allows for the rapid identification and characterization of preferentially expressed genes in different tissues, as well as the discovery of novel genes (Adams *et al.* 1991 Science 252:1651-1656; Okubo *et al.* 1992 Nature Genet. 1:173-179).

In 1995, the first systematic analysis of the *Neurospora* genome was undertaken by the *Neurospora* Genome Project at the University of New Mexico (Nelson *et al.* 1997 Fungal Genet. Biol. 21:348-363). Initially, three cDNA libraries were constructed for this project, using mRNA isolated from conidial (germinating asexual spores), starved mycelial (branching hyphae), and perithecial (fertilized fruiting bodies) tissues. Single-pass, partial sequencing of cDNA clones was used to determine the nature of the encoded products. Following the initial phase, subtractive hybridization was used to remove the most abundantly expressed genes from the cDNA libraries. In addition, a fourth cDNA library (Westergaard) was constructed using mRNA from unfertilized tissue grown under mating conditions (Westergaard and Mitchell 1947 Amer. J. Botany 34:573-577). cDNA clones from these subtracted libraries (conidial, mycelial and perithecial) and the Westergaard library have been sequenced and analyzed in this, the second phase of the *Neurospora* Genome Project at UNM.

The *Neurospora* Proteome represents the first systematic, functional classification of the known genes of a filamentous fungus. Proteome refers to the complement of proteins expressed by a genome or tissue. In order to identify putative protein homologs to the expressed genes of *Neurospora*, the BLASTX algorithm (Altschul *et al.* 1990 J. Mol. Biol. 215:403-410; Altschul *et al.* 1997 Nucl. Acids Res. 25:3389-3402) was used to translate each EST nucleotide sequence into the six possible reading frames and compare the predicted protein sequences with the protein sequence database available through the National Center for Biotechnology Information (NCBI, Bethesda, MD). Low complexity regions that could generate artificially high scores were removed by filtering, using the SEG program available through NCBI. The database matches were divided into groups according to statistical significance values (P or E values): highly significant (P/E values = 10⁻²⁰), moderately significant (10⁻⁵ to 10⁻¹⁹), weakly significant (10⁻² to 10⁻⁴), and not statistically significant (>10⁻²).

A total of 3,397 cDNA clones were analyzed for this version of the *Neurospora* Proteome (summarized in Table 1). Significantly more highly and moderately significant matches were detected in the conidial and Westergaard libraries (66.5% and 70.0%, respectively) than in the mycelial and perithecial libraries (37.0% and 40.5%). Correspondingly fewer cDNAs showing no similarity to any previously characterized genes were present in the conidial and Westergaard libraries (33.5% and 30.0%, respectively), while the mycelial and perithecial libraries had greater percentages of cDNAs encoding apparently novel genes (63.0% and 59.5%, respectively).

Those cDNA clones encoding products with highly or moderately significant matches in the NCBI nonredundant (nr) database are identified in Table 2, for a total of 680 different genes. They are categorized according to the classification scheme utilized by the Expressed Gene Anatomy Database, or EGAD, developed at The Institute for Genomic Research (TIGR, Rockville, MD), and available at: http://www.tigr.org/docs/tigr-scripts/egad_scripts/role_report.spl (White and Kerlavage 1996 Methods Enzymol. 266:24-40). Division into these major functional categories (I-VII) facilitates examination of the tissue-specific expression of functional classes of genes.

The pattern of tissue-specific gene expression has remained very similar to that identified in the first phase of the *Neurospora* Genome Project (Nelson *et al.* 1997 Fungal Genet. Biol. 21:348-363). The majority of identified genes from all four libraries encode products involved in metabolism or protein synthesis. Interestingly, the new Westergaard library appeared to mirror the conidial library in its pattern of expression, e.g., of genes involved in sugar metabolism, 38% and 50% were in the Westergaard and conidial libraries, respectively, and genes for ribosomal proteins were 39.4% and 49.6%, respectively. 80% of

the genes involved in secondary metabolism were found only in the perithecial library, and the remaining 20% were from the mycelial library. An unexpected finding was the high expression of the *nmt1* and *nmt2* genes, particularly *nmt1*, in unfertilized sexual tissue (the Westergaard library). 10.4% of the Westergaard cDNA clones are *nmt1* homologs, as compared with 1.1%, 0.3% and 0.1% of the conidial/subtracted conidial, mycelial/subtracted mycelial and perithecial/subtracted perithecial libraries, respectively. Both of these genes encode products involved in the biosynthesis of thiamine (Maundrell 1990 J. Biol. Chem. 265:10857-10864; Manetti *et al.* 1994 Yeast 10:1075-1082).

The burgeoning field of genomics has provided molecular biologists a revolutionary opportunity for large-scale study of complete genomes, their transcriptional expression patterns, and the products encoded by identified genes, i.e., the proteome. The *Neurospora* Proteome represents the systematic, *in silico* classification of those genes that appear to be expressed in specific developmental stages of *N. crassa*, as well as the first of what will likely be many such proteomes of the filamentous fungi.

Acknowledgements

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Table 1: Summary of cDNA clones^a

Library ^b	Percent with Putative Identification	Percent Previously Uncharacterized (Novel)	Number cDNAs Analyzed
Conidial (C)	66.5%	33.5%	872
Mycelial (M)	37.0%	63.0%	1,104
Perithecial (P)	40.5%	59.5%	730
Westergaard (W)	70.0%	30.0%	691
Total	52.90	48.0%	3,397

^aThose cDNAs with P/E values equal to or less than 10^{-5} were classified as encoding proteins with putative identifications, while those with P/E values greater than 10^{-5} were classified as novel genes.

^bEach library includes clones from both subtracted and unsubtracted libraries.

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	P22126	24 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

Clone ID ^a	MatchAcc ^b	Identification ^c	P/E value ^d	Tissues ^e
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	P40319	SUR4 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	P35169	TOR1, 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 (Trb)	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

Clone ID ^a	MatchAcc ^b	Identification ^c	P/E value ^d	Tissue ^e
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/peroxidase (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 Hsp70 (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

Clone ID ^a	MatchAcc ^b	Identification ^c	P/E value ^d	Tissues ^e
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	nm1 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

Clone ID ^a	MatchAcc ^b	Identification ^c	P/E value ^d	Tissues ^e
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	fumarate (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

Clone ID ^a	MatchAcc ^b	Identification ^c	P/E value ^d	Tissues ^e
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	P25087	delta (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	P28811	3-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	P/E 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 (Rh)	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 (Psp)	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	P32775	1,4-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 bisphosphate 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

Clone ID ^a	MatchAccb	Identification ^c	P/E value ^d	Tissues ^e
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	P38720	6-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 guanylyltransferase (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	Lpz11p, 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 Scl 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	P/E 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/Cselp 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 SPI1 (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) (Yl)	4.3e-10	1P
NP4C9	NP_015173	similar to phosphotyrosyl phosphatase activator Rrd2p (Sc)	2.0e-26	1P
SC3D1	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 (Yl)	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

Clone ID ^a	MatchAcc ^b	Identification ^c	P/E value ^d	Tissues ^e
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				
NP2B1	Q01291	40S ribosomal proteins (assorted) (Nc)	1.7e-131	71C, 11M, 6P, 58W
NC5F7	P14126	60S 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

Clone ID ^a	MatchAcc ^b	Identification ^c	P/E value ^d	Tissues ^e
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 (Yl)	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	cgg-1, glucose-repressible gene protein (Nc)	2.2e-44	11M, 6P, 7W

Clone ID ^a	MatchAcc ^b	Identification ^c	P/E value ^d	Tissues ^e
NC2C2	Q04571	cgc-2 (hydrophobin precursor; rodlet protein; blue light induced protein 7) (Nc)	2.3e-57	17C
NM9C1	gi 1184781	cgc-4, putative polypeptide 1 or 2 (Nc)	4.3e-59	1C, 18M, 5P
NM9D7	gi 1184784	cgc-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	P38248	ORF YBR0727, hypothetical 48.3 kD protein homologous to Sps2p	6.0e-9	1M
NP5E3	P38286	ORF YBR159w	2.8e-19	1P
W13F11	P38297	ORF YBR179c, hypothetical ATP binding protein	5.3e-13	1C, 1W
SM4D11	P25618	ORF 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	P53173	ORF YGL054c, hypothetical 15.9 kD protein	1.2e-15	1C
SP1E11	P53134	ORF YGL114w, hypothetical 80.0 kD protein	1.4e-35	1P
NM6B4	CAA97021.1	ORF YGR033c	5.6e-13	1M
NM7F2	P32793	ORF YHR016c, SH3 domain containing protein	4.5e-13	1M
NM5G5	P38860	ORF YHR168w, hypothetical GTP-binding protein	3.8e-26	1M
NP4E4	P47111	ORF YJR044c, probable membrane protein	3.7e-32	1P
SC1G9	P47179	ORF 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	P40157	ORF YNL212w, hypothetical 88.8 kD protein	1.8e-47	1C
W07G1	P40345	ORF 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

Clone ID ^a	MatchAcc ^b	Identification ^c	P/E value ^d	Tissues ^e
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 YFY6 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	P50197	2,5-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

Clone ID ^a	MatchAcc ^b	Identification ^c	<i>P/E</i> value ^d	Tissues ^e
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

Legend and Footnotes to Table 2:

The EGAD cellular role classification scheme (White and Kerlavage 1996 Methods Enzymol. 266:24-40) has been used whenever possible. Those identified *Neurospora* ORFs lacking homologs in the EGAD classification were classified as appropriate under Secondary metabolism, etc. Only those sequences with BLASTX *P/E* values of 10^{-5} or lower (highly or moderately significant) are reported in this table, except as noted. Fourteen sequences falling within this range were determined to reflect spurious matches (e.g., proline-rich regions) and not actual homology; those sequences were not included in this table. As additional sequence information becomes available, expanded versions of this table can be accessed at our web site: <http://www.unm.edu/~ngp/>.

^a A single representative clone ID is given in those cases in which multiple (duplicate) cDNAs have been identified.

^b MatchAcc generally indicates the best match (identified by its accession number) to a sequence in the NCBI nonredundant protein database; however, in those cases in which the best match was to an unidentified open reading frame, a less optimal match to an identified sequence is shown.

^c Identification refers to the reported match in the NCBI protein database. The organism of the best match is indicated in parenthesis (see list of abbreviations below).

^d The BLASTX *P/E* value is that obtained with the respective *Neurospora* cDNA clone and the sequence identified in the MatchAcc and Identification columns.

^e The tissues from which the respective cDNAs were isolated are identified, where C indicates conidial, M denotes mycelial, P is perithecial and W is Westergaard (unfertilized sexual tissue). The number preceding these abbreviations indicates the number of duplicate cDNAs isolated from each tissue.

^f The BLASTN *P* value is reported. The corresponding BLASTX *P* value was greater than 10^{-5} , and so was not considered significant (see text).

^g The following 40S ribosomal proteins were identified: MRP2, P40 homolog B, RP10, RP41, S2-18, S20-22, S24-28, S30-31, S33 and the putative ribosome-associated protein similar to ribosomal protein SA. The identified 60S ribosomal proteins included: L1-5, L7, L9-19, L22-23, L25-30, L32, L35, L37, L39-40 and the acidic ribosomal proteins P0, P1 and P2.

^h The unclassified genes do not include genes identified only by putative homology to ESTs.

Aa, <i>Alternaria alternata</i>	Pa, <i>Pichia angusta</i>
Ab, <i>Agaricus bisporus</i>	Pg, <i>Pyricularia grisea</i>
Ac, <i>Ajellomyces capsulatus</i>	Phi, <i>Phytophthora infestans</i>
Acb, <i>Acinetobacter</i> sp.	Pip, <i>Pichia pastoris</i>
Ae, <i>Alcaligenes eutrophus</i>	Pm, <i>Pichia methanolica</i>
Al, <i>Ascobolus immersus</i>	Pnch, <i>Penicillium chrysogenum</i>
Am, <i>Amanita muscaria</i>	Pnci, <i>Penicillium citrinum</i>
Aspa, <i>Aspergillus awamorii</i>	Pnj, <i>Penicillium janthinellum</i>
Aspac, <i>Aspergillus aculeatus</i>	Pnp, <i>Penicillium patulum</i>
Aspfl, <i>Aspergillus flavus</i>	Pnpur, <i>Penicillium purporogenum</i>
Aspfu, <i>Aspergillus fumigatus</i>	Pp, <i>Physcomitrella patens</i>
Aspn, <i>Aspergillus niger</i>	Psae, <i>Pseudomonas aeruginosa</i>
Aspo, <i>Aspergillus oryzae</i>	Pspc, <i>Pseudomonas paucimobilis</i>
Aspp, <i>Aspergillus parasiticus</i>	Pspt, <i>Pseudomonas putida</i>
At, <i>Arabidopsis thaliana</i>	Pss, <i>Pseudomonas syringae</i>
Av, <i>Agrobacterium vitis</i>	Pyh, <i>Pyrococcus horikoshii</i>
Bn, <i>Brassica napus</i>	Rh, <i>Rosa hybrida</i>
Bs, <i>Bacillus subtilis</i>	Rhrh, <i>Rhodococcus rhodochrous</i>
Bt, <i>Bos taurus</i>	Rhz, <i>Rhizobium</i> sp.
Ca, <i>Candida albicans</i>	Rn, <i>Rattus norvegicus</i>
Cc, <i>Cochliobolus carbonum</i>	Rr, <i>Rattus rattus</i>
Ce, <i>Caenorhabditis elegans</i>	Sa, <i>Sulfolobus acidocaldarius</i>
Cg, <i>Colletotrichum gloeosporioides</i> (valvae)	Sc, <i>Saccharomyces cerevisiae</i>
Ci, <i>Coccidioides immitis</i>	Sf, <i>Saccharomycopsis fibuligera</i>
Ck, <i>Cercospora kikuchii</i>	Sm, <i>Streptococcus mutans</i>
Cl, <i>Cylindrocarpum lichenicola</i>	Som, <i>Sordaria macrospora</i>
Cm, <i>Candida maltosa</i>	Sp, <i>Schizosaccharomyces pombe</i>
Ct, <i>Candida tropicalis</i>	Spp, <i>Sphingomonas paucimobilis</i>
Ctl, <i>Colletotrichum lagenarium</i>	Ssd, <i>Sus scrofa domestica</i>
Cum, <i>Cucurbita maxima</i>	Strc, <i>Streptomyces coelicolor</i>
Dd, <i>Dictyostelium discoideum</i>	Strg, <i>Streptomyces griseus</i>
Dm, <i>Drosophila melanogaster</i>	Strr, <i>Streptomyces reticuli</i>
Dr, <i>Deinococcus radiodurans</i>	Strv, <i>Streptomyces violaceoruber</i>
Ec, <i>Escherichia coli</i>	Syn, <i>Synechocystis</i> sp.
En, <i>Emericella nidulans</i>	Tc, <i>Trypanosoma cruzi</i>
Fn, <i>Filobasidiella neoformans</i>	Tl, <i>Thermococcus litoralis</i>
Fo, <i>Fusarium oxysporum</i>	Tm, <i>Thermatoga maritima</i>
Fs, <i>Fusarium sporotrichioides</i>	Trh, <i>Trichoderma harzianum</i>
Galg, <i>Gallus gallus</i>	Trm, <i>Trichophyton mentagrophytes</i>
Gc, <i>Glomerella cingulata</i>	Trr, <i>Trichoderma reesei</i>
Gg, <i>Gaeumannomyces graminis</i> (graminis)	Um, <i>Ustilago maydis</i>
Hh, <i>Halobacterium halobium</i>	Vc, <i>Volvox carteri</i>
Hi, <i>Haemophilus influenzae</i>	Yl, <i>Yarrowia lipolytica</i>
Hp, <i>Hansenula polymorpha</i>	
Hs, <i>Homo sapiens</i>	
Hui, <i>Humicola insolens</i>	
Hv, <i>Hordeum vulgare</i>	
Km, <i>Kluyveromyces marxianus</i> var. <i>lactis</i>	
Le, <i>Lycopersicon esculentum</i>	
Lj, <i>Lotus japonicus</i>	
Lm, <i>Leishmania major</i>	
Ma, <i>Metarhizium anisopliae</i>	
Mg, <i>Magnaporthe grisea</i>	
Mm, <i>Mus musculus</i>	
Mor, <i>Moraxella</i> sp.	
Mp, <i>Mycoplasma pneumoniae</i>	
Mt, <i>Mycobacterium tuberculosis</i>	
Mx, <i>Myxococcus xanthus</i>	
Nc, <i>Neurospora crassa</i>	
Nh, <i>Nectria haematococca</i>	
Nt, <i>Nicotiana tabacum</i>	
Oc, <i>Oryctolagus cuniculus</i>	
Os, <i>Oryza sativa</i>	