

SUPPLEMENTAL TABLE S2. Identified proteins and normalized relative abundance calculated by NSAF. Proteins are ordered by differential presence on microsomes (decreasing G-score values). Blue cells: over-represented on sorbitol; orange cells: over-represented on xylose. BR: biological replicate; NSAF: normalized spectral abundance factor; Sorb: sorbitol addition; TMD: transmembrane domains; Xyl.: xylose addition.

LOCUS TAG	NCBI/JGI DESCRIPTION	TMD	LENGTH AMINO ACIDS	SPECTRAL COUNTS				NSAF.10 ⁴		G-score
				Sorb.		Xyl.		Sorb	Xyl.	
				BR1	BR2	BR1	BR2			
An18g06700	strong similarity to proteasome 20S subunit Pre7 - <i>Saccharomyces cerevisiae</i>	0	260	0	0	14	17	0.5	21.9	26.20
An04g09170	strong similarity to valosin-containing protein like AAA-ATPase Cdc48 - <i>Saccharomyces cerevisiae</i>	0	820	3	1	93	2	1.4	21.0	20.47
An01g09960	xylosidase xlnD - <i>Aspergillus niger</i>	0	804	0	0	41	19	0.2	13.6	17.28
An15g00510	strong similarity to proteasome 20S subunit C2 - <i>Rattus norvegicus</i>	0	262	0	0	10	11	0.5	14.8	16.83
An01g03740	D-xylose reductase xyrA - <i>Aspergillus niger</i>	0	319	0	0	20	2	0.4	12.7	14.57
An10g00820	strong similarity to carboxyphosphoenolpyruvate phosphonmutase bcpA - <i>Streptomyces hygroscopicus</i>	0	299	20	32	104	43	45.7	89.0	14.17
An16g02130	similarity to novel cell death-regulatory protein GRIM19 - <i>Mus musculus</i>	0	109	0	1	5	7	3.6	20.7	13.33
An02g10790	strong similarity to proteasome 20S subunit Pre6 - <i>Saccharomyces cerevisiae</i>	0	270	0	0	8	8	0.5	11.0	11.95
An02g12510	strong similarity to plasma membrane H(+)-ATPase pmaA - <i>Aspergillus nidulans</i> [putative frameshift]	9	990	6	14	50	76	5.4	23.1	11.81
An04g05640	mitochondrial proton-pumping NADH:ubiquinone reductase nuo51 - <i>Aspergillus niger</i>	0	496	1	11	32	35	6.6	24.5	11.08
An01g12210	strong similarity to core protein I of ubiquinol--cytochrome-c reductase β -MPP - <i>Neurospora crassa</i>	0	479	9	16	56	42	13.9	37.1	11.00
An07g08300	cyclophilin-like peptidyl prolyl cis-trans isomerase cypA - <i>Aspergillus niger</i>	0	174	14	29	13	18	65.1	32.7	10.95
An16g03590	strong similarity to phosphatidylinositol-phosphatidylcholine transfer protein Sec14 - <i>Saccharomyces cerevisiae</i>	0	322	8	7	1	1	12.5	1.4	10.22
An01g03820	strong similarity to ER protein-translocation complex subunit Sbh2 - <i>Saccharomyces cerevisiae</i>	1	127	7	5	1	4	25.6	7.8	9.99
An11g06720	strong similarity to proteasome 20S subunit Pre9 - <i>Saccharomyces cerevisiae</i>	0	255	0	0	7	6	0.5	9.6	9.91
An07g09990	strong similarity to heat shock protein 70 hsp70 - <i>Ajellomyces capsulatus</i> [putative frameshift]	0	637	89	88	61	80	72.5	40.1	9.49
An02g12270	strong similarity to glycine-rich RNA-binding protein grrbp2 - <i>Euphorbia esula</i>	0	116	6	4	3	1	23.6	7.0	9.48
An05g02300	similarity to secreted protein SEQ ID NO:127 from patent WO200061779-A1 - <i>Homo sapiens</i>	1	290	0	2	17	5	2.2	14.0	9.47
An02g07040	strong similarity to proteasome 20S subunit Scl1 - <i>Saccharomyces cerevisiae</i>	0	244	1	0	6	10	1.6	12.2	9.23
An16g04770	strong similarity to aldo/keto reductase Gcy1 - <i>Saccharomyces cerevisiae</i>	0	319	12	8	4	2	16.7	3.7	9.04
An18g05980	strong similarity to GTP-binding protein rho1p - <i>Schizosaccharomyces pombe</i>	0	193	11	13	47	18	33.0	61.2	8.56
An18g06800	strong similarity to proteasome 20S subunit Pre10 - <i>Saccharomyces cerevisiae</i>	0	274	3	0	8	15	3.3	15.5	8.52
An07g02010	strong similarity to proteasome 20S subunit Pre8 - <i>Saccharomyces cerevisiae</i>	0	279	3	0	9	14	3.3	15.2	8.36

An07g07390	strong similarity to subunit IV of cytochrome c oxidase Cox4 - <i>Saccharomyces cerevisiae</i>	0	194	2	5	15	14	10.1	27.4	8.36
An14g03400	ornithine carbamoyltransferase argB - <i>Aspergillus niger</i> [putative sequencing error]	0	371	8	15	2	6	16.5	4.1	7.92
An12g05040	similarity to hypothetical protein lin-10 - <i>Caenorhabditis elegans</i> -	0	99	1	2	0	0	9.2	0.9	7.90
An18g00950	weak similarity to hypothetical acetyltransferase MK0549 - <i>Methanopyrus kandle</i> -	0	251	8	7	5	0	16.1	4.0	7.86
An06g01890	similarity to histidine triad protein Hnt1 - <i>Saccharomyces cerevisiae</i> -	0	135	3	4	1	1	14.5	3.3	7.49
An02g03400	strong similarity to proteasome 20S subunit Pup2 - <i>Saccharomyces cerevisiae</i>	0	246	0	0	4	6	0.5	7.7	7.48
An01g03570	strong similarity to cytochrome-b5 reductase Mcr1 - <i>Saccharomyces cerevisiae</i>	0	322	6	14	36	28	16.6	36.1	7.44
An01g12420	strong similarity to cytoplasmic ribosomal protein of the large subunit L17 - <i>Rattus norvegicus</i>	0	184	27	14	14	19	58.7	32.8	7.40
An07g03070	strong similarity to mitochondrial carrier protein ARALAR2 - <i>Homo sapiens</i>	0	695	5	20	58	38	9.5	25.0	7.20
An18g05020	strong similarity to cytoplasmic ribosomal protein of the large subunit Rpl27 - <i>Saccharomyces cerevisiae</i>	0	135	9	13	9	7	43.4	22.0	7.08
An09g06670	strong similarity to suppressor gene of mitochondrial histone Yhm2 - <i>Saccharomyces cerevisiae</i>	0	316	0	6	13	17	5.4	17.4	6.72
An07g10010	strong similarity to mitochondrial carrier protein Yhm1 - <i>Saccharomyces cerevisiae</i>	0	309	2	7	18	19	8.0	21.9	6.71
An09g03300	xylosidase AxlA, with strong similarity to α -xylosidase XylS - <i>Sulfolobus solfataricus</i>	0	736	0	0	13	10	0.2	5.8	6.64
An08g10530	strong similarity to mitochondrial aconitate hydratase Aco1 - <i>Saccharomyces cerevisiae</i>	0	777	4	5	48	8	3.2	13.1	6.50
An08g08740	strong similarity to cytoplasmic ribosomal protein of the small subunit S18 - <i>Homo sapiens</i>	0	155	19	20	13	21	66.3	40.2	6.50
An04g02470	strong similarity to GTP-binding protein ypt5p - <i>Schizosaccharomyces pombe</i>	0	218	0	0	6	2	0.6	7.0	6.39
An11g11030	strong similarity to cytoplasmic ribosomal protein of the large subunit L28 - <i>Saccharomyces cerevisiae</i>	0	149	10	10	9	5	35.8	17.6	6.37
An07g04570	strong similarity to hex1 - <i>Aspergillus nidulans</i> [putative frameshift]	0	216	19	22	14	19	50.0	28.0	6.31
An17g02330	strong similarity to phosphoglycerate dehydrogenase serA - <i>Escherichia coli</i>	0	480	18	20	6	14	20.9	7.7	6.31
An01g06180	strong similarity to cytochrome c1 of ubiquinol--cytochrome c reductase CYT-1 - <i>Neurospora crassa</i>	0	316	1	21	28	36	18.5	36.8	6.16
An08g01930	similarity to precursor of 3-oxoacyl-(acyl-carrier-protein) reductase - <i>Cuphea lanceolata</i>	0	338	0	0	10	1	0.4	6.1	6.12
An01g02500	strong similarity to thioredoxin - <i>Aspergillus nidulans</i>	0	108	5	4	1	4	22.9	9.2	6.05
An04g02070	strong similarity to clathrin heavy chain - <i>Bos taurus</i>	0	1711	108	98	34	108	31.4	15.0	5.91
An11g03340	acid α -amylase - <i>Aspergillus niger</i>	0	505	1	1	22	1	1.3	8.4	5.83
An06g01830	strong similarity to cytosolic leucine--tRNA ligase - <i>Neurospora crassa</i>	0	1126	2	1	41	3	0.8	7.1	5.78
An12g00020	strong similarity to D-lactate dehydrogenase dld - <i>Kluyveromyces lactis</i>	0	601	0	0	14	3	0.2	5.3	5.76
An09g03950	strong similarity to cytosolic tryptophan--tRNA ligase Wrs1 - <i>Saccharomyces cerevisiae</i> -	0	433	8	6	0	3	8.7	1.5	5.74
An14g00010	secretion related GTPase srgA - <i>Aspergillus niger</i>	0	206	0	0	6	1	0.6	6.6	5.70
An14g04080	strong similarity to iron-sulfur subunit of ubiquinol--cytochrome c reductase rip1p - <i>S.pombe</i>	0	238	6	9	28	16	16.9	33.7	5.66
An15g01710	strong similarity to F1Fo-ATP synthase subunit 7 ATP7 - <i>Kluyveromyces lactis</i>	0	173	2	12	15	23	21.8	40.1	5.51
An05g00140	similarity to signal recognition particle receptor β chain Srp102 - <i>Saccharomyces cerevisiae</i>	1	320	11	20	11	9	25.6	11.6	5.45
An02g11940	strong similarity to aminopeptidase METPRO02 from patent EP939131-A2 - <i>Homo sapiens</i>	0	497	3	0	11	14	1.8	9.3	5.43
An08g04240	strong similarity to alternative NADH:ubiquinone reductase NDH2 - <i>Yarrowia lipolytica</i>	0	567	1	4	21	12	2.5	10.7	5.40
An07g01290	strong similarity to xylitol dehydrogenase xdh - <i>Galactocandida mastotermitis</i>	0	369	24	24	23	13	34.2	17.8	5.23
An02g13840	strong similarity to cytoplasmic ribosomal protein of the small subunit S9 - <i>Homo sapiens</i>	0	193	24	21	24	17	61.4	38.8	5.13
An02g13850	strong similarity to cytoplasmic ribosomal protein of the large subunit Urp1 - <i>Saccharomyces cerevisiae</i>	0	158	7	5	5	2	20.6	8.6	5.11
An11g07020	similarity to hypothetical protein BAB52928.1 - <i>Mesorhizobium loti</i>	0	260	0	1	10	1	1.5	8.0	4.86
An09g06850	strong similarity to 78 kD subunit of NADH:ubiquinone reductase NDUFS1 - <i>Bos taurus</i>	0	737	6	42	59	73	17.1	32.4	4.80
An07g02180	strong similarity to dihydrolipoamide acetyltransferase Lat1 - <i>Saccharomyces cerevisiae</i>	0	675	7	71	31	27	30.3	15.6	4.75
An01g07200	similarity to N-acetylglucosaminyltransferases chain p110 - <i>Rattus norvegicus</i>	0	833	0	0	18	1	0.2	4.2	4.72

An11g00890	strong similarity to hypothetical protein Afu6g10450 - <i>Aspergillus fumigatus</i>	0	192	1	0	2	7	2.0	8.9	4.68
An08g01740	strong similarity to uronate dehydrogenase from patent DE19604798-A1 - <i>Saccharomyces cerevisiae</i>	0	298	0	0	7	1	0.4	5.1	4.67
An12g04940	strong similarity to mitochondrial heat shock protein Hsp60 - <i>Saccharomyces cerevisiae</i>	0	587	22	38	35	111	26.8	45.0	4.66
An07g06760	strong similarity to cytoplasmic ribosomal protein of the small subunit S20 - <i>Saccharomyces cerevisiae</i> -	0	116	3	2	1	1	12.3	3.9	4.63
An11g04870	strong similarity to ribonucleoprotein autoantigen Sm-D - <i>Homo sapiens</i>	0	121	0	0	3	1	1.1	6.7	4.54
An04g02460	strong similarity to heart muscle protein mitofilin HMP - <i>Homo sapiens</i>	1	631	1	15	28	31	6.8	17.0	4.52
An14g01010	strong similarity to cytoplasmic ribosomal protein of the large subunit L7 - <i>Saccharomyces cerevisiae</i>	0	273	26	20	27	13	44.3	26.8	4.39
An09g06250	strong similarity to vacuolar aminopeptidase Ysci - <i>Saccharomyces cerevisiae</i>	0	516	1	0	8	8	0.8	5.8	4.36
An10g00170	strong similarity to protein sequence 79 from patent WO0129221 - <i>Homo sapiens</i>	0	330	2	0	6	9	2.0	8.5	4.36
An16g08100	similarity to hypothetical ureidoglycolate hydrolase SPAC19G12.04 - <i>Schizosaccharomyces pombe</i> -	0	254	1	3	0	0	4.6	0.4	4.33
An01g00060	strong similarity to fatty acid synthase α subunit fas2p - <i>Schizosaccharomyces pombe</i>	0	1862	116	166	146	94	39.5	23.3	4.22
An01g04240	strong similarity to cytoplasmic acidic ribosomal protein P0 - <i>Saccharomyces cerevisiae</i>	0	312	16	10	53	12	22.1	37.9	4.19
An05g00160	strong similarity to cystathionine β -synthase Cys4 - <i>Saccharomyces cerevisiae</i> -	0	587	4	4	0	0	3.8	0.2	4.14
202202	strong similarity to actin-bundling protein Sac6, putative [<i>Neosartorya fischeri</i> NRRL 181]	0	644	16	19	10	9	14.3	5.5	4.13
An08g06540	strong similarity to antiproliferative protein prohibitin Phb1 - <i>Saccharomyces cerevisiae</i>	0	279	2	10	12	24	11.7	23.6	4.12
An07g03440	similarity to hypothetical protein YHR045w - <i>Saccharomyces cerevisiae</i>	2	564	3	7	32	9	4.8	13.3	4.08
An18g01000	similarity to hypothetical protein EAA30505.1 - <i>Neurospora crassa</i>	1	284	3	12	19	23	14.2	27.0	4.04
An01g04740	strong similarity to ribosomal protein of the large subunit L12 - <i>Mus musculus</i>	0	165	12	6	10	4	29.2	15.9	4.00
An02g12940	strong similarity to EST an 3344 - <i>Aspergillus niger</i> -	0	253	2	5	1	1	7.7	1.8	3.99
An11g11230	strong similarity to citrate transport protein Ctp1 - <i>Saccharomyces cerevisiae</i>	0	296	0	0	3	4	0.4	4.6	3.97
An02g03950	strong similarity to cytoplasmic ribosomal protein of the large subunit L3 - <i>Saccharomyces cerevisiae</i>	0	392	27	30	30	19	38.2	22.8	3.93
An06g01390	strong similarity to 21.3 kD subunit of NADH:ubiquinone reductase - <i>Neurospora crassa</i>	3	195	1	8	9	17	12.7	24.5	3.83
An01g08800	strong similarity to glutamine synthase Gln1 - <i>Saccharomyces cerevisiae</i>	0	375	25	11	75	10	25.3	41.1	3.79
An07g01640	strong similarity to calmodulin 6 CaM6 - <i>Arabidopsis thaliana</i> -	0	143	4	1	1	1	10.0	3.2	3.75
An02g01580	strong similarity to vesicular transport protein SEC17 - <i>Pichia pastoris</i>	0	294	1	6	16	9	6.6	15.6	3.75
An04g01870	strong similarity to proteasome 20S subunit Pre1 - <i>Saccharomyces cerevisiae</i> [putative sequencing error]	0	203	0	0	3	2	0.6	4.9	3.70
An01g03460	cytoplasmic ribosomal protein of the large subunit L15 rpl15 - <i>Aspergillus niger</i>	0	203	5	4	22	4	12.2	23.5	3.68
An11g09500	strong similarity to cytoplasmic ribosomal protein of the small subunit S4.e - <i>Saccharomyces cerevisiae</i>	0	258	26	28	30	22	55.0	36.7	3.66
An01g09840	strong similarity to hypothetical protein AN0630.2 - <i>Aspergillus nidulans</i>	1	74	0	1	3	2	5.3	13.4	3.66
An18g04310	strong similarity to cytoplasmic ribosomal protein of the small subunit S12 - <i>Sus scrofa</i>	0	150	4	2	15	3	11.3	22.2	3.66
An02g11440	strong similarity to hypothetical protein SPCC1450.12 - <i>Schizosaccharomyces pombe</i> -	0	919	2	15	2	1	5.0	0.7	3.64
An01g05800	similarity to lactone-specific esterase estf1 - <i>Pseudomonas fluorescens</i>	0	296	1	0	7	3	1.3	6.4	3.64
An03g06550	glucan 1,4- α -glucosidase glaA - <i>Aspergillus niger</i>	0	640	19	44	111	35	25.8	41.3	3.60
An13g01530	weak similarity to hypothetical protein ycnE - <i>Bacillus subtilis</i> -	0	102	1	2	1	0	8.9	2.7	3.59
An01g13600	strong similarity to mitochondrial phosphate transport protein Mir1 - <i>Saccharomyces cerevisiae</i>	0	314	15	41	57	59	46.8	66.9	3.57
An12g01190	strong similarity to syntaxin-related protein (T-SNARE) Sso2 - <i>Saccharomyces cerevisiae</i>	1	308	0	2	4	9	2.1	7.9	3.57
An02g07010	strong similarity to ubiquitin ubi1 - <i>Aspergillus nidulans</i>	0	154	0	0	4	0	0.8	5.3	3.57
An01g12810	similarity to BAX-associated protein fragment SEQ ID NO:242 from patent WO200264766-A2 - <i>Saccharomyces cerevisiae</i>	2	222	16	13	9	16	34.6	20.7	3.51
An04g00990	NADP-dependent glutamate dehydrogenase gdhA from patent WO9951756-A - <i>Aspergillus niger</i>	0	460	57	51	152	61	61.4	83.7	3.45

An02g11910	similarity to mitochondrial pyruvate dehydrogenase complex protein Pdx1 - <i>Saccharomyces cerevisiae</i>	0	289	4	24	16	6	25.7	14.0	3.45
An12g05360	strong similarity to cholesterol 24-hydroxylase - <i>Mus musculus</i>	0	569	32	50	22	51	37.7	23.3	3.45
An03g02430	strong similarity to mannitol dehydrogenase mtlD - <i>Pseudomonas fluorescens</i> -	0	488	3	8	3	0	6.1	1.3	3.43
An07g02800	strong similarity to hypothetical protein 2E4.30 - <i>Neurospora crassa</i> -	3	346	3	6	1	2	7.1	1.8	3.37
An16g08180	similarity to palmitylated serine/threonine kinase PKL12 - <i>Mus musculus</i> [putative frameshift]	0	375	0	1	8	3	1.0	5.5	3.37
An04g04970	strong similarity to Yta11 - <i>Saccharomyces cerevisiae</i>	1	803	0	4	11	17	1.5	6.4	3.36
An01g11340	strong similarity to methionyl aminopeptidase Map1 - <i>Saccharomyces cerevisiae</i> -	0	379	4	4	0	2	5.8	1.2	3.35
An06g01550	strong similarity to glucan synthase FKS - <i>Paracoccidioides brasiliensis</i>	16	1897	4	29	86	38	4.6	11.8	3.30
An18g06290	strong similarity to calcium P-type ATPase nca-1 - <i>Neurospora crassa</i>	9	1008	48	58	49	38	27.5	15.7	3.29
An16g08740	strong similarity to 17.8 kD subunit of NADH:ubiquinone reductase Nuo-17.8 - <i>Neurospora crassa</i>	0	172	0	1	3	4	2.3	7.9	3.27
An07g03850	strong similarity to transaldolase Tal1 - <i>Saccharomyces cerevisiae</i>	0	324	23	27	32	14	40.6	25.9	3.27
An03g04790	strong similarity to mitochondrial outer membrane protein Tom70 - <i>Podospora anserina</i>	1	629	8	13	37	26	8.9	18.2	3.27
An07g06030	strong similarity to coatomer γ subunit 2 copg2 - <i>Homo sapiens</i>	0	916	17	15	2	13	9.2	3.1	3.26
An07g03770	strong similarity to Cu Zn superoxide dismutase sodC - <i>Aspergillus fumigatus</i>	0	154	7	7	7	4	24.5	13.5	3.25
An16g07380	strong similarity to hypothetical cDNA MGC:7080 - <i>Mus musculus</i>	3	283	1	0	4	5	1.4	6.1	3.17
An08g10690	strong similarity to 40 kD subunit of NADH-ubiquinone reductase NUO-40 - <i>Neurospora crassa</i>	0	372	1	20	24	30	15.0	26.4	3.17
An09g05180	strong similarity to cytoplasmic ribosomal protein of the large subunit L4 - <i>Saccharomyces cerevisiae</i>	0	372	30	27	29	24	40.2	25.9	3.11
An02g12070	strong similarity to mitochondrial phosphate transport protein G7 - <i>Glycine max</i>	0	379	0	0	5	2	0.3	3.6	3.10
An02g05860	strong similarity to rac-family serine/threonine protein kinase homolog dagA - <i>Dictyostelium discoideum</i> -	0	626	6	6	1	2	5.2	1.0	3.09
An02g11680	strong similarity to translation initiation factor eIF-4A - <i>Schizosaccharomyces pombe</i>	0	398	24	15	15	17	25.8	14.7	3.08
An05g00110	strong similarity to hypothetical protein YNR020c - <i>Saccharomyces cerevisiae</i>	0	237	0	1	2	6	1.6	6.5	3.06
An04g03360	strong similarity to acidic Ca(2+)-independent phospholipase A2 aiPLA2 - <i>Rattus norvegicus</i>	0	212	7	3	2	4	12.9	5.5	3.02
An12g07830	strong similarity to cytoplasmic ribosomal protein of the large subunit L30 - <i>Kluyveromyces lactis</i>	0	159	6	3	2	4	15.6	7.4	2.98
An18g02900	strong similarity to hypothetical protein SPAC8A4.09c - <i>Schizosaccharomyces pombe</i> -	0	372	2	2	0	0	3.1	0.2	2.95
An11g04180	dnaK-type molecular chaperone bipA - <i>Aspergillus niger</i>	1	672	68	117	89	107	71.8	52.7	2.94
An16g07040	similarity to β -1,3-glucanosyltransferase bgt1 - <i>Aspergillus fumigatus</i> [truncated ORF]	0	423	1	3	17	2	2.8	8.3	2.91
An08g01590	similarity to membrane associated protein SLP-2 - <i>Homo sapiens</i>	0	436	1	5	9	15	3.9	10.1	2.89
An18g02170	strong similarity to mannosyltransferase Ktr5 - <i>Saccharomyces cerevisiae</i>	1	502	6	9	28	17	8.0	16.4	2.89
An04g07440	similarity to endoplasmic reticulum membrane protein Shr3 - <i>Saccharomyces cerevisiae</i> [truncated ORF]	3	192	6	13	8	8	26.4	15.5	2.88
An03g06880	strong similarity to carboxypeptidase Y-sorting protein Pep1 - <i>Saccharomyces cerevisiae</i>	2	1472	2	12	41	23	2.6	7.9	2.86
An12g08720	similarity to hypothetical protein AAG27909.1 - <i>Arabidopsis thaliana</i>	0	521	10	25	51	33	17.7	29.3	2.86
An14g04170	cytochrome c oxidase subunit V cox5 - <i>Aspergillus niger</i>	0	198	2	8	11	15	13.8	24.1	2.85
An03g04340	strong similarity to ER membrane translocation facilitator Sec61 - <i>Yarrowia lipolytica</i>	10	478	14	26	14	18	22.1	12.3	2.83
An07g08850	strong similarity to cytoplasmic ribosomal protein of the small subunit Rps11b - <i>Saccharomyces cerevisiae</i>	0	160	2	2	11	2	7.3	15.2	2.83
An02g07650	strong similarity to phosphoglucomutase pgmB - <i>Aspergillus nidulans</i> -	0	555	6	11	8	0	8.2	2.8	2.82
An02g12770	strong similarity to succinate dehydrogenase Sdh1 - <i>Saccharomyces cerevisiae</i>	0	646	8	46	72	51	22.0	34.5	2.80
An02g02530	strong similarity to ATP-dependent RNA helicase p68 - <i>Homo sapiens</i>	0	565	9	22	7	14	14.5	6.9	2.80
An12g04750	strong similarity to prohibitin Phb2 - <i>Saccharomyces cerevisiae</i>	1	306	4	8	11	22	10.6	19.7	2.78
An01g10880	similarity to F1F0-ATP synthase subunit g homolog Atp20 - <i>Saccharomyces cerevisiae</i>	0	198	3	3	6	12	8.5	16.9	2.77
An11g04620	strong similarity to proteasome 20S subunit Pup1 - <i>Saccharomyces cerevisiae</i>	0	272	0	0	3	2	0.5	3.6	2.76

An17g01420	strong similarity to hypothetical transport protein SPCC830.08c - Schizosaccharomyces pombe	3	169	21	15	11	26	56.2	40.0	2.73
An08g03450	strong similarity to 3-ketosphinganine reductase Tsc10 - Saccharomyces cerevisiae-	0	322	4	5	3	1	7.7	2.5	2.73
An18g04220	strong similarity to mitochondrial ADP/ATP carrier anc1p - Schizosaccharomyces pombe	4	319	29	85	96	111	93.4	117.3	2.72
An07g01470	strong similarity to hypothetical v-snare binding protein SPAC56F8.08 - Schizosaccharomyces pombe-	0	324	1	4	1	0	4.4	0.8	2.68
An01g02320	strong similarity to GTP-binding protein a-ras - Aspergillus nidulans	0	212	2	2	2	12	5.5	12.3	2.67
An02g01750	strong similarity to chaperone involved in mitochondrial protein import Mge1 - Saccharomyces cerevisiae	0	240	0	2	7	3	2.7	7.9	2.64
An16g07290	strong similarity to F1Fo-ATP synthase subunit 4 ATP4 - Kluyveromyces lactis	0	244	3	14	14	26	18.7	29.9	2.64
An04g08060	hypothetical protein	0	210	0	0	3	1	0.6	3.9	2.62
An04g09250	strong similarity to protein involved in vacuolar protein sorting Mvp1 - Saccharomyces cerevisiae	0	558	2	3	14	9	2.6	7.6	2.60
An02g06130	strong similarity to cytoplasmic ribosomal protein of the small subunit S14.e - Neurospora crassa	0	150	12	9	10	10	37.3	24.7	2.60
An01g04040	secretion-associated GTP-binding protein sarA - Aspergillus niger	0	189	9	19	5	22	39.2	26.2	2.60
An02g05890	strong similarity to protein disulfide-isomerase pdi1 - Caenorhabditis elegans	1	731	11	38	73	42	17.6	28.5	2.59
An18g05000	strong similarity to host infection protein cap20 - Colletotrichum gloeosporioides-	0	188	2	5	0	4	10.4	4.3	2.58
An01g13390	similarity to hypothetical protein CAD21062.1 - Neurospora crassa	0	374	0	0	4	2	0.3	3.1	2.57
An15g00760	strong similarity to translation elongation factor eEF-1 γ chain - Artemia sp.	0	412	27	29	31	22	35.7	23.4	2.56
An01g13930	similarity to succinate dehydrogenase - Saccharomyces cerevisiae	0	220	0	1	5	2	1.8	6.1	2.56
An11g01180	weak similarity to immunoglobulin kappa light chain - Mus musculus	1	282	1	2	7	6	3.2	8.6	2.56
An11g00530	strong similarity to ATP citrate lyase - Homo sapiens	0	485	45	44	52	38	48.0	33.7	2.54
An01g00050	similarity to fatty-acyl-CoA synthase β chain Fas1 - Saccharomyces cerevisiae [truncated ORF]	0	1464	86	115	129	62	35.8	23.6	2.53
An18g00260	strong similarity to cytochrome P450 monooxygenase avnA - Aspergillus parasiticus	1	513	5	14	7	4	9.9	4.0	2.53
An18g05670	strong similarity to 23 kD subunit of NADH:ubiquinone reductase - Bos taurus	0	224	1	3	7	7	5.2	11.7	2.52
An04g01540	strong similarity to diphosphomevalonate decarboxylase Erg19 - Saccharomyces cerevisiae-	0	404	2	5	2	0	4.8	1.1	2.50
An03g03360	strong similarity to carnitine/acyl carnitine carrier acuH - Aspergillus nidulans	1	325	1	3	8	8	3.6	9.2	2.50
An18g04180	strong similarity to cytoplasmic ribosomal protein of the small subunit S19 - Saccharomyces cerevisiae-	0	147	2	1	1	0	6.2	1.8	2.49
An04g05430	strong similarity to hypothetical protein CAD21051.1 - Neurospora crassa	1	588	2	6	18	12	3.8	9.4	2.46
An14g00300	strong similarity to 1-acyldihydroxyacetone-phosphate reductase Ayr1 - Saccharomyces cerevisiae	0	295	0	1	5	3	1.3	5.2	2.46
An08g01370	strong similarity to Oxodicarboxylate carrier Odc2 - Saccharomyces cerevisiae	0	305	1	7	13	11	7.3	14.5	2.46
An14g00060	strong similarity to 20.9 kD subunit of NADH:ubiquinone reductase - Neurospora crassa	2	188	0	7	7	12	10.4	18.7	2.42
An11g09390	strong similarity to 21 kD subunit of NADH:ubiquinone reductase nuo-21 - Neurospora crassa	0	219	0	14	14	19	17.2	27.6	2.42
An08g03970	strong similarity to hypothetical protein CAE47902.1 - Aspergillus fumigatus	1	396	8	9	6	5	11.5	5.2	2.40
An08g03430	strong similarity to cytoplasmic ribosomal protein of the large subunit L6 - Saccharomyces cerevisiae	0	202	21	21	26	18	54.8	39.7	2.40
An16g08020	strong similarity to valine--tRNA ligase cyt-20 - Neurospora crassa [putative frameshift]	0	1054	3	1	25	2	1.1	4.7	2.39
An04g00110	strong similarity to 21/29 kD subunit of NADH:ubiquinone reductase - Neurospora crassa	0	280	0	5	8	9	5.1	11.3	2.38
An11g01760	strong similarity to proteasome 20S subunit Pre2 - Saccharomyces cerevisiae	0	379	1	0	5	4	1.0	4.5	2.37
An07g07840	strong similarity to cytoplasmic ribosomal protein of the large subunit L23 - Saccharomyces cerevisiae-	0	140	2	2	2	0	8.4	3.2	2.37
An14g02090	similarity to hypothetical protein BAE64442.1 - Aspergillus oryzae	2	174	0	1	4	2	2.2	6.7	2.35
An02g08820	strong similarity to hypothetical protein SPBC31F10.16 - Schizosaccharomyces pombe	0	708	6	9	4	2	5.7	1.7	2.35
An13g01210	strong similarity to proteasome 20S subunit Pre3 - Saccharomyces cerevisiae	0	199	3	0	7	4	4.6	10.4	2.34
An12g10380	strong similarity to chitin synthase C chsC - Aspergillus fumigatus	8	884	0	1	8	7	0.4	3.2	2.32

An09g05490	strong similarity to COP-coated vesicle membrane protein P24 homolog lbrA - Polysphondylium pallidum	2	239	1	4	9	7	6.0	12.5	2.31
An05g02320	similarity to α -1,6-mannosyltransferase from patent JP09003097-A - Pichia pastoris	0	406	2	0	9	3	1.6	5.6	2.31
An12g08570	similarity to type 2 peroxiredoxin PrxII - Brassica napus	0	168	6	8	8	4	22.5	13.4	2.30
An03g03570	strong similarity to hypothetical protein Afu2g14370 - Aspergillus fumigatus	5	513	0	0	6	1	0.3	2.6	2.29
An10g00360	strong similarity to nuclear pore-associated DEAD-box protein Dbp5 - Saccharomyces cerevisiae	0	482	6	4	2	2	5.7	1.7	2.28
An02g04020	strong similarity to adenylosuccinate lyase ADSL - Homo sapiens-	0	483	2	2	0	0	2.4	0.2	2.28
An02g14930	strong similarity to dolichyl-diphosphooligosaccharide-protein glycotransferase γ chain Ost3 - S.cerevisiae	3	335	1	9	18	10	8.2	15.3	2.23
An04g01200	strong similarity to 14 kD subunit of ubiquinol--cytochrome c reductase Qcr7 - Saccharomyces cerevisiae	0	122	0	1	3	2	3.2	8.1	2.22
An09g00650	similarity to hypothetical protein F9K20.18 - Arabidopsis thaliana-	0	242	3	2	2	0	5.9	1.9	2.22
An07g07150	strong similarity to single-stranded nucleic acid binding protein CBP - Mus musculus	0	360	10	3	5	3	9.8	4.3	2.22
An03g03050	strong similarity to cDNA gene trap ankyrin repeat containing protein Gtar - Mus musculus-	0	826	1	9	1	1	3.3	0.5	2.20
An12g05170	similarity to hypothetical protein AAM35689.1 - Xanthomonas axonopodis	0	295	5	3	18	5	7.5	14.4	2.20
An07g03760	strong similarity to 100 kDa coactivator snd1 - Homo sapiens	0	883	5	4	29	7	2.8	7.5	2.19
An18g01170	strong similarity to poly(ADP-ribose) polymerase NAP protein from patent WO200004173-A1 - Zea mays-	0	650	1	4	0	0	2.2	0.1	2.19
An11g01960	similarity to transsulphurylation protein hxB - Aspergillus nidulans [putative sequencing error]	0	345	0	0	2	3	0.4	2.9	2.18
An04g04750	strong similarity to oxoglutarate dehydrogenase (lipoamide) Kgd1 - Saccharomyces cerevisiae	0	1055	16	8	50	21	6.0	12.2	2.13
An16g02990	strong similarity to phosphoglycerate mutase pgm - Bacillus subtilis	0	520	11	11	8	7	11.3	5.4	2.13
An16g07150	strong similarity to soluble cytoplasmic fumarate reductase YEL047c - Saccharomyces cerevisiae	0	629	5	12	2	7	7.2	2.7	2.12
An12g00030	strong similarity to L-iditol 2-dehydrogenase Sor1 - Saccharomyces cerevisiae	0	358	0	0	3	2	0.4	2.8	2.10
An01g08010	strong similarity to iron and manganese transporter Ccc1 - Saccharomyces cerevisiae	3	303	0	2	3	7	2.1	6.3	2.09
An02g06710	strong similarity to suppressor of tom1 protein Mpt4 - Saccharomyces cerevisiae	0	303	2	0	7	3	2.1	6.3	2.09
An11g06200	strong similarity to 31 kD subunit of NADH:ubiquinone reductase - Neurospora crassa	0	280	1	11	16	14	11.6	19.6	2.09
An16g01830	glyceraldehyde-3-phosphate dehydrogenase gpdA - Aspergillus niger	0	336	18	12	14	13	23.6	14.8	2.06
An01g06960	strong similarity to hypothetical phosphatidyl synthase SPAC22A12.08c - Schizosaccharomyces pombe	0	364	0	0	3	2	0.4	2.7	2.06
An08g06130	strong similarity to GTP-binding regulatory protein α chain fadA - Aspergillus nidulans	0	353	0	1	4	4	1.1	4.3	2.06
An01g09310	similarity to β -ketoacyl reductase rhlG - Pseudomonas aeruginosa-	0	262	3	2	0	2	5.5	1.7	2.05
An18g01590	strong similarity to carnitine O-acetyltransferase cat2 - Candida tropicalis	0	643	8	10	7	3	7.5	2.9	2.05
56930	strong similarity to small oligopeptide transporter, OPT family [Aspergillus clavatus NRRL 1]	15	786	2	3	14	10	1.8	5.6	2.04
An02g14800	protein disulfide isomerase A pdiA - Aspergillus niger	0	515	44	105	82	86	75.6	59.0	2.04
An02g05880	strong similarity to 29.9 kD subunit of NADH:ubiquinone reductase - Neurospora crassa	0	237	0	10	5	20	11.5	19.4	2.03
An11g10790	similarity to serum paraoxonase/arylesterase 2 PON2 - Gallus gallus	1	422	3	7	1	4	6.5	2.4	2.00
An09g06480	similarity to hypothetical protein YJL145w - Saccharomyces cerevisiae	0	477	10	11	12	3	11.7	5.9	2.00
An16g07410	strong similarity to mitochondrial F1-ATPase α -subunit Atp1 - Saccharomyces cerevisiae	0	556	31	37	71	65	32.1	44.3	1.97
An14g02250	strong similarity to flavocytochrome b2 L-lactate dehydrogenase CYB2 - Pichia anomala	0	500	9	5	4	4	7.5	3.1	1.95
An09g05630	strong similarity to hypothetical protein encoded by gene B18D24.80 - Neurospora crassa	1	130	0	2	3	4	5.0	10.4	1.93
An08g00610	strong similarity to cytoplasmic ribosomal protein of the large subunit L9.b - Saccharomyces cerevisiae	0	192	13	12	11	14	34.6	24.0	1.93
An16g05020	strong similarity to protein vip1p - Schizosaccharomyces pombe	0	257	2	0	5	4	2.5	6.7	1.93
An15g01240	strong similarity to protein required for accurate mitotic chromosome segregation Cse1 - S.cerevisiae	0	962	3	1	19	4	1.2	4.4	1.92
An12g10210	similarity to hypothetical protein CAD21295.1 - Neurospora crassa	1	289	0	0	3	1	0.5	2.8	1.90
An08g05300	strong similarity to heat shock protein Hsp70 ss1p - Schizosaccharomyces pombe-	0	712	2	15	48	0	6.4	12.3	1.89

An10g00400	strong similarity to 1,3- β -glucanosyltransferase gel1 - <i>Aspergillus fumigatus</i>	1	458	0	3	11	3	2.0	5.7	1.88
An04g02640	strong similarity to protein pescadillo - <i>Homo sapiens</i>	0	673	1	0	6	5	0.6	3.1	1.88
An17g01977	strong similarity to glycine-tRNA ligase Grs1 - <i>Saccharomyces cerevisiae</i>	0	626	0	0	6	1	0.2	2.2	1.88
An04g02480	strong similarity to lipid phosphoinositide phosphatase Sac1 - <i>Saccharomyces cerevisiae</i>	2	687	32	56	36	52	33.5	23.2	1.88
An08g05400	strong similarity to peroxisomal acetyl-CoA C-acyltransferase POT1 - <i>Yarrowia lipolytica</i> -	0	418	1	2	0	0	2.2	0.2	1.87
An07g01520	strong similarity to nucleoporin Nup170 - <i>Saccharomyces cerevisiae</i>	0	1350	18	7	1	10	4.9	1.5	1.86
An02g02230	strong similarity to hypothetical protein SPAC824.01 - <i>Schizosaccharomyces pombe</i>	0	741	1	3	10	10	1.6	5.0	1.86
An01g04730	strong similarity to secretory protein Sec23 - <i>Saccharomyces cerevisiae</i>	0	768	19	7	8	9	9.0	4.1	1.86
An18g05640	strong similarity to hypothetical mold-specific protein MS8 - <i>Ajellomyces capsulatus</i>	0	198	1	6	7	11	9.9	16.9	1.85
An08g07470	similarity to VAMP-7 vesicle-associated membrane protein-7 - <i>Rattus norvegicus</i>	1	269	0	2	4	5	2.4	6.4	1.84
An11g00470	strong similarity to ribose 5-phosphate isomerase RPI - <i>Mus musculus</i> -	0	273	3	3	3	0	6.2	2.3	1.84
An01g03050	similarity to polyadenylate-binding protein Pabp - <i>Saccharomyces cerevisiae</i>	0	731	25	24	24	18	17.6	10.5	1.83
An12g05750	strong similarity to high-affinity inorganic phosphate/H ⁺ symporter Pho84 - <i>Saccharomyces cerevisiae</i>	9	645	0	0	4	3	0.2	2.1	1.82
An01g11010	strong similarity to cell wall protein Crh1 - <i>Saccharomyces cerevisiae</i>	0	396	0	3	9	4	2.3	6.1	1.82
An04g04060	strong similarity to cytochrome-c peroxidase precursor Ccp1 - <i>Saccharomyces cerevisiae</i>	0	364	22	41	37	30	45.4	33.5	1.82
An16g04430	strong similarity to membrane steroid hormone-binding protein MSBP - <i>Bos taurus</i>	1	169	4	11	7	7	23.9	15.5	1.80
An01g07320	strong similarity to embryogenesis protein H β 58 - <i>Mus musculus</i>	0	352	6	6	4	4	9.2	4.4	1.80
An16g06850	strong similarity to translation initiation factor eIF-4F Tif4631 - <i>Saccharomyces cerevisiae</i>	0	1315	7	8	2	2	3.1	0.6	1.78
An18g03780	strong similarity to hypothetical protein 9G6.250 - <i>Neurospora crassa</i>	9	986	2	3	18	7	1.5	4.7	1.78
An01g09270	strong similarity to isocitrate lyase acuD - <i>Aspergillus nidulans</i>	0	538	2	12	34	4	7.0	12.9	1.77
An04g00060	strong similarity to 19.3 kD subunit of NADH:ubiquinone reductase - <i>Neurospora crassa</i>	0	232	0	1	3	3	1.7	5.1	1.77
An04g05420	strong similarity to α -aminoadipate reductase large subunit lys2 - <i>Penicillium chrysogenum</i> -	0	1430	8	3	45	0	2.1	5.7	1.77
An02g03270	strong similarity to methylenetetrahydrofolate reductase Met13 - <i>Saccharomyces cerevisiae</i> -	0	626	3	1	0	0	1.9	0.1	1.76
An01g12230	strong similarity to nucleolar protein Nop1 - <i>Saccharomyces cerevisiae</i>	0	313	5	1	13	5	5.4	10.7	1.75
An06g01440	similarity to heterogeneous nuclear ribonucleoprotein (hnRNP) Tom34 - <i>Saccharomyces cerevisiae</i>	0	336	17	12	10	17	22.9	14.8	1.75
An08g01610	strong similarity to hypothetical GTP-binding protein SPAC27E2.03c - <i>Schizosaccharomyces pombe</i>	0	394	13	8	7	10	14.2	8.0	1.75
An01g13190	strong similarity to cytoplasmic ribosomal protein of the small subunit S5.e - <i>Saccharomyces cerevisiae</i>	0	215	18	16	14	22	41.8	30.6	1.72
An18g06350	strong similarity to hypothetical protein Afu6g06700 - <i>Aspergillus fumigatus</i>	0	209	0	0	1	2	0.6	3.0	1.72
An14g00100	strong similarity to nucleoporin-interacting protein Nic96 - <i>Saccharomyces cerevisiae</i>	0	993	10	10	6	4	5.4	1.9	1.72
An09g06490	strong similarity to oxide squalene cyclising enzyme from patent JP08308568-A - <i>Rattus rattus</i>	0	735	1	5	19	5	2.3	6.0	1.72
An17g01150	strong similarity to acyl-CoA dehydrogenase MCAD - <i>Rattus norvegicus</i> -	0	446	3	3	0	2	3.8	1.0	1.72
An06g01870	strong similarity to cytoplasmic ribosomal protein of the small subunit S10 - <i>Saccharomyces cerevisiae</i>	0	154	6	6	7	4	21.1	13.5	1.71
An08g02260	strong similarity to phosphoglycerate kinase pgkA - <i>Aspergillus nidulans</i>	0	417	13	10	10	9	14.7	8.4	1.70
An05g01890	strong similarity to hypothetical protein related to host-specific AK-toxin Akt2 B23L21.350 - <i>Neurospora crassa</i>	0	461	2	1	0	0	2.0	0.2	1.70
An01g11100	strong similarity to hypothetical membrane protein YBR287w - <i>Saccharomyces cerevisiae</i>	6	443	0	0	1	4	0.3	2.2	1.69
An12g04110	strong similarity to precursor of mitochondrial nuclease Nuc1 - <i>Saccharomyces cerevisiae</i>	1	334	1	3	3	11	3.5	7.8	1.69
An01g06230	strong similarity to translation initiation factor 3 subunit eIF3 β - <i>Homo sapiens</i>	0	740	9	8	43	4	6.2	11.6	1.69
An08g03000	strong similarity to H ⁺ -transporting ATPase chain C Vma5 - <i>Saccharomyces cerevisiae</i>	0	388	6	3	1	4	6.4	2.6	1.68
An04g05310	strong similarity to vacuolar H(+)-transporting ATPase subunit Vph1 - <i>Saccharomyces cerevisiae</i>	6	850	13	33	54	49	14.2	22.0	1.66
An02g04520	strong similarity to H ⁺ -transporting ATP synthase δ chain precursor Atp5 - <i>Saccharomyces cerevisiae</i>	0	228	4	4	13	7	9.7	16.2	1.66

An07g02690	similarity to hypothetical regulational protein PBK1 - Homo sapiens-	0	407	6	2	4	0	5.4	2.0	1.66
An01g08570	strong similarity to thioredoxin reductase TrxB - Penicillium chrysogenum-	0	367	2	2	1	0	3.2	0.7	1.65
An18g06470	strong similarity to DnaJ-like protein MTJ1 - Mus musculus-	2	397	4	5	0	5	6.2	2.5	1.65
An16g06820	strong similarity to hypothetical pathogenicity protein PATH531 - Magnaporthe grisea	2	323	10	7	3	11	14.1	8.1	1.64
An15g04100	strong similarity to salicylaldehyde dehydrogenase doxF - Pseudomonas sp.-	0	478	1	2	0	0	1.9	0.2	1.64
An08g01030	strong similarity to vacuolar protein sorting protein Vps29 - Saccharomyces cerevisiae	0	195	5	2	3	2	10.0	5.1	1.63
An02g12410	strong similarity to translation initiation factor eIF3 subunit Tif34 - Saccharomyces cerevisiae	0	337	0	0	3	1	0.4	2.4	1.63
An02g02910	strong similarity to orotate reductase pyrE - Aspergillus nidulans	0	544	2	4	8	13	3.1	7.1	1.62
An14g00150	similarity to hypothetical protein B24H17.110 - Neurospora crassa-	0	207	1	3	1	1	5.7	2.2	1.60
An07g05520	strong similarity to O-methyltransferase B omtB - Aspergillus parasiticus-	0	380	9	14	20	0	16.1	9.7	1.58
An11g02400	strong similarity to cytosolic lysine--tRNA ligase Krs1 - Saccharomyces cerevisiae	0	618	0	0	5	1	0.2	1.9	1.55
An14g02460	strong similarity to flavohemoglobin Fhp - Alcaligenes eutrophus	0	417	8	8	7	5	10.3	5.4	1.55
An02g13300	similarity to hypothetical protein ID880 - Bradyrhizobium japonicum	0	907	0	0	2	6	0.1	1.7	1.54
An01g08400	strong similarity to sorting nexin-1-like protein Vps5 - Saccharomyces cerevisiae-	0	567	3	2	0	1	2.5	0.5	1.53
An04g02120	strong similarity to cytoplasmic ribosomal protein of the large subunit L16 - Saccharomyces cerevisiae	0	176	11	7	10	8	27.4	19.0	1.53
An01g10730	similarity to plasma membrane bound receptor from patent DE19627237-A1 - Sus scrofa	0	213	1	7	3	3	10.4	5.5	1.52
An18g06820	strong similarity to glutamine-fructose-6-phosphate transaminase Gfa1 - Saccharomyces cerevisiae	0	694	16	18	16	12	12.9	7.4	1.52
An01g10190	similarity to mitochondrial tricarboxylate carrier - Rattus sp.	1	370	0	1	2	5	1.1	3.7	1.52
An15g05770	strong similarity to hypothetical sulphite reductase SPAC4C5.05c - Schizosaccharomyces pombe	0	1472	48	39	68	8	15.5	9.4	1.51
211877	strong similarity to cytochrome P450 oxidoreductase [Aspergillus fumigatus Af293]	2	541	42	56	61	47	47.4	36.2	1.51
An15g01420	strong similarity to glucosidase I Cwh41 - Saccharomyces cerevisiae	0	822	9	34	71	24	13.8	21.0	1.50
An10g00800	strong similarity to purine nucleoside permease NUP - Candida albicans-	0	407	1	3	1	0	2.9	0.7	1.49
An07g06730	strong similarity to cut3p - Schizosaccharomyces pombe-	0	1309	2	10	0	3	2.5	0.5	1.48
An11g02230	strong similarity to lanosterol 14 α -demethylase (P450(14DM)) CYP51 - Penicillium italicum	2	512	2	5	16	6	3.8	7.9	1.47
An04g05620	strong similarity to acetate--CoA ligase facA - Aspergillus nidulans	0	670	21	16	19	13	14.6	8.8	1.47
53033	strong similarity to 1,3- β -glucanosyltransferase, putative [Neosartorya fischeri NRRL 181]	0	537	0	5	16	2	2.7	6.2	1.46
An05g00930	strong similarity to NADP-dependent malate dehydrogenase mdh - Homo sapiens-	0	596	3	2	1	0	2.4	0.5	1.46
An15g00190	strong similarity to mitochondrial import receptor MOM38 - Neurospora crassa	0	354	5	17	21	26	16.5	24.2	1.45
An05g01760	similarity to hard surface induced protein 3 chip3 - Glomerella cingulata	7	501	0	1	7	1	0.8	3.1	1.45
An01g12150	β -galactosidase lacA - Aspergillus niger	0	1007	0	1	9	3	0.4	2.2	1.44
An06g01510	strong similarity to class I α -mannosidase AAB62720.1 - Spodoptera frugiperda	1	869	4	14	40	9	5.5	10.3	1.44
An01g03110	similarity to ribosomal protein of the small subunit Rsm7 - Saccharomyces cerevisiae-	0	422	3	1	0	1	2.8	0.6	1.44
An15g00560	strong similarity to actin γ - Aspergillus nidulans	0	375	36	41	45	42	53.8	42.1	1.43
An18g02490	strong similarity to ARF guanine-nucleotide exchange factor 2 Gea2 - Saccharomyces cerevisiae-	0	1554	6	7	0	3	2.3	0.4	1.42
An18g06680	strong similarity to proteasome 20S subunit Pre4 - Saccharomyces cerevisiae	0	260	1	1	4	4	2.5	5.9	1.41
An02g06400	strong similarity to small Ras-like GTPase Vps21 - Saccharomyces cerevisiae	0	262	0	2	4	4	2.5	5.9	1.40
An06g01200	strong similarity to endosomal protein Emp70 - Saccharomyces cerevisiae	9	645	0	1	7	2	0.6	2.7	1.39
An15g01920	strong similarity to methylcitrate synthase mcsA - Aspergillus nidulans	0	465	1	9	5	1	5.9	2.5	1.38
An09g02930	strong similarity to high-affinity glucose transporter HGT1 - Kluyveromyces lactis	12	527	0	1	3	5	0.7	2.9	1.38
An08g06810	strong similarity to pentafunctional enzyme aroM - Aspergillus nidulans	0	1587	2	0	16	3	0.4	2.2	1.37

An12g04780	strong similarity to 24 kD subunit of NADH:ubiquinone reductase Nuo24 - <i>Neurospora crassa</i>	0	269	2	5	7	11	7.3	12.4	1.36
An02g02360	strong similarity to chitin synthase with a myosin motor-like domain csmA - <i>Aspergillus nidulans</i>	2	1855	0	0	10	3	0.1	1.3	1.36
An16g04020	strong similarity to peroxisomal membrane protein Pex14 - <i>Hansenula polymorpha</i>	0	370	1	5	2	1	4.6	1.7	1.36
An16g04970	strong similarity to arginine-specific carbamoyl-phosphate synthase subunit Cpa2 - <i>Saccharomyces cerevisiae</i>	0	1173	18	34	26	17	11.6	6.7	1.36
An02g06450	strong similarity to hypothetical protein Afu3g10780 - <i>Aspergillus fumigatus</i>	6	351	1	9	1	6	7.8	3.9	1.35
An03g01310	strong similarity to CTP synthase Ura7 - <i>Saccharomyces cerevisiae</i> -	0	579	2	1	0	0	1.6	0.2	1.35
An18g05590	strong similarity to mitochondrial carrier protein Ymc1 - <i>Saccharomyces cerevisiae</i>	0	304	0	1	3	3	1.3	3.9	1.35
An02g05470	strong similarity to 49 kD subunit of NADH:ubiquinone reductase - <i>Neurospora crassa</i>	0	476	3	23	26	30	14.5	21.4	1.34
An02g03940	strong similarity to glucose repression mediator protein Ssn6 - <i>Saccharomyces cerevisiae</i> -	0	858	3	3	0	1	2.0	0.3	1.34
An07g09530	strong similarity to α subunit E1 of the pyruvate dehydrogenase complex Pda1 - <i>Saccharomyces cerevisiae</i>	0	404	0	17	10	4	11.3	6.5	1.31
An08g02700	strong similarity to S-adenosylmethionine synthase eth-1 - <i>Neurospora crassa</i>	0	387	16	13	9	19	19.8	13.3	1.31
An07g03130	strong similarity to mitochondrial cation transporter Mmt1 - <i>Saccharomyces cerevisiae</i>	0	486	1	1	6	4	1.3	3.9	1.31
An12g00580	weak similarity to heat shock protein dnaJ - <i>Brucella ovis</i>	2	364	4	5	2	4	6.8	3.2	1.30
An11g04360	strong similarity to polyribosome binding protein Scp160 - <i>Saccharomyces cerevisiae</i>	0	1172	6	4	24	11	2.3	5.5	1.29
An09g02830	strong similarity to acylaminoacyl-peptidase DPP V - <i>Aspergillus fumigatus</i>	0	750	3	5	24	2	2.9	6.4	1.29
An17g01360	strong similarity to cytoplasmic ribosomal protein of the large subunit L8.e Pl2b - <i>Saccharomyces cerevisiae</i>	0	254	6	2	5	1	8.7	4.6	1.28
An06g01030	strong similarity to hypothetical protein Afu6g14120 - <i>Aspergillus fumigatus</i>	6	500	2	0	5	5	1.3	3.8	1.27
An01g00100	strong similarity to pyruvate dehydrogenase β chain precursor Pdb1 - <i>Saccharomyces cerevisiae</i>	0	374	1	31	16	16	22.6	15.7	1.26
An07g08140	strong similarity to cytosolic phenylalanine--tRNA ligase β subunit Frs2 - <i>Saccharomyces cerevisiae</i>	0	481	3	1	1	0	2.4	0.6	1.26
An15g01780	strong similarity to 2-methylcitrate dehydratase PrpD - <i>Salmonella typhimurium</i>	0	502	5	8	8	1	7.0	3.4	1.26
An15g06440	strong similarity to karyopherin α Srp1 - <i>Saccharomyces cerevisiae</i>	0	549	11	10	13	4	10.2	5.8	1.25
An01g02880	strong similarity to cytoplasmic ubiquitin / ribosomal fusion protein Cep52 - <i>Saccharomyces cerevisiae</i>	0	128	1	2	7	1	7.1	12.0	1.25
An02g09200	strong similarity to translational factor CaYST1 - <i>Candida albicans</i>	0	298	20	14	20	16	30.1	22.1	1.24
An14g06830	strong similarity to hypothetical membrane protein Ptm1 - <i>Saccharomyces cerevisiae</i>	7	536	0	5	10	7	2.7	5.9	1.24
An01g14080	strong similarity to cytoplasmic ribosomal protein of the small subunit Ys24 - <i>Saccharomyces cerevisiae</i>	0	130	11	8	11	10	39.0	29.8	1.23
An04g01310	similarity to protein involved in regulation of the inositol biosynthesis Scs2 - <i>Saccharomyces cerevisiae</i>	1	286	7	4	5	4	10.5	6.0	1.23
An04g01730	strong similarity to ubiquitin fusion degradation protein Ufd2 - <i>Saccharomyces cerevisiae</i>	0	1073	6	12	8	2	4.5	1.8	1.23
An17g01945	strong similarity to protein Rvs161 - <i>Saccharomyces cerevisiae</i>	0	261	2	5	2	3	7.5	3.8	1.22
An04g01800	strong similarity to proteasome 20S subunit Pup3 - <i>Saccharomyces cerevisiae</i>	0	206	2	0	4	3	3.2	6.6	1.22
An02g07930	strong similarity to precursor of linoleate diol synthase - <i>Gaeumannomyces graminis</i>	0	1110	1	6	14	13	1.8	4.5	1.22
An02g06390	strong similarity to cytoplasmic ribosomal protein of the small subunit Rp30 - <i>Saccharomyces cerevisiae</i>	0	200	17	12	12	20	38.4	29.3	1.22
An02g06050	strong similarity to cytoplasmic ribosomal protein of the small subunit S16.e - <i>Saccharomyces cerevisiae</i>	0	143	5	11	8	9	30.0	22.1	1.22
An16g02520	strong similarity to threonine synthase Thr4 - <i>Saccharomyces cerevisiae</i> -	0	520	4	9	9	0	6.8	3.3	1.22
An04g06380	strong similarity to mitochondrial aspartate aminotransferase mAspAT - <i>Mus musculus</i>	0	429	27	26	32	25	32.5	24.2	1.21
An07g07000	strong similarity to mitochondrial m-AAA protease subunit Yta12 - <i>Saccharomyces cerevisiae</i>	0	898	4	4	11	16	2.5	5.5	1.20
An01g04630	strong similarity to γ chain precursor of the H ⁺ -transporting ATP synthase Atp3 - <i>Saccharomyces cerevisiae</i>	0	297	2	3	7	7	4.8	8.8	1.18
An13g00670	strong similarity to mitochondrial protein Mia1 - <i>Saccharomyces cerevisiae</i> -	0	135	1	2	1	1	6.7	3.3	1.17
An16g01810	strong similarity to histone H2A variant pht1p - <i>Schizosaccharomyces pombe</i> -	0	138	1	1	0	1	4.7	2.0	1.17
An15g00140	similarity to transcription repressor Tup1 - <i>Saccharomyces cerevisiae</i> -	0	583	4	4	4	0	3.8	1.4	1.16
An07g08220	strong similarity to clathrin associated epsin 2A - <i>Homo sapiens</i> -	0	525	3	1	0	1	2.2	0.5	1.16

An04g06210	strong similarity to homocitrate synthase lys1 - <i>Penicillium chrysogenum</i> -	0	465	3	2	1	1	3.1	1.0	1.15
An11g01640	similarity to phospholipase C type Isc2 - <i>Saccharomyces cerevisiae</i>	2	477	0	0	3	1	0.3	1.7	1.15
An11g01770	strong similarity to 135 kD subunit of DNA-directed RNA polymerase I - <i>Neurospora crassa</i>	0	1213	0	0	7	1	0.1	1.3	1.15
An02g01510	strong similarity to component of the endoplasmic reticulum protein translocation machinery Sec62 - <i>Saccharomyces cerevisiae</i>	2	465	9	16	13	10	14.3	9.1	1.15
An07g02160	strong similarity to mitochondrial malate dehydrogenase Mdh1 - <i>Saccharomyces cerevisiae</i>	0	340	8	20	20	35	21.8	29.4	1.14
An02g02170	strong similarity to tryptophan synthase Trp5 - <i>Saccharomyces cerevisiae</i>	0	723	5	6	5	1	4.1	1.6	1.14
An02g10660	strong similarity to methionine adenosyltransferase regulatory β subunit MAT II - <i>Homo sapiens</i> -	0	324	1	2	1	0	2.8	0.8	1.13
An04g09030	strong similarity to mitochondrial succinate-fumarate transporter Sfc1 - <i>Saccharomyces cerevisiae</i>	0	325	0	2	2	6	2.0	4.7	1.13
An08g01960	strong similarity to adenosylhomocysteinase - <i>Homo sapiens</i>	0	449	28	19	76	13	27.5	36.0	1.12
An14g01560	strong similarity to zuotin Zuo1 - <i>Saccharomyces cerevisiae</i>	0	447	0	2	8	1	1.5	3.8	1.11
An12g07020	strong similarity to α -1,6-mannosyltransferase Hoc1 - <i>Saccharomyces cerevisiae</i>	1	421	0	3	6	5	2.2	4.9	1.11
An11g10150	strong similarity to phosphoribosylaminoimidazolesuccinocarboxamide synthase Ade1 - <i>S.cerevisiae</i>	0	300	2	2	2	0	3.9	1.5	1.10
An15g06790	strong similarity to suppressor of the septation mutant cdc11 sce3p - <i>Schizosaccharomyces pombe</i> -	0	489	4	1	2	0	2.9	0.9	1.10
An04g02540	similarity to bladder tumour EST encoded protein 16 from patent DE19818619-A1 - <i>Homo sapiens</i> -	1	491	1	4	1	1	2.9	0.9	1.09
An11g07010	strong similarity to alkane-inducible cytochrome P450 alk2 - <i>Candida tropicalis</i>	0	502	2	4	16	2	3.4	6.6	1.09
An01g06370	strong similarity to hypothetical protein YKR065c - <i>Saccharomyces cerevisiae</i>	2	248	1	0	3	2	1.6	4.0	1.09
An08g04280	similarity to polyadenylated RNA-binding protein Pub1 - <i>Saccharomyces cerevisiae</i> -	0	497	3	2	2	0	2.9	0.9	1.08
An13g00320	strong similarity to hypothetical protein Afu7g03900 - <i>Aspergillus fumigatus</i>	4	432	0	3	1	10	2.1	4.8	1.08
An11g04510	strong similarity to suppressor 2 Sup2 - <i>Saccharomyces cerevisiae</i>	0	727	1	1	10	1	0.9	2.9	1.08
An08g01640	strong similarity to small glutamine-rich tetratricopeptide protein SGT - <i>Homo sapiens</i> -	0	341	2	1	1	0	2.7	0.8	1.07
An12g01260	strong similarity to nitrilase NIT1 - <i>Arabidopsis thaliana</i>	0	320	4	7	11	14	9.4	14.4	1.07
An02g12980	strong similarity to cis-Golgi t-SNARE Sed5 - <i>Saccharomyces cerevisiae</i> -	1	343	2	1	0	1	2.7	0.8	1.07
An02g11420	dipeptidyl aminopeptidase type IV dapB - <i>Aspergillus niger</i>	1	901	0	0	5	1	0.1	1.3	1.06
An11g06670	strong similarity to α subunit of assimilatory sulfite reductase Met10 - <i>Saccharomyces cerevisiae</i> -	0	1045	10	10	13	0	5.1	2.3	1.06
An02g03120	strong similarity to GDP dissociation inhibitor in the secretory pathway Gdi1 - <i>Saccharomyces cerevisiae</i>	0	468	0	2	8	1	1.4	3.7	1.06
An08g00210	strong similarity to glycerol-3-phosphate dehydrogenase gdm1 - <i>Mus musculus</i>	1	704	8	32	43	39	15.0	21.1	1.06
An03g06670	weak similarity to myosin-like protein Mlp1 - <i>Saccharomyces cerevisiae</i>	0	2080	28	94	120	128	15.3	21.6	1.06
An02g07320	strong similarity to AU-specific RNA-binding protein / enoyl-CoA hydratase AUH - <i>Homo sapiens</i> -	0	302	3	2	0	3	4.7	2.1	1.05
An08g07520	strong similarity to levodione reductase lvr - <i>Corynebacterium aquaticum</i> -	0	314	2	2	0	2	3.7	1.4	1.05
An02g03090	similarity to Not2p - <i>Homo sapiens</i>	0	523	0	0	3	1	0.2	1.6	1.05
203715	strong similarity to outer mitochondrial membrane protein porin [<i>Aspergillus clavatus</i> NRRL 1]	0	350	7	34	29	47	30.9	39.4	1.05
An14g00810	strong similarity to hypothetical protein EAA61688.1 - <i>Aspergillus nidulans</i>	0	343	0	0	2	1	0.4	1.8	1.05
An17g01530	alcohol-dehydrogenase adhA from patent WO8704464-A - <i>Aspergillus niger</i> -	0	350	2	1	0	1	2.6	0.8	1.05
An04g05270	strong similarity to transcription activator Adr1 - <i>Saccharomyces cerevisiae</i>	0	327	4	6	7	1	8.4	4.7	1.05
An04g01260	strong similarity to golgi α -1,6 mannosyltransferase subunit Anp1 - <i>Saccharomyces cerevisiae</i>	0	411	4	20	31	18	15.5	21.7	1.04
An18g03570	β -glucosidase bgl1 - <i>Aspergillus niger</i>	0	860	3	15	33	12	5.6	9.5	1.04
An01g08410	strong similarity to polypeptide HFIZG53 from patent EP892050-A2 - <i>Homo sapiens</i>	0	242	0	2	5	2	2.7	5.6	1.04
An13g00840	strong similarity to general amino acid permease Gap1 - <i>Saccharomyces cerevisiae</i>	12	585	4	10	14	20	6.5	10.6	1.04
An14g01140	strong similarity to guanine deaminase Gda - <i>Mus musculus</i> [putative frameshift]	1	531	0	0	3	1	0.2	1.5	1.03

An18g05070	strong similarity to 26S proteasome subunit 9 - Homo sapiens	0	424	10	8	8	8	11.4	7.0	1.03
An18g02680	strong similarity to cytochrome P450 monooxygenase avnA - Aspergillus parasiticus	1	493	15	33	24	27	25.6	18.8	1.03
An02g04860	strong similarity to cytochrome-b5 reductase - Saccharomyces cerevisiae	0	305	4	13	20	15	14.9	21.0	1.03
An12g07790	strong similarity to transcription factor btf3p - Schizosaccharomyces pombe-	0	155	1	2	2	0	5.9	2.9	1.02
An14g04160	strong similarity to cofilin Cof1 - Saccharomyces cerevisiae-	0	155	1	2	2	0	5.9	2.9	1.02
An11g05700	similarity to hypothetical membrane protein YGR235c - Saccharomyces cerevisiae	0	252	0	4	4	7	4.6	8.2	1.01
An02g11810	strong similarity to hypothetical conserved protein 12F11.50 - Neurospora crassa	7	551	0	0	1	3	0.2	1.5	1.00
An11g07970	strong similarity to hypothetical protein SPBC16H5.12c - Schizosaccharomyces pombe	0	702	16	5	29	19	8.0	12.5	1.00
An04g03750	strong similarity to hypothetical protein YMR099c - Saccharomyces cerevisiae-	0	320	2	3	3	0	4.5	2.0	1.00
An15g02490	similarity to 3-isopropylmalate dehydrogenase leuB - Sulfolobus sp.	0	361	0	0	1	2	0.4	1.7	1.00
An08g10480	strong similarity to cytoplasmic ribosomal protein of the large subunit L7 - Schizosaccharomyces pombe	0	263	23	35	35	34	57.9	47.7	0.99
An11g09120	strong similarity to cytoplasmic ribosomal protein of the large subunit L26 - Saccharomyces cerevisiae	0	134	5	8	8	6	26.2	19.5	0.98
46101	weak similarity to predicted protein [Aspergillus terreus NIH2624]	1	278	0	1	3	2	1.4	3.6	0.97
An04g02050	similarity to hypoxia-induced protein #21 from patent WO200246465-A2 - Homo sapiens-	5	348	2	2	1	1	3.4	1.3	0.95
An08g04880	strong similarity to hypothetical protein CAD27304.1 - Aspergillus fumigatus	3	263	0	3	3	6	3.5	6.5	0.95
An16g02490	strong similarity to β -adaptn BAD1 - Drosophila melanogaster-	0	748	3	4	0	3	2.6	0.8	0.95
An07g05110	strong similarity to septin aspA - Aspergillus nidulans	0	379	5	1	14	2	4.5	7.9	0.95
An04g08730	strong similarity to hypothetical conserved protein SPAC12B10.16c - Schizosaccharomyces pombe	0	536	0	6	1	2	3.2	1.2	0.94
An01g04430	strong similarity to translation initiation factor eIF-3 - Schizosaccharomyces pombe	0	1052	16	15	44	26	7.8	12.1	0.94
An01g09590	strong similarity to voltage-gated potassium channel β subunit Kv β 1 - Rattus norvegicus-	0	341	3	2	0	3	4.2	1.9	0.93
An03g03640	strong similarity to mitochondrial sulfide dehydrogenase (coenzyme Q2) SPBC2G5.06c - S. pombe	0	527	3	8	11	16	5.7	9.4	0.93
An01g08430	strong similarity to methylmalonate-semialdehyde dehydrogenase MMSDH - Rattus norvegicus	0	600	1	18	5	11	8.5	5.0	0.92
An01g08870	strong similarity to component of COPII-coated vesicles Erv25 - Saccharomyces cerevisiae	1	211	5	8	15	11	16.7	22.7	0.92
An04g05260	strong similarity to saccharopine reductase LYS3 - Magnaporthe grisea	0	448	0	1	5	1	0.9	2.6	0.91
An08g01480	strong similarity to tRNA ligase Trl1 - Saccharomyces cerevisiae	0	821	0	0	5	0	0.2	1.2	0.91
An01g13530	strong similarity to protein involved in the attachment of GPI-anchors to proteins Gpi8 - S. cerevisiae	0	402	1	2	1	0	2.3	0.7	0.91
An04g08330	strong similarity to orotidine-5-monophosphate pyrophosphorylase - Ajellomyces capsulatus [truncated ORF]-	0	191	3	2	4	0	7.5	4.3	0.91
An08g03590	strong similarity to precursor of protein Emp24 - Saccharomyces cerevisiae	0	203	2	7	12	7	12.2	17.3	0.90
An14g00370	strong similarity to cytoplasmic ribosomal protein of the large subunit L13 - Rattus norvegicus	0	225	13	5	11	8	21.4	15.6	0.90
An16g05420	strong similarity to glucose-6-phosphate isomerase Pgi1 - Saccharomyces cerevisiae	0	553	35	28	58	12	29.9	23.0	0.90
An16g02460	strong similarity to α subunit of the coatomer complex Ret1 - Saccharomyces cerevisiae	0	1206	15	30	26	14	9.8	6.1	0.90
An01g08960	strong similarity to iron transport multicopper oxidase Fet3 - Candida albicans	1	613	0	0	1	3	0.2	1.3	0.90
An12g02120	similarity to hypothetical mold-specific protein MS8 - Ajellomyces capsulatus	0	353	3	3	2	2	4.8	2.3	0.90
An07g05920	strong similarity to estrogen receptor-binding cyclophilin cypD - Bos primigenius taurus	0	372	2	7	6	1	6.6	3.6	0.89
An02g13220	strong similarity to lysophospholipase phospholipase B - Penicillium notatum	0	640	1	3	9	5	1.8	4.1	0.88
An08g02280	strong similarity to hypothetical protein YKR018c - Saccharomyces cerevisiae-	0	692	1	3	1	0	1.7	0.4	0.88
An07g01340	weak similarity to phosphoenolpyruvate carboxylase - Escherichia coli	0	346	17	8	20	6	19.2	13.8	0.88
An18g05810	strong similarity to cytoplasmic ribosomal protein of the small subunit S26 - Homo sapiens	0	119	1	3	4	5	9.8	14.4	0.86
An18g02020	disulfide isomerase tigA - Aspergillus niger	0	359	16	29	25	26	33.0	25.9	0.86
An05g01350	strong similarity to hypothetical protein AN2579.2 - Aspergillus nidulans	1	419	0	0	2	1	0.3	1.5	0.86

An14g01050	similarity to serine/threonine protein kinase Yak1 - <i>Saccharomyces cerevisiae</i> -	0	895	4	2	0	2	1.9	0.5	0.85
An18g05050	strong similarity to hypothetical protein encoded by B7F18.130 - <i>Neurospora crassa</i> -	7	388	1	3	0	2	3.0	1.2	0.85
An18g06250	strong similarity to phosphopyruvate hydratase ENO1 - <i>Candida albicans</i>	0	438	8	5	26	3	8.0	12.1	0.85
An11g03480	strong similarity to hypothetical protein encoded by An01g01140 - <i>Aspergillus niger</i> -	0	434	1	2	1	0	2.1	0.6	0.84
An04g03130	strong similarity to mannosylation protein Lec35 - <i>Cricetulus griseus</i> [putative sequencing error]	2	299	1	1	5	2	2.2	4.5	0.84
An04g01520	similarity to nuclear envelope protein cut11p - <i>Schizosaccharomyces pombe</i>	0	565	6	3	1	5	4.4	2.1	0.84
An11g10070	strong similarity to hypothetical protein Afu3g06270 - <i>Aspergillus fumigatus</i>	0	323	0	1	2	3	1.2	3.1	0.84
An05g01770	strong similarity to hypothetical protein Afu6g14020 - <i>Aspergillus fumigatus</i>	1	438	1	1	5	3	1.5	3.5	0.84
An04g05320	strong similarity to hypothetical protein TEMO - <i>Rattus norvegicus</i>	0	1963	0	3	15	4	0.5	1.8	0.83
An15g05740	strong similarity to GTP-binding protein Rab6 - <i>Homo sapiens</i>	0	209	4	12	3	14	20.5	15.1	0.83
An01g03580	strong similarity to cytoplasmic ribosomal protein of the large subunit L18a Rpl20 - <i>Saccharomyces cerevisiae</i>	0	198	15	15	21	14	40.1	32.3	0.83
An08g04450	similarity to hypothetical guanosine-diphosphatase - <i>Schizosaccharomyces pombe</i>	1	561	6	13	23	18	9.0	13.3	0.83
An14g01590	strong similarity to sterol transmethylase ERG6 - <i>Candida albicans</i>	0	377	14	18	35	25	22.4	28.9	0.83
An17g00090	weak similarity to translocation protein Sec72 - <i>Saccharomyces cerevisiae</i>	0	194	0	3	3	5	4.7	7.9	0.83
An18g03480	strong similarity to sterol δ 14 15-reductase erg-3 - <i>Neurospora crassa</i>	8	497	0	1	2	4	0.8	2.4	0.82
An04g09130	similarity to peroxisomal membrane protein PMP22 - <i>Arabidopsis thaliana</i>	3	224	2	4	1	4	7.6	4.4	0.82
An11g09690	strong similarity to proteasome 19S regulatory particle subunit Rpn5 - <i>Saccharomyces cerevisiae</i>	0	488	7	8	8	5	8.3	5.0	0.82
An15g02200	strong similarity to alcohol oxidase AOD1 - <i>Candida boidinii</i> -	0	602	6	16	20	0	9.7	6.1	0.82
An07g07520	strong similarity to vacuolar alkaline phosphatase Pho8 - <i>Saccharomyces cerevisiae</i>	1	595	6	10	18	18	7.2	11.1	0.82
An02g12140	glucose-6-phosphate 1-dehydrogenase gsdA - <i>Aspergillus niger</i>	0	510	14	14	17	11	14.5	10.1	0.81
An11g11210	strong similarity to ATP-dependent RNA helicase ste13p - <i>Schizosaccharomyces pombe</i>	0	505	1	0	5	1	0.8	2.3	0.81
An08g04070	strong similarity to mitochondrial receptor complex chain MOM22 - <i>Neurospora crassa</i>	0	153	3	5	3	5	14.5	10.0	0.81
An01g07190	strong similarity to component of the translocase of mitochondrial inner membrane Tim54 - <i>S. cerevisiae</i>	0	447	0	0	2	1	0.3	1.4	0.80
An18g04730	strong similarity to hypothetical protein SPCC622.11 - <i>Schizosaccharomyces pombe</i>	9	687	0	0	2	2	0.2	1.2	0.80
An02g13450	weak similarity to protein CAP59 - <i>Cryptococcus neoformans</i>	1	794	1	1	7	3	0.8	2.4	0.80
An01g01820	catalase R catR - <i>Aspergillus niger</i>	0	730	6	24	21	41	10.9	15.4	0.80
An07g08990	pyruvate kinase pkiA - <i>Aspergillus niger</i>	0	526	15	8	12	10	11.6	7.7	0.80
An09g06590	heat shock protein sspB - <i>Aspergillus niger</i>	0	702	65	61	106	44	46.9	38.7	0.79
An18g02700	similarity to cytochrome P-450 cyp509A1 - <i>Cunninghamella elegans</i>	1	529	2	9	20	6	5.7	9.0	0.78
An16g05570	strong similarity to aspartate transaminase - <i>Sus scrofa</i>	0	419	11	11	15	7	14.0	9.7	0.78
An18g01200	strong similarity to O-methylsterigmatocystin oxidoreductase ord1 - <i>Aspergillus flavus</i>	0	527	1	0	3	3	0.7	2.2	0.78
An04g08980	strong similarity to cytoplasmic ribosomal protein of the large subunit L43a - <i>Saccharomyces cerevisiae</i>	0	92	0	2	3	2	7.1	10.8	0.78
An02g07570	strong similarity to ergosterol biosynthesis protein Kes1 - <i>Saccharomyces cerevisiae</i>	0	415	2	4	3	1	4.1	2.0	0.76
An09g06750	strong similarity to hypothetical protein B13I18.120 - <i>Neurospora crassa</i>	0	277	3	11	14	14	13.6	18.6	0.76
An16g01870	strong similarity to mRNA cleavage factor I 25 kDa subunit CFIM25 - <i>Homo sapiens</i>	0	277	3	5	3	4	8.0	4.9	0.76
An11g09570	strong similarity to cytoplasmic ribosomal protein of the large subunit L37.b - <i>Saccharomyces cerevisiae</i>	0	95	1	1	3	2	6.8	10.4	0.75
An05g00900	strong similarity to hypothetical protein SPAC32A11.02c - <i>Schizosaccharomyces pombe</i>	0	748	0	1	4	3	0.5	1.8	0.75
An11g10380	strong similarity to 26S proteasome regulatory subunit rpn3p - <i>Schizosaccharomyces pombe</i> -	0	645	6	1	4	0	3.0	1.3	0.75
An02g00890	strong similarity to phosphoserine transaminase Ser1 - <i>Saccharomyces cerevisiae</i> -	0	424	4	1	3	0	3.4	1.5	0.75
An16g09320	strong similarity to cytosolic alanine--tRNA ligase Ala1 - <i>Saccharomyces cerevisiae</i>	0	961	9	8	39	2	4.7	7.8	0.75

An07g04940	strong similarity to α -1,6-mannosyltransferase Hoc1 - <i>Saccharomyces cerevisiae</i>	0	362	0	1	4	1	1.1	2.7	0.75
An08g05580	strong similarity to precursor of isocitrate dehydrogenase (NAD ⁺) chain Idh2 - <i>Saccharomyces cerevisiae</i>	0	438	1	21	8	14	13.4	9.3	0.75
An13g00440	strong similarity to uridine-monophosphate kinase Ura6 - <i>Saccharomyces cerevisiae</i> -	0	212	1	2	2	0	4.3	2.1	0.75
An14g04920	triose-phosphate-isomerase tpiA from patent WO8704464-A - <i>Aspergillus niger</i> -	0	249	2	3	12	0	5.7	9.1	0.75
An07g09170	strong similarity to breast cancer resistance protein 1 BCRP1 - <i>Mus musculus</i>	7	1034	2	4	13	7	1.6	3.6	0.74
An04g02060	strong similarity to 5-aminoimidazole-4-carboxamide ribotide transformylase Ade17 - <i>S. cerevisiae</i>	0	646	16	11	23	3	11.1	7.4	0.74
An01g09500	strong similarity to cytosolic threonine--tRNA ligase Ths1 - <i>Saccharomyces cerevisiae</i>	0	718	6	8	25	8	5.3	8.4	0.74
An04g01080	strong similarity to ribonucleotide reductase from patent JP10014582-A - <i>Homo sapiens</i>	0	865	2	0	9	1	0.8	2.2	0.73
An02g02750	strong similarity to catalase cta1p - <i>Schizosaccharomyces pombe</i> -	0	501	2	1	0	1	1.8	0.5	0.73
An08g01410	strong similarity to ER-Golgi transport protein Sft2 - <i>Saccharomyces cerevisiae</i> -	4	217	2	1	0	2	4.2	2.1	0.73
An04g01750	strong similarity to 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase Met6 - <i>Saccharomyces cerevisiae</i>	0	774	105	77	179	45	61.4	52.3	0.72
An02g10450	strong similarity to GTP-binding protein Vps1 - <i>Saccharomyces cerevisiae</i>	0	697	9	16	22	30	9.5	13.6	0.72
An17g02390	strong similarity to cytoplasmic ribosomal protein of the small subunit Rp10b - <i>Saccharomyces cerevisiae</i>	0	256	19	16	21	20	36.1	29.2	0.72
An17g01670	strong similarity to succinyl coenzyme A synthase α subunit SYRTSA - <i>Rattus norvegicus</i>	0	332	6	4	4	5	8.2	5.2	0.71
An11g09350	strong similarity to mitochondrial NADH dehydrogenase ndh64 - <i>Neurospora crassa</i>	3	700	1	1	1	8	0.9	2.4	0.71
An12g04660	strong similarity to thiamin-phosphate pyrophosphorylase/hydroxyethylthiazole kinase Thi6 - <i>S. cerevisiae</i>	0	519	0	2	6	2	1.3	3.0	0.71
An09g06330	similarity to protein fragment SEQ ID NO:5981 from patent EP1108790-A2 - <i>Corynebacterium glutamicum</i>	3	679	3	7	4	3	4.0	2.0	0.70
An02g02830	strong similarity to protein RER1 - <i>Homo sapiens</i>	3	189	7	6	8	6	18.6	13.8	0.70
An08g02460	strong similarity to SNARE protein of Golgi compartment Gos1 - <i>Saccharomyces cerevisiae</i> -	1	227	1	2	0	2	4.0	2.0	0.70
An03g04940	strong similarity to Erv41 - <i>Saccharomyces cerevisiae</i>	0	399	7	4	12	12	7.5	11.1	0.69
An04g02130	similarity to U1 and U2 snRNPs component SmB - <i>Homo sapiens</i>	0	220	1	0	3	1	1.8	3.7	0.69
An02g04690	strong similarity to serine-type carboxypeptidase I cdpS - <i>Aspergillus saitoi</i> [putative sequencing error]	0	524	0	0	2	1	0.2	1.2	0.69
An11g01510	similarity to the protein involved in sister chromatid segregation Src1 - <i>Saccharomyces cerevisiae</i>	1	733	2	4	2	1	2.3	0.9	0.69
An16g08570	strong similarity to translation initiation factor 3 47 kDa subunit stt3p - <i>Schizosaccharomyces pombe</i>	13	741	15	17	43	21	11.4	15.7	0.68
An07g03680	strong similarity to repressor protein qutR - <i>Aspergillus nidulans</i> -	6	272	3	3	0	5	6.2	3.6	0.68
An07g01960	strong similarity to stearyl-CoA desaturase P-ole1 - <i>Pichia angusta</i>	3	456	13	32	29	22	26.0	20.4	0.68
An02g08100	strong similarity to translin-like protein TRAX - <i>Gallus gallus</i> -	0	235	2	1	1	1	3.9	1.9	0.67
An15g06740	strong similarity to cytoplasmic ribosomal protein of the large subunit L32 - <i>Drosophila subobscura</i>	0	179	11	5	12	6	24.0	18.6	0.67
An03g06950	strong similarity to dynamin-related protein Dnm1 - <i>Saccharomyces cerevisiae</i>	0	798	11	20	3	27	10.3	6.9	0.67
An01g03160	strong similarity to cytoplasmic ribosomal protein of the large subunit S8 - <i>Rattus norvegicus</i>	0	200	8	9	9	10	22.8	17.6	0.67
An06g01900	similarity to polyphosphoinositide binding protein Ssh2p - <i>Glycine max</i>	0	475	2	4	1	3	3.6	1.7	0.67
An07g03920	strong similarity to bile acid transporter Ybt1 - <i>Saccharomyces cerevisiae</i>	16	1643	6	22	41	25	4.5	7.3	0.66
An01g01000	similarity to hypothetical protein BAC11036.1 - <i>Homo sapiens</i>	1	410	1	0	4	1	1.0	2.4	0.66
An03g02990	similarity to α -N-acetylglucosamine transferase GNT1 - <i>Kluyveromyces lactis</i>	0	410	1	0	4	1	1.0	2.4	0.66
An08g10400	strong similarity to UDP-galactose transport protein SpUGT - <i>Schizosaccharomyces pombe</i>	8	410	1	0	1	4	1.0	2.4	0.66
An17g00880	strong similarity to endometrium tumour EST encoded protein 137 from patent DE19817948-A1 - <i>H. sapiens</i>	0	483	2	3	3	0	3.0	1.3	0.66
An16g01820	strong similarity to hypothetical inorganic phosphate transporter and regulator of Pho81p Pho88 - <i>Saccharomyces cerevisiae</i>	1	203	15	25	21	28	51.9	44.0	0.66
An08g03270	strong similarity to β -COP Sec26 - <i>Saccharomyces cerevisiae</i>	0	955	20	5	9	13	6.9	4.3	0.66

An02g09350	strong similarity to sulfate transport protein shst2 - <i>Stylosanthes hamata</i>	10	730	6	5	2	6	4.1	2.1	0.66
An15g01510	strong similarity to P-type ATPase Drs2 - <i>Saccharomyces cerevisiae</i>	9	1193	0	2	7	4	0.5	1.7	0.66
An08g00600	similarity to glutaredoxin - <i>Oryza sativa</i> -	1	252	1	3	1	2	4.6	2.5	0.65
An11g01120	strong similarity to NADPH-dependent aldehyde reductase - <i>Sporobolomyces salmonicolor</i>	0	381	4	5	17	3	6.5	9.7	0.64
An14g00900	strong similarity to glycosylphosphatidylinositol anchor synthesis protein Mcd4 - <i>Saccharomyces cerevisiae</i>	13	996	5	10	5	6	4.1	2.1	0.64
An11g11280	strong similarity to dihydrolipoamide succinyltransferase kgd2 - <i>Aspergillus fumigatus</i>	0	469	7	1	11	8	4.7	7.5	0.64
An01g09480	strong similarity to phosphatidylserine synthase pS232 - <i>Triticum aestivum</i>	4	236	0	1	3	1	1.7	3.4	0.64
An07g09570	strong similarity to phosphatidate cytidyltransferase Cds1 - <i>Saccharomyces cerevisiae</i>	8	453	2	5	14	3	4.3	7.0	0.63
An09g05970	strong similarity to cytosolic glutamate--tRNA ligase - <i>Arabidopsis thaliana</i>	0	712	4	2	13	4	2.4	4.4	0.63
An17g02180	similarity to hypothetical eIF-3 p110 subunit - <i>Caenorhabditis elegans</i>	4	255	1	2	4	4	3.6	6.0	0.63
An04g03495	similarity to oligosaccharyltransferase δ subunit Swp1 - <i>Saccharomyces cerevisiae</i>	4	287	8	10	19	15	16.8	21.7	0.63
An16g02210	strong similarity to proteasome 19S regulatory particle subunit Rpn12 - <i>Saccharomyces cerevisiae</i> -	0	278	2	3	4	0	5.1	2.9	0.62
An01g03120	strong similarity to phosphate transport protein Pho90 - <i>Saccharomyces cerevisiae</i>	12	881	0	0	3	1	0.1	0.9	0.62
53357	strong similarity to aldehyde dehydrogenase [<i>Aspergillus terreus</i> NIH2624]	0	513	5	2	5	0	3.8	1.9	0.62
An02g06300	similarity to naaladase II - <i>Homo sapiens</i> -	1	888	0	0	2	2	0.1	0.9	0.62
An17g02340	strong similarity to cytosolic serine--tRNA ligase Ses1 - <i>Saccharomyces cerevisiae</i>	0	474	6	8	10	3	8.0	5.1	0.61
42743	strong similarity to methyltransferase family protein [<i>Aspergillus flavus</i> NRRL3357]	0	263	11	8	19	2	19.3	14.7	0.61
An01g10460	similarity to hypothetical protein CAD21056.1 - <i>Neurospora crassa</i> -	1	544	2	2	1	1	2.2	0.8	0.61
An05g00200	strong similarity to ankyrin repeat-containing protein Akr1 - <i>Saccharomyces cerevisiae</i>	5	731	5	8	19	11	4.8	7.5	0.60
An17g00320	strong similarity to hypothetical membrane protein YDR326c - <i>Saccharomyces cerevisiae</i>	1	1252	0	0	4	1	0.1	0.8	0.60
An12g04860	strong similarity to cytoplasmic ribosomal protein of the large subunit L30 - <i>Saccharomyces cerevisiae</i>	0	106	2	6	4	5	20.9	16.2	0.60
An11g09890	strong similarity to mannosyltransferase 1 PMT1 - <i>Candida albicans</i>	10	944	8	19	13	12	7.6	4.9	0.59
An11g05680	similarity to cytochrome P450 3A13 - <i>Mus musculus</i>	1	539	10	6	7	8	8.0	5.2	0.59
An01g02900	strong similarity to translation initiation factor Eif-5a.2 - <i>Saccharomyces cerevisiae</i>	0	160	6	0	5	1	10.6	7.3	0.59
An15g06310	strong similarity to phosphatidylethanolamine methyltransferase cho2p - <i>Schizosaccharomyces pombe</i>	7	1077	17	26	25	18	10.5	7.3	0.59
An08g00430	strong similarity to precursor of carboxypeptidase Kex1 - <i>Saccharomyces cerevisiae</i>	1	612	0	0	2	1	0.2	1.0	0.59
An12g00510	strong similarity to cytoplasmic ribosomal protein of the small subunit S24.e - <i>Saccharomyces cerevisiae</i>	0	133	6	10	9	10	32.3	26.4	0.58
An02g02980	strong similarity to protein influencing Itr1 expression Die2 - <i>Saccharomyces cerevisiae</i>	9	566	2	6	3	3	3.9	2.1	0.57
An13g00540	strong similarity to hypothetical protein Afu7g04060 - <i>Aspergillus fumigatus</i>	1	265	0	2	4	2	2.5	4.4	0.57
208521	strong similarity to FAD binding domain protein [<i>Aspergillus clavatus</i> NRRL 1]	1	581	1	3	2	0	2.0	0.8	0.57
An18g05770	strong similarity to component of chaperonin-containing T-complex Cct7 - <i>Saccharomyces cerevisiae</i>	0	631	0	0	1	2	0.2	1.0	0.57
An03g02530	similarity to hypothetical proteinase encoded by SCD8A.14c - <i>Streptomyces coelicolor</i>	0	328	2	3	8	4	4.4	6.9	0.57
An08g10500	strong similarity to hypothetical protein EAA62682.1 - <i>Aspergillus nidulans</i>	0	268	1	0	1	3	1.5	3.0	0.56
An04g06920	extracellular α -glucosidase agIU - <i>Aspergillus niger</i>	0	985	2	3	13	3	1.5	3.0	0.56
An16g02360	strong similarity to pyridoxine 4-dehydrogenase PLR - <i>Schizosaccharomyces pombe</i> -	0	329	5	1	5	0	5.1	3.0	0.56
An17g00210	strong similarity to hypothetical oxidoreductase CAB46711.1 - <i>Schizosaccharomyces pombe</i>	0	360	4	2	11	3	4.7	7.3	0.55
An12g01350	strong similarity to cytoplasmic ribosomal protein of the small subunit S4 - <i>Saccharomyces cerevisiae</i>	0	259	15	18	34	23	33.7	40.0	0.55
An12g04500	strong similarity to transport ATPase Drs2 - <i>Saccharomyces cerevisiae</i>	7	1358	0	0	3	2	0.1	0.7	0.55
An01g04570	strong similarity to capsular associated protein CAP10 - <i>Filobasidiella neoformans</i>	9	997	0	0	3	1	0.1	0.8	0.55
An03g03900	similarity to single-stranded DNA-binding protein Rim1 - <i>Saccharomyces cerevisiae</i>	0	148	2	3	2	3	9.7	6.7	0.54

An15g04150	strong similarity to oxidoreductase, actinorhodin production encoded by Orf11 - Streptomyces lividans-	0	293	2	1	2	0	3.1	1.5	0.54
An08g05670	strong similarity to nitrate permease crnA - Aspergillus nidulans	12	504	0	1	1	4	0.8	2.0	0.54
An15g05290	strong similarity to bile acid transporter Ybt1 - Saccharomyces cerevisiae	14	1542	6	18	28	27	4.1	6.5	0.53
An15g07040	strong similarity to phospholipase D Spo14 - Saccharomyces cerevisiae	0	1214	2	10	7	1	2.7	1.3	0.52
An04g07060	strong similarity to peptide ABC transporter protein Mdl1 - Saccharomyces cerevisiae	5	787	0	1	1	5	0.5	1.5	0.52
An17g02240	strong similarity to cytoplasmic ribosomal protein of the large subunit L23a - Rattus norvegicus	0	154	3	2	4	1	9.3	6.4	0.52
An11g04730	prolyl aminopeptidase papA - Aspergillus niger	0	511	3	2	8	5	2.8	4.8	0.52
An08g05640	strong similarity to nitrite reductase (NADH) niiA - Aspergillus nidulans	0	1097	31	25	36	24	13.4	9.9	0.51
An04g00410	strong similarity to dipeptidyl peptidase III - Rattus norvegicus-	0	707	7	13	41	0	7.5	10.6	0.51
An01g02810	strong similarity to cytochrome P450 sterol δ 22-desaturase Erg5 - Saccharomyces cerevisiae	0	531	1	0	3	2	0.7	1.9	0.51
An13g00620	strong similarity to 80K protein H precursor G19P1 - Homo sapiens	0	568	11	25	20	20	16.7	12.9	0.51
An08g07420	strong similarity to multifunctional pyrimidine biosynthesis enzyme pyrABCN - Aspergillus nidulans	0	2277	10	4	30	10	1.7	3.2	0.50
An09g06800	strong similarity to leucyl aminopeptidase Ape2 - Saccharomyces cerevisiae-	0	882	4	9	30	0	4.0	6.2	0.50
An04g07080	similarity to hypothetical protein SPBC2G5.01 - Schizosaccharomyces pombe	1	433	6	13	3	17	11.7	8.5	0.50
An07g01970	strong similarity to cytoplasmic metalloproteinase mepB - Aspergillus fumigatus-	0	716	1	5	16	0	2.4	4.2	0.50
An04g04940	strong similarity to hypothetical protein Afu4g11550 - Aspergillus fumigatus	4	303	2	5	6	9	6.4	9.2	0.50
An11g06860	strong similarity to multidrug transporter bmr3 - Bacillus subtilis	12	550	1	0	3	2	0.7	1.8	0.49
An05g02280	similarity to esterase from patent WO9802556-A2 - Alcaligenes sp.	0	375	1	5	1	4	4.5	2.6	0.49
An08g07360	strong similarity to mitochondrial import receptor TOM20 - Neurospora crassa	1	167	4	9	4	11	21.0	16.7	0.49
53656	strong similarity to Pc24g00650 [Penicillium chrysogenum Wisconsin 54-1255]	0	134	3	1	4	0	8.7	6.1	0.49
An12g00410	strong similarity to RNA binding protein 47 RBP47 - Nicotiana glauca	0	402	1	6	4	2	4.9	2.9	0.49
An02g02020	strong similarity to vacuolar H(+)-transporting ATPase subunit B Vma2 - Saccharomyces cerevisiae	0	507	19	14	18	19	17.2	13.3	0.49
An12g08610	glucokinase glkA - Aspergillus niger-	0	495	6	10	16	0	8.7	6.0	0.49
An15g03940	strong similarity to monosaccharide transporter AmMst-1 - Amanita muscaria	10	527	2	2	6	5	2.2	3.9	0.48
An07g09190	strong similarity to very long-chain fatty acyl-CoA synthase Fat1 - Saccharomyces cerevisiae	3	655	1	5	1	3	2.6	1.2	0.48
An07g10350	protein O-mannosyl transferase pmtA - Aspergillus niger	9	741	8	18	26	25	9.3	12.5	0.48
An08g03690	strong similarity to ADP-ribosylation factor arf1 - Ajellomyces capsulatus	0	183	2	1	5	2	5.0	7.4	0.47
An02g14210	strong similarity to hypothetical agmanitase - Escherichia coli	0	422	3	3	9	5	4.0	6.2	0.47
An05g01070	strong similarity to 7-aminocholesterol resistance protein Rta1 - Saccharomyces cerevisiae	7	320	0	1	3	1	1.2	2.5	0.47
An01g03350	strong similarity to C-8 sterol isomerase erg-1 - Neurospora crassa	1	215	6	12	7	14	22.4	18.0	0.47
An14g02280	strong similarity to hypothetical protein Afu4g03090 - Aspergillus fumigatus	1	342	0	3	5	3	2.7	4.5	0.47
An04g08820	strong similarity to glucosyltransferase Alg8 - Saccharomyces cerevisiae	10	580	0	1	4	1	0.7	1.7	0.47
An11g10260	strong similarity to α N-acetylglucosamine transferase - Kluyveromyces lactis	1	345	2	1	6	2	2.6	4.4	0.46
An16g08470	similarity to hypothetical cell growth regulator OS-9 - Homo sapiens	0	509	4	6	6	3	5.4	3.4	0.46
An03g05000	similarity to human transmembrane protein HTPN-73 from patent WO9961471-A2 - Homo sapiens	7	457	3	5	3	4	4.8	3.0	0.46
An08g10710	strong similarity to proteasome 19S regulatory particle subunit Rpn9 - Saccharomyces cerevisiae	0	381	3	2	2	2	3.8	2.1	0.46
An03g03650	strong similarity to hypothetical protein Afu3g04020 - Aspergillus fumigatus	0	332	0	1	3	1	1.2	2.4	0.45
An08g02770	strong similarity to vacuolar H(+)-ATPase activator subunit Vma13 - Saccharomyces cerevisiae	0	478	11	8	7	13	10.6	7.7	0.45
An01g04250	strong similarity to uroporphyrinogen decarboxylase from patent WO9925839-A1 - Thielavia terrestris-	0	363	1	3	3	0	3.2	1.7	0.45
An04g04990	strong similarity to mannose-1-phosphate guanyltransferase MPG1 - Trichoderma reesei-	0	364	3	1	1	2	3.2	1.7	0.45

An12g03990	strong similarity to hypothetical protein EAA57923.1 - <i>Aspergillus nidulans</i>	0	769	5	23	11	18	9.6	6.9	0.45
An01g12570	strong similarity to histidinol dehydrogenase his-3 - <i>Neurospora crassa</i>	0	866	5	4	21	1	2.9	4.7	0.45
An06g00710	similarity to β -lactamase from patent FR2792651-A1 - <i>Pyrococcus abyssi</i>	0	1084	4	3	2	2	1.8	0.7	0.45
An18g02480	strong similarity to DNA repair protein XAB2 - <i>Homo sapiens</i> -	0	822	1	2	0	1	1.1	0.3	0.45
An04g05630	similarity to nuclear pore complex subunit Nup100 - <i>Saccharomyces cerevisiae</i> -	0	1949	3	2	0	1	0.7	0.1	0.45
An08g06400	strong similarity to actin-related protein arp2p - <i>Schizosaccharomyces pombe</i> [truncated ORF]	0	341	1	0	2	2	1.1	2.4	0.44
An15g01350	strong similarity to hypothetical cleft lip and palate transmembrane protein 1 CLPTM1 - <i>Homo sapiens</i>	5	601	4	8	7	4	5.4	3.5	0.44
An12g00720	strong similarity to 138 kD subunit of DNA-dependent RNA polymerase II rpb2p - <i>S. pombe</i>	0	1256	0	0	3	1	0.1	0.6	0.44
An07g04850	An02g01510	0	346	1	0	3	1	1.1	2.3	0.44
An12g04870	strong similarity to cytoplasmic ribosomal protein of the large subunit L10 - <i>Saccharomyces cerevisiae</i>	0	223	27	18	26	31	53.1	46.5	0.44
An08g05610	nitrate reductase (NADPH) niaD - <i>Aspergillus niger</i> -	0	867	6	2	20	0	2.6	4.3	0.44
An07g10420	strong similarity to cell division cycle protein Cdc50 - <i>Saccharomyces cerevisiae</i>	2	402	1	3	7	3	2.9	4.7	0.43
An15g00170	strong similarity to protein kinase skp1p - <i>Schizosaccharomyces pombe</i>	0	394	6	5	6	5	7.6	5.3	0.42
An16g08550	strong similarity to ATP synthase coupling factor (F0) subunit e Tim11 - <i>Saccharomyces cerevisiae</i>	1	92	2	4	4	7	18.4	22.5	0.42
An17g00910	strong similarity to 4-aminobutyrate transaminase gatA - <i>Aspergillus nidulans</i>	0	498	0	8	1	6	4.4	2.7	0.42
An08g02310	similarity to HC-toxin non-ribosomal peptide synthase HTS1 - <i>Cochliobolus carbonum</i>	0	6242	25	15	10	14	1.7	0.7	0.41
An11g09670	strong similarity to cytoplasmic ribosomal protein of the small subunit S27 - <i>Homo sapiens</i>	0	82	1	2	4	2	11.1	14.3	0.40
An02g01830	cytochrome c cyc - <i>Aspergillus niger</i>	0	112	5	8	4	12	31.4	26.6	0.40
An09g05290	strong similarity to exonuclease II SPAC17A5.14 - <i>Schizosaccharomyces pombe</i>	0	1406	2	7	19	5	1.8	3.1	0.40
An15g06390	strong similarity to ribosomal RNA processing protein Rrp5 - <i>Saccharomyces cerevisiae</i>	0	1822	3	0	12	1	0.5	1.3	0.40
An08g05730	strong similarity to cytoplasmic ribosomal protein of the large subunit L1 - <i>Saccharomyces cerevisiae</i>	0	300	3	2	10	1	4.8	6.9	0.40
An18g06440	strong similarity to COPII vesicle component Yip3 - <i>Saccharomyces cerevisiae</i>	3	173	5	3	10	5	12.8	16.2	0.39
An07g03200	strong similarity to adaptor complex AP-1 medium chain AP47 - <i>Mus musculus</i>	0	418	3	1	2	1	2.8	1.5	0.39
An02g07120	strong similarity to viral integration site protein int-6/EIF-3 P48 - <i>Mus musculus</i>	0	452	12	19	18	18	18.1	14.6	0.39
181397	strong similarity to fatty-acyl coenzyme A oxidase (Pox1), putative [<i>Aspergillus fumigatus</i> A1163]	0	694	1	0	4	1	0.6	1.4	0.39
An02g14560	oligosaccharyltransferase α subunit ostA - <i>Aspergillus niger</i>	1	503	23	56	46	53	41.1	35.7	0.39
An16g04640	strong similarity to hypothetical protein SPCC1281.03c - <i>Schizosaccharomyces pombe</i>	2	186	0	2	4	1	3.5	5.3	0.38
An15g01890	strong similarity to β -glucosidase precursor bgl2 - <i>Coccidioides immitis</i>	0	936	0	0	2	1	0.1	0.7	0.38
An02g03860	strong similarity to hypothetical protein B1D1.160 - <i>Neurospora crassa</i> -	0	1265	6	6	9	0	2.6	1.4	0.38
An01g02600	strong similarity to γ 1-adaptin - <i>Homo sapiens</i>	0	848	4	4	4	2	2.6	1.4	0.38
An02g03520	strong similarity to G protein-binding protein CRFG - <i>Homo sapiens</i>	0	655	3	0	4	5	1.4	2.6	0.38
An02g03570	strong similarity to membrane protein YBR159w - <i>Saccharomyces cerevisiae</i>	3	346	8	19	19	13	20.7	16.9	0.37
An04g01830	similarity to hypothetical DEC1 protein homolog - <i>Schizosaccharomyces pombe</i>	0	937	2	2	9	3	1.2	2.4	0.37
An02g02410	similarity to high density lipoprotein-binding protein HBP - <i>Homo sapiens</i>	0	976	0	0	2	1	0.1	0.6	0.37
An16g07390	strong similarity to endoplasmic reticulum signal peptidase subunit Spc2 - <i>Saccharomyces cerevisiae</i>	2	209	2	7	4	6	11.8	9.1	0.37
An01g09260	strong similarity to aldehyde dehydrogenase (NADP+) - <i>Homo sapiens</i>	0	500	3	6	11	8	4.9	7.0	0.37
An09g06580	strong similarity to ras-GTPase-activating protein SH3-domain binding protein G3BP - <i>Mus musculus</i>	0	537	5	2	4	2	3.6	2.2	0.37
An08g03190	strong similarity to tubulin β chain β -tubulin - <i>Aspergillus flavus</i>	0	447	28	30	29	43	34.1	29.3	0.36
An07g05160	similarity to hypothetical protein C01B10.8 - <i>Caenorhabditis elegans</i>	5	542	2	5	3	3	3.6	2.2	0.36
An04g01780	strong similarity to hypothetical protein YAR002c-a - <i>Saccharomyces cerevisiae</i>	1	232	3	6	9	8	10.7	13.6	0.36

An07g07880	similarity to ORFX ORF2689 polypeptide sequence SEQ ID NO:5378 from patent WO200058473-A2 - Homo sapiens	0	517	0	5	7	5	2.8	4.4	0.36
An16g04160	strong similarity to galactokinase Gal1 - Saccharomyces cerevisiae-	0	524	3	3	5	0	3.2	1.9	0.35
An16g02820	strong similarity to fatty acid omega-hydroxylase CYP505 - Fusarium oxysporum	0	1104	6	8	5	7	3.4	2.0	0.35
An12g00800	strong similarity to C2-domain family vesicle protein GLUT4 - Rattus norvegicus	1	1520	19	21	58	20	6.9	9.3	0.35
An11g02620	strong similarity to alanine transaminase ALA2 - Hordeum vulgare-	0	567	2	5	6	0	3.4	2.1	0.35
An11g10320	strong similarity to cytoskeleton assembly control protein homolog Sla2 - Saccharomyces cerevisiae	0	1015	3	1	10	2	1.2	2.2	0.34
An03g01280	strong similarity to glutamine--tRNA ligase - Saccharomyces cerevisiae	0	625	3	4	12	4	3.1	4.8	0.34
An04g09890	strong similarity to hypothetical cell wall α -glucan synthase ags1p - Schizosaccharomyces pombe	13	2397	0	4	8	8	0.5	1.2	0.34
An04g00670	strong similarity to hypothetical coiled-coil protein similar to human congenital heart disease protein CAC05252.1 - Schizosaccharomyces pombe	1	196	1	3	2	2	6.0	4.1	0.33
An01g05650	strong similarity to tubulin α -1 chain tubA - Aspergillus nidulans	0	448	19	13	23	15	18.9	15.5	0.33
An17g00540	similarity to suppressor of S.cerevisiae sin4 mutation Rlr1 - Saccharomyces cerevisiae	0	2274	0	0	3	2	0.1	0.4	0.33
An08g03960	strong similarity to hypothetical endoplasmic reticulum associated protein - Schizosaccharomyces pombe	7	254	4	5	10	7	9.7	12.4	0.33
An07g05820	strong similarity to hypothetical transmembrane protein usgS - Aspergillus nidulans	4	366	4	10	13	13	10.3	13.1	0.32
An07g06840	strong similarity to precursor of dihydrolipoamide dehydrogenase Lpd1 - Saccharomyces cerevisiae	0	514	26	41	57	27	34.2	29.7	0.32
An16g08830	strong similarity to component of ER protein-translocation subcomplex Sec71 from patent WO9949028-A1 - Saccharomyces cerevisiae	1	270	5	15	11	13	19.8	16.4	0.32
An08g06770	strong similarity to cytoplasmic isoleucine--tRNA ligase IIs1 - Saccharomyces cerevisiae-	0	1077	8	3	25	0	2.8	4.3	0.32
An15g00690	strong similarity to 14.8 kD subunit of NADH:ubiquinone reductase - Neurospora crassa	0	123	0	6	3	8	13.8	16.9	0.32
An02g14450	secretory pathway Ca ²⁺ -ATPase pmrA - Aspergillus niger	6	1028	2	6	3	3	2.2	1.1	0.32
An03g01320	strong similarity to hypothetical protein mlr2056 - Mesorhizobium loti	1	256	2	4	9	3	6.6	8.8	0.32
An16g02560	strong similarity to hypothetical β -lactamase XF1621 - Xylella fastidiosa-	0	506	1	2	1	1	1.8	0.9	0.31
An02g07690	strong similarity to chromosome segregation protein mal3p - Schizosaccharomyces pombe	0	246	6	3	6	4	10.1	7.7	0.31
An18g04030	similarity to Topoisomerase I TopoI - Filobasidiella neoformans-	0	514	1	2	2	0	1.8	0.9	0.31
An02g12750	strong similarity to cytoskeleton specific chaperonin subunit Cct4 - Saccharomyces cerevisiae	0	536	2	2	1	2	2.2	1.2	0.31
An11g05000	strong similarity to Niemann-Pick C1 protein - Homo sapiens	14	1277	1	8	12	10	1.9	3.2	0.30
An04g03400	strong similarity to aldehyde dehydrogenase aldA - Aspergillus niger	0	502	6	4	7	3	5.4	3.8	0.30
An12g01020	strong similarity to acetamidase amdS - Aspergillus nidulans	0	579	6	17	19	23	10.6	13.2	0.30
An02g08660	strong similarity to hypothetical protein H04M03.4 - Caenorhabditis elegans	0	510	17	12	28	6	15.1	12.2	0.30
An02g11200	similarity to 13 kD subunit of NADH:ubiquinone reductase - Bos taurus	0	292	0	3	1	6	3.1	4.6	0.30
An03g00730	strong similarity to copper amine oxidase AO-I from patent JP08070872-A - Aspergillus niger-	0	668	2	5	6	0	2.9	1.8	0.29
An12g03980	strong similarity to hypothetical protein AAN52526.1 - Pichia angusta	2	176	1	2	1	2	5.2	3.6	0.29
An08g07290	aldehyde dehydrogenase aldA - Aspergillus niger	0	497	19	14	42	15	17.5	20.9	0.29
An14g01030	strong similarity to translation initiation factor eIF-3 subunit - Homo sapiens [truncated ORF]	0	505	11	15	29	17	13.7	16.6	0.29
An09g06650	strong similarity to core protein II of ubiquinol--cytochrome c reductase CAA42214.1 - Bos primigenius taurus	0	458	32	48	61	42	45.7	40.8	0.29
An12g02080	strong similarity to cytochrome P450 monooxygenase stcS - Aspergillus nidulans [putative frameshift]	0	510	3	10	9	16	6.9	9.0	0.29
An02g05870	strong similarity to coatomer β subunit copB2 - Homo sapiens [putative frameshift]	0	873	6	7	24	3	4.0	5.7	0.28
An02g01690	strong similarity to p150 component of the COPII coat of secretory pathway vesicles Sec31 - S. cerevisiae	0	1259	2	1	7	3	0.7	1.5	0.28
An01g14730	similarity to cis cis-muconate lactonizing enzyme I TcMLE - Trichosporon cutaneum	0	391	2	5	5	2	5.0	3.5	0.28

An11g02040	strong similarity to phosphogluconate dehydrogenase Gnd1 - <i>Saccharomyces cerevisiae</i>	0	508	62	52	103	46	58.7	53.1	0.28
An14g03050	strong similarity to hypothetical protein of the UPF0028 family - <i>Schizosaccharomyces pombe</i>	2	1482	1	0	4	2	0.3	0.8	0.28
An02g03010	strong similarity to chromosome segregation protein cut14p - <i>Schizosaccharomyces pombe</i>	0	1179	2	6	3	3	1.9	1.0	0.28
An17g01330	strong similarity to adenosine kinase - <i>Cricetulus griseus</i>	0	353	3	4	13	1	5.5	7.4	0.27
An11g00010	similarity to antiviral GTPase Mx1 - <i>Oncorhynchus mykiss</i>	0	802	2	17	8	12	6.3	4.6	0.27
An07g10400	strong similarity to cell division control protein Cdc68 - <i>Saccharomyces cerevisiae</i>	0	1020	0	1	4	1	0.4	1.0	0.27
An07g02770	strong similarity to hypothetical protein YKL195w - <i>Saccharomyces cerevisiae</i>	0	270	0	2	2	3	2.4	3.7	0.26
An01g06040	strong similarity to hypothetical membrane protein YOL077c - <i>Saccharomyces cerevisiae</i>	0	358	3	3	5	1	4.7	3.3	0.26
An02g09290	hypothetical protein-	0	608	1	2	1	1	1.5	0.7	0.26
An18g02990	similarity to mitochondrial ribosomal protein Mrp20 - <i>Saccharomyces cerevisiae</i> -	0	196	1	2	1	2	4.6	3.2	0.26
An08g00880	strong similarity to hypothetical branched-chain α -ketoacid dehydrogenase E1 β subunit - <i>Homo sapiens</i>	0	375	8	13	9	16	14.9	12.3	0.26
An07g07340	strong similarity to luminal ER-protein retention receptor ERD2 - <i>Kluyveromyces marxianus</i>	6	335	2	1	6	1	2.7	4.0	0.26
An14g02360	strong similarity to U2 snRNA-specific protein A - <i>Homo sapiens</i>	0	253	3	1	2	2	4.6	3.2	0.26
An04g01940	strong similarity to translation initiation factor eIF2 γ chain Gcd11 - <i>Saccharomyces cerevisiae</i>	0	513	9	4	9	5	6.8	5.1	0.26
An12g08560	strong similarity to proteinase SlpE - <i>Streptomyces lividans</i>	2	624	0	3	7	1	1.5	2.5	0.26
An15g06020	strong similarity to ubiquitin activating protein Uba1 - <i>Saccharomyces cerevisiae</i> -	0	1034	6	8	29	0	3.6	5.1	0.26
An04g01230	strong similarity to hypothetical ECM33 homolog SPCC1223.12c - <i>Schizosaccharomyces pombe</i>	0	401	1	3	5	4	2.9	4.3	0.26
An08g03490	similarity to elongation factor 1 β EF-1 - <i>Oryctolagus cuniculus</i>	0	302	6	3	7	3	8.2	6.3	0.25
An03g04060	strong similarity to cadmium resistance protein Ycf1 - <i>Saccharomyces cerevisiae</i>	12	1541	5	23	32	23	4.8	6.5	0.25
An02g07500	strong similarity to saccharopine dehydrogenase LYS1 - <i>Candida albicans</i> -	0	377	3	3	6	0	4.5	3.1	0.25
An13g00090	strong similarity to eburicol 14 α -demethylase cyp51 - <i>Uncinula necator</i>	2	556	5	13	19	14	8.7	10.9	0.25
An12g08760	strong similarity to vacuolar ATPase subunit E Vma-4 - <i>Neurospora crassa</i>	0	231	4	7	6	7	13.0	10.5	0.25
An11g11310	strong similarity to histone H2B - <i>Aspergillus nidulans</i>	0	141	4	5	8	3	17.5	14.7	0.25
An05g00070	strong similarity to leukotriene-A4 hydrolase - <i>Mus musculus</i> -	0	664	1	3	3	0	1.8	1.0	0.25
An17g02170	strong similarity to centromere/microtubule-binding protein Cbf5 - <i>Saccharomyces cerevisiae</i>	0	485	4	1	8	3	3.0	4.3	0.24
An08g00310	strong similarity to septin aspD - <i>Aspergillus nidulans</i>	0	346	5	4	16	1	7.1	9.1	0.24
An13g00080	strong similarity to hypothetical conserved protein B2F7.100 - <i>Neurospora crassa</i>	0	238	1	0	2	1	1.6	2.7	0.24
An14g04180	strong similarity to H ⁺ -transporting ATP synthase β chain - <i>Neurospora crassa</i> [truncated ORF]	0	417	71	70	134	85	88.3	95.0	0.24
An15g02340	strong similarity to argininosuccinate synthase Arg1 - <i>Saccharomyces cerevisiae</i>	0	417	6	4	17	2	6.6	8.4	0.24
An02g12120	strong similarity to cytoplasmic ribosomal protein of the large subunit Rpl37b - <i>Saccharomyces cerevisiae</i>	0	109	3	2	4	2	13.1	10.8	0.24
An16g07120	strong similarity to regulator protein Sin3 - <i>Saccharomyces cerevisiae</i>	0	1531	0	0	2	1	0.1	0.4	0.23
An01g12380	strong similarity to ATP-binding cassette transporter PMR1 - <i>Penicillium digitatum</i>	13	1539	0	0	1	2	0.1	0.4	0.23
An07g04190	strong similarity to dolichyl-diphosphooligosaccharide-protein glycosyltransferase DDOST - <i>Gallus gallus</i>	1	458	30	44	41	55	42.3	38.0	0.23
An01g09220	weak similarity to tyrosinase melC2 - <i>Streptomyces lincolnensis</i> -	0	406	2	4	6	0	4.2	2.9	0.23
An03g04560	strong similarity to morphine dehydrogenase - <i>Pseudomonas putida</i> -	0	283	3	1	4	0	4.1	2.9	0.23
An03g03660	strong similarity to glutathione reductase Glr1 - <i>Saccharomyces cerevisiae</i> -	0	472	2	5	7	0	4.1	2.9	0.23
An18g03100	strong similarity to hypothetical precursor of secretory protein Ssp120 - <i>Saccharomyces cerevisiae</i>	0	199	6	4	7	5	13.7	11.3	0.23
An02g10310	strong similarity to glycogen synthase - <i>Neurospora crassa</i>	0	713	3	1	1	2	1.6	0.9	0.23
An01g04280	strong similarity to dnaJ protein homolog Ydj1 - <i>Saccharomyces cerevisiae</i>	0	413	5	1	3	3	4.1	2.8	0.23
An16g07470	similarity to mediator of 40S ribosomal subunit assembly gar2p - <i>Schizosaccharomyces pombe</i>	0	381	3	0	5	2	2.4	3.6	0.23

An09g04170	strong similarity to protein Sly1 - <i>Saccharomyces cerevisiae</i>	0	705	3	0	6	2	1.3	2.2	0.23
An01g09520	strong similarity to mitogen-activated protein kinase mPKA - <i>Aspergillus nidulans</i>	0	421	5	1	2	4	4.0	2.8	0.22
An08g06090	similarity to nucleoporin nup184p - <i>Schizosaccharomyces pombe</i>	0	1832	1	0	2	4	0.2	0.6	0.22
An07g08170	strong similarity to IMP dehydrogenase IMH3 - <i>Candida albicans</i>	0	533	16	8	21	21	12.0	14.4	0.22
An02g07210	aspartic protease pepE - <i>Aspergillus niger</i>	0	398	8	12	16	8	13.4	11.1	0.22
An08g05500	strong similarity to mitochondrial ribosomal protein of the large subunit Yml3 - <i>Saccharomyces cerevisiae</i>	0	371	4	1	1	4	3.9	2.7	0.22
An07g06990	strong similarity to hypothetical protein SPCC594.04c - <i>Schizosaccharomyces pombe</i>	2	373	1	4	1	4	3.8	2.7	0.21
An08g04470	strong similarity to mitochondrial elongation factor Tu - <i>Arabidopsis thaliana</i>	0	440	4	10	3	13	8.6	6.8	0.21
An12g00820	strong similarity to UTP-glucose-1-phosphate uridylyltransferase Ugp1 - <i>Saccharomyces cerevisiae</i>	0	521	34	12	50	26	23.2	26.5	0.21
An18g02760	similarity to hypothetical protein T21J18.40 - <i>Arabidopsis thaliana</i>	0	1689	0	0	1	2	0.1	0.4	0.21
An03g01090	similarity to α -1,6-mannosyltransferase Hoc1 - <i>Saccharomyces cerevisiae</i>	0	413	2	1	6	1	2.2	3.3	0.21
An18g00730	strong similarity to capsule-associated protein CAP59 - <i>Cryptococcus neoformans</i>	1	430	3	7	7	4	6.4	4.8	0.21
An01g04320	strong similarity to COPII vesicle coat component protein Erv46 - <i>Saccharomyces cerevisiae</i>	2	406	8	11	24	9	12.5	14.9	0.21
An04g06200	strong similarity to dihydrosphingosine/sphingosine phosphate lyase Dpl1 - <i>Saccharomyces cerevisiae</i>	0	636	6	7	10	4	5.5	4.1	0.21
An04g03680	similarity to glucanase ZmGnsN4 from patent WO200073470-A2 - <i>Zea mays</i>	0	281	0	1	2	1	1.4	2.2	0.20
An18g06230	strong similarity to proteasome 19S regulatory particle subunit Rpt4 - <i>Saccharomyces cerevisiae</i> -	0	393	3	2	0	5	3.6	2.5	0.20
An15g01680	strong similarity to signal peptide-containing protein SIGP from patent WO9933981-A2 - <i>Homo sapiens</i>	5	355	0	2	3	2	1.8	2.8	0.20
55153	strong similarity to nonribosomal peptide synthetase; NRPS [<i>Hypocrea virens</i>]	0	5640	19	6	4	14	1.2	0.6	0.20
An15g00160	strong similarity to transcription regulator CaGCR3 - <i>Candida albicans</i> -	0	849	4	4	17	0	2.6	3.7	0.20
An02g06530	strong similarity to protein required for dispersion of mitochondria cluA - <i>Dictyostelium discoideum</i>	0	1249	6	3	16	4	2.0	3.0	0.20
An15g03090	strong similarity to C-3 sterol dehydrogenase/C-4 decarboxylase ERG26 - <i>Candida albicans</i>	0	412	4	2	10	2	4.1	5.5	0.20
An15g01690	strong similarity to cytoplasmic ribosomal protein of the large subunit L14.a - <i>Saccharomyces cerevisiae</i>	0	149	8	9	11	11	30.6	27.2	0.19
An18g02470	strong similarity to vacuolar ATPase subunit D Vma-8 - <i>Neurospora crassa</i> -	0	266	2	1	1	2	3.4	2.4	0.19
An18g05180	strong similarity to hypothetical membrane protein YCR044c - <i>Saccharomyces cerevisiae</i>	7	374	1	1	3	2	1.7	2.7	0.19
An14g05020	strong similarity to armadillo repeat-containing protein Vac8 - <i>Saccharomyces cerevisiae</i> -	0	576	2	5	0	7	3.4	2.3	0.19
An08g09230	strong similarity to isotrichodermin C-15 hydroxylase Tri11 - <i>Fusarium sporotrichioides</i>	1	500	3	3	2	4	3.4	2.3	0.19
An16g02940	strong similarity to protein fragment SEQ ID NO:69506 from patent EP1033405-A2 - <i>Zea mays</i>	0	267	4	3	5	3	7.3	5.7	0.19
An16g05050	similarity to importin RanBP7 - <i>Homo sapiens</i>	0	1045	4	3	5	1	1.9	1.1	0.19
An03g05070	strong similarity to proclavaminc acid amidino hydrolase pah - <i>Streptomyces clavuligerus</i>	0	382	2	0	3	2	1.7	2.6	0.19
An12g07510	similarity to secreted protein #70 from patent WO9925825-A2 - <i>Homo sapiens</i>	1	176	0	3	3	3	5.2	6.7	0.19
An04g02020	strong similarity to cyclophilin cypB - <i>Aspergillus nidulans</i>	2	212	6	24	29	19	37.4	41.3	0.19
An02g12430	precursor of mitochondrial isocitrate dehydrogenase icdA - <i>Aspergillus niger</i>	0	413	5	4	2	8	6.0	4.6	0.19
An07g08740	weak similarity to 75 kDa invariant surface glycoprotein ISG75 - <i>Trypanosoma brucei</i>	0	314	0	1	2	1	1.2	2.0	0.18
An12g07850	strong similarity to fumarate hydratase fumR - <i>Rhizopus oryzae</i>	0	533	7	14	13	12	10.5	8.6	0.18
An08g00520	strong similarity to protein sonA - <i>Aspergillus nidulans</i>	0	359	2	2	2	2	3.3	2.3	0.18
An09g06790	secretion related GTPase srgB - <i>Aspergillus niger</i>	0	201	6	12	13	10	24.0	21.1	0.18
An07g10040	strong similarity to coproporphyrinogen oxidase III Hem13 - <i>Saccharomyces cerevisiae</i>	0	440	0	5	4	1	3.3	2.3	0.18
An02g14080	strong similarity to asparagine--tRNA ligase ASNS - <i>Thermus aquaticus</i>	0	574	4	7	11	1	5.2	3.9	0.18
An07g10110	strong similarity to 26S proteasome regulatory chain 12 rp12 - <i>Homo sapiens</i>	0	356	3	2	6	4	4.0	5.3	0.18
An01g08420	strong similarity to calcium-binding protein precursor cnx1p - <i>Schizosaccharomyces pombe</i>	1	562	31	60	95	49	42.4	46.4	0.18

An02g14100	similarity to cDNA RNA-binding protein TIA-1 - Mus musculus	0	833	0	1	3	1	0.5	1.0	0.18
An08g07840	NADPH cytochrome P450 oxidoreductase cprA - Aspergillus niger [possible sequencing error]	1	695	20	51	80	35	26.8	30.0	0.18
An11g09790	strong similarity to sulfate adenylyltransferase sC - Aspergillus nidulans	0	574	18	13	22	16	14.3	12.1	0.18
An01g02430	strong similarity to D-amino-acid oxidase DAO - Fusarium solani-	0	363	3	1	4	0	3.2	2.2	0.18
An09g00620	similarity to estradiol 17- β -dehydrogenase HSD17B1 - Rattus norvegicus	0	283	5	9	11	13	13.3	15.6	0.18
An01g12720	similarity to tumour suppressor protein TSA305 from patent WO9928457-A1 - Homo sapiens	0	689	2	6	5	3	3.2	2.2	0.18
An15g00410	strong similarity to acetate-inducible gene aciA - Aspergillus nidulans	0	360	9	9	21	1	13.4	11.3	0.18
An09g02800	strong similarity to serine O-acetyltransferase cysA - Aspergillus nidulans	14	1779	1	4	1	2	0.8	0.4	0.18
An14g06530	similarity to nucleoporin Nup192 - Saccharomyces cerevisiae-	0	1786	4	1	0	3	0.8	0.4	0.18
An04g02800	strong similarity to pyrroline-5-carboxylate reductase ProC - Pseudomonas aeruginosa	0	286	6	1	1	7	6.8	5.4	0.18
An08g04100	strong similarity to serine palmitoyltransferase 2 Lcb2 - Saccharomyces cerevisiae	1	676	3	2	8	3	2.1	3.1	0.18
An04g03270	strong similarity to proteasome 19S regulatory particle subunit Rpn2 - Saccharomyces cerevisiae	0	1147	4	2	12	2	1.5	2.3	0.17
An16g01860	strong similarity to protease involved in a-factor processing Ste23 - Saccharomyces cerevisiae	0	1167	0	6	10	4	1.4	2.2	0.17
An18g06760	strong similarity to NAD(+)-isocitrate dehydrogenase subunit I idh1 - Ajellomyces capsulatus	0	385	1	3	2	2	3.0	2.1	0.17
An07g02990	similarity to RNA-binding protein AUF1 - Homo sapiens	0	315	7	0	7	6	6.2	7.7	0.17
An08g08600	similarity to protein cw11p - Schizosaccharomyces pombe	4	325	4	10	6	11	11.6	9.7	0.17
An01g06060	strong similarity to GTP-binding protein rab11 - Rattus norvegicus	0	211	6	11	13	15	21.6	24.4	0.17
An12g00220	strong similarity to hypothetical protein EAA61911.1 - Aspergillus nidulans	1	154	1	4	2	4	9.3	7.6	0.17
An14g00220	strong similarity to hypothetical protein SPAC17C9.06 - Schizosaccharomyces pombe	0	514	9	17	21	23	13.4	15.6	0.17
An16g05910	strong similarity to cholesterol 7 α -hydroxylase CYP7 - Sus scrofa	1	499	3	3	4	8	3.4	4.5	0.16
An04g05300	strong similarity to fructose-1,6-bisphosphatase fbpA - Aspergillus oryzae	0	355	1	0	2	1	1.1	1.8	0.16
An08g10490	strong similarity to spindle pole body-associated protein dis1p - Schizosaccharomyces pombe	0	935	1	0	3	1	0.4	0.9	0.16
An16g04940	strong similarity to cytoplasmic ribosomal protein of the small subunit S12 AS1 - Podospora anserina	0	153	4	4	4	6	14.5	12.4	0.16
An02g04530	strong similarity to cyclopropane-fatty-acyl-phospholipid synthase - Escherichia coli	2	510	3	11	13	12	7.4	9.0	0.16
An16g04100	strong similarity to transcription regulator protein Cdc39 - Saccharomyces cerevisiae-	0	2361	7	6	11	0	1.5	0.9	0.16
An09g05950	strong similarity to plasma membrane ATPase PMA1 - Kluyveromyces lactis	9	1019	1	1	0	1	0.6	0.3	0.16
An13g01080	strong similarity to ATP phosphoribosyltransferase his1p - Schizosaccharomyces pombe	0	307	3	1	7	1	3.8	5.0	0.16
An04g02150	similarity to amino acid system N transporter SN1 - Rattus norvegicus	11	750	1	4	7	4	1.9	2.8	0.16
An04g05930	strong similarity to very long chain fatty acid synthase Tsc13 - Saccharomyces cerevisiae	6	309	0	4	5	3	3.8	5.0	0.16
An04g05000	strong similarity to hypothetical protein AN80 from patent WO9924580-A2 - Aspergillus nidulans	0	420	1	3	1	3	2.8	1.9	0.16
An06g02180	weak similarity to Traf2 and NCK interacting kinase (splice variant 8) - Homo sapiens	0	1053	3	1	2	1	1.1	0.6	0.16
An16g04270	strong similarity to vacuolar protein sorting-associated protein Vps35 - Saccharomyces cerevisiae	0	866	15	22	10	35	11.3	9.5	0.15
An02g03250	strong similarity to 3-isopropylmalate dehydratase LEU2 - Phycomyces blakesleeana	0	772	5	0	10	1	1.9	2.7	0.15
An01g13160	strong similarity to α -isopropylmalate synthase Leu4 - Saccharomyces cerevisiae-	0	626	3	3	6	0	2.7	1.9	0.15
An07g02190	strong similarity to protein Sec7 - Saccharomyces cerevisiae	0	1793	1	0	1	4	0.2	0.6	0.15
An16g02970	strong similarity to cytoplasmic serine hydroxymethyltransferase Shm2 - Saccharomyces cerevisiae	0	471	27	17	54	17	24.6	27.4	0.15
An08g06330	strong similarity to ϵ -COP - Cricetulus griseus	0	324	1	3	3	5	3.6	4.7	0.15
An12g01890	strong similarity to squalene synthase ERG9 - Candida utilis	1	472	18	28	42	32	25.6	28.5	0.15
An01g13070	strong similarity to signal recognition particle receptor Sec63 - Saccharomyces cerevisiae	3	653	15	27	22	31	16.9	14.8	0.15
An08g01790	strong similarity to eukaryotic initiation factor 3H1 subunit TIF3H1 - Arabidopsis thaliana	0	365	4	3	7	6	5.3	6.7	0.15

An11g01260	similarity to hypothetical protein - Magnaporthe grisea	2	492	1	1	2	3	1.3	2.0	0.15
An01g00150	strong similarity to nuclear protein Enp1 - Saccharomyces cerevisiae	0	493	2	0	3	2	1.3	2.0	0.15
An03g04280	strong similarity to pyridoxine synthesis component pyroA - Aspergillus nidulans	0	309	8	12	19	14	17.3	19.6	0.14
An02g14380	hexokinase hxk - Aspergillus niger-	0	490	6	6	14	0	6.6	5.3	0.14
An01g07860	strong similarity to hypothetical membrane transport protein YGR125w - Saccharomyces cerevisiae	10	1066	1	0	2	2	0.4	0.8	0.14
An17g00370	strong similarity to hypothetical single-stranded TG1-3 binding protein tcg - Schizosaccharomyces pombe	0	361	10	4	14	10	10.5	12.2	0.14
An10g00150	strong similarity to cytochrome P450 monooxygenase TRI4 - Myrothecium roridum	2	508	2	0	2	3	1.3	2.0	0.14
An05g00050	strong similarity to prolidase - Suberites domuncula-	0	466	2	2	4	0	2.5	1.7	0.14
204514	strong similarity to UV excision repair protein (RadW), putative [Aspergillus clavatus NRRL 1]	0	369	2	1	1	2	2.5	1.7	0.14
An02g10440	strong similarity to H ⁺ -transporting ATPase vma-1 - Neurospora crassa	0	604	14	14	27	20	12.3	14.2	0.14
An04g01530	strong similarity to transport vesicle docking protein Pep12 - Saccharomyces cerevisiae	1	273	4	11	6	19	14.8	16.8	0.14
An17g02140	strong similarity to vanadate resistance protein Van2 - Saccharomyces cerevisiae	9	381	7	7	14	10	9.9	11.6	0.13
An14g07200	strong similarity to catalase C catC - Aspergillus nidulans-	0	490	2	2	4	0	2.4	1.7	0.13
An05g00880	strong similarity to dnaJ protein homolog Scj1 - Saccharomyces cerevisiae	0	416	6	8	14	3	9.1	7.6	0.13
An04g08800	strong similarity to mitochondrial carrier Leu5 - Saccharomyces cerevisiae	1	435	0	1	2	1	0.9	1.5	0.13
An04g01720	similarity to DnaJ protein SIS1 - Cryptococcus curvatus	0	355	3	6	7	9	7.0	8.4	0.13
An18g05910	strong similarity to hypothetical glycosyl transferase SPCC330.08 - Schizosaccharomyces pombe	1	545	1	1	3	2	1.2	1.8	0.13
An02g04000	strong similarity to pyruvate dehydrogenase kinase isoform 2 - Zea mays	0	438	0	1	1	2	0.9	1.4	0.13
An18g04840	strong similarity to translation elongation factor 1 α - Podospora anserina [putative sequencing error]	0	460	84	59	128	67	81.2	76.7	0.13
An02g10700	strong similarity to alkane-hydroxylating cytochrome P-450 CYP52A3-A - Candida maltosa	1	506	2	2	2	2	2.3	1.6	0.13
An09g05260	strong similarity to cell division control protein Cdc12 - Saccharomyces cerevisiae	0	383	2	2	7	1	3.1	4.0	0.13
An06g01540	strong similarity to serine C-palmitoyltransferase chain Lcb1 - Saccharomyces cerevisiae	0	504	4	4	6	3	4.4	3.4	0.13
An14g00990	strong similarity to trifunctional protein of the β -oxidation fox-2 - Neurospora crassa	0	901	4	4	15	1	2.5	3.3	0.13
An16g03320	strong similarity to transport protein Sec24A - Homo sapiens	0	1009	6	2	4	4	2.2	1.5	0.12
An03g05200	strong similarity to carboxypeptidase S1 - Penicillium janthinellum	0	566	9	3	10	4	5.7	4.6	0.12
An16g07110	strong similarity to acetyl-CoA hydrolase Ach1 - Saccharomyces cerevisiae	0	525	3	5	5	4	4.2	3.3	0.12
An01g10340	similarity to hypothetical fatty acid elongation protein Sur4 - Saccharomyces cerevisiae	5	543	10	17	20	14	13.2	11.5	0.12
An09g04010	strong similarity to chitin synthase C chsC - Aspergillus fumigatus	7	914	0	7	2	5	2.1	1.5	0.12
An07g09320	similarity to 2-hydroxyruconate-semialdehyde hydrolase phnD - Pseudomonas sp.	0	408	2	2	5	3	2.9	3.8	0.12
An03g02040	strong similarity to cyclopropane-fatty-acyl-phospholipid synthase - Escherichia coli-	0	428	2	1	0	3	2.1	1.5	0.12
An14g03020	similarity to secreted protein SEQ ID NO:58 from patent WO9957132-A1 - Homo sapiens	5	737	2	1	1	6	1.2	1.8	0.12
An02g09370	similarity to translation initiation factor eIF-2 α chain EIF2A - Homo sapiens	0	332	3	3	7	4	5.1	6.2	0.12
An09g00670	strong similarity to GPI-anchored β (1-3)glucanosyltransferase gel3 - Aspergillus fumigatus	1	541	2	6	5	4	4.1	3.2	0.12
An02g09250	strong similarity to subunit of the vacuolar ATPase Vma6 - Saccharomyces cerevisiae	0	362	6	5	9	10	8.3	9.7	0.12
An15g02810	similarity to phosphatidylinositol phosphate phosphatase Inp52 - Saccharomyces cerevisiae	1	441	2	1	1	2	2.1	1.4	0.12
An08g03910	strong similarity to cytoplasmic ribosomal protein of the large subunit L10a - Rattus norvegicus	0	217	28	14	33	32	51.0	54.5	0.11
An02g08450	secretory AAA-ATPase nsfA - Aspergillus niger	0	728	5	4	11	6	3.4	4.3	0.11
An08g02210	strong similarity to RNase L inhibitor - Homo sapiens [putative sequencing error]	0	782	7	5	12	10	4.2	5.2	0.11
An14g03360	strong similarity to choline-transport mutant SCT1 suppressor protein - Saccharomyces cerevisiae	4	711	5	11	12	7	6.0	4.9	0.11
An02g14750	strong similarity to actin-related protein - Homo sapiens	0	472	0	3	2	1	1.9	1.3	0.11

An16g00920	strong similarity to peroxisomal membrane protein PMP20 - <i>Candida boidinii</i>	0	166	1	1	3	1	3.9	4.9	0.11
An08g05790	strong similarity to glycogen phosphorylase Gph1 - <i>Saccharomyces cerevisiae</i>	0	881	16	17	38	3	9.9	8.5	0.11
An16g08490	strong similarity to dolichyl-phosphate-D-mannose--protein O-mannosyltransferase Pmt4 – <i>S. cerevisiae</i>	10	771	4	10	11	14	4.9	6.0	0.11
An08g07020	similarity to mannosyl transferase Alg9 - <i>Saccharomyces cerevisiae</i>	10	602	3	5	3	6	3.7	2.8	0.11
An13g00740	similarity to cyclopropane-fatty-acyl-phospholipid synthase - <i>Escherichia coli</i>	2	517	10	30	35	29	20.4	22.5	0.10
An01g03550	strong similarity to urease URE1 - <i>Cryptococcus neoformans</i>	0	831	1	2	6	1	1.1	1.6	0.10
An16g04580	strong similarity to hypothetical protein HSPC021 - <i>Homo sapiens</i>	2	476	13	15	18	18	15.6	13.8	0.10
An16g09200	strong similarity to U5 snRNP-specific protein U5-116kD - <i>Mus musculus</i>	0	990	3	1	6	3	1.2	1.7	0.10
An18g01670	6-phosphofructokinase pfkA - <i>Aspergillus niger</i>	0	783	4	2	10	2	2.2	2.9	0.10
An02g13670	similarity to human secreted protein fragment from patent WO9909155-A1 - <i>Homo sapiens</i>	6	492	4	3	5	3	4.0	3.1	0.10
An07g07830	similarity to hypothetical protein YIL039w - <i>Saccharomyces cerevisiae</i>	2	564	1	0	1	2	0.7	1.1	0.10
An02g03580	strong similarity to lipid metabolism protein YER044c from patent WO200058521-A2 - <i>S. cerevisiae</i>	0	149	0	4	3	2	7.9	6.7	0.10
An02g08080	strong similarity to cytoplasmic ribosomal protein of the large subunit L22 - <i>Xenopus laevis</i>	0	124	5	7	10	6	26.2	24.0	0.10
An02g09160	strong similarity to hypothetical protein YOR311c - <i>Saccharomyces cerevisiae</i>	5	384	1	5	5	2	4.4	3.5	0.10
An01g08590	strong similarity to hypothetical protein YKR088c - <i>Saccharomyces cerevisiae</i> -	5	340	2	1	6	0	2.7	3.4	0.10
An04g08830	similarity to Golgi membrane protein Emp47 - <i>Saccharomyces cerevisiae</i>	1	415	7	21	23	22	17.9	19.8	0.10
An11g03970	similarity to hypothetical AAA family ATPase SCD8A.32c - <i>Streptomyces coelicolor</i>	0	596	7	4	9	4	5.0	4.1	0.10
An01g06120	strong similarity to 4- α -glucanotransferase / amylo-16-glucosidase Gdb1 - <i>Saccharomyces cerevisiae</i>	0	1539	1	13	15	0	2.5	1.8	0.09
An14g04190	strong similarity to 14- α -glucan branching enzyme Glc3 - <i>Saccharomyces cerevisiae</i>	0	692	2	2	4	0	1.7	1.2	0.09
An07g08280	strong similarity to 3-Hydroxy-3-methylglutaryl-CoA reductase HMGR - <i>Gibberella fujikuroi</i>	6	1114	9	25	13	29	8.1	6.9	0.09
An01g01550	strong similarity to catalase cat1 - <i>Aspergillus fumigatus</i>	0	727	6	18	18	12	8.8	7.6	0.09
An16g04330	strong similarity to mannose phospho-dolichol synthase dpm1 - <i>Hypocrea jecorina</i>	0	245	9	15	14	18	26.0	23.9	0.09
An01g13220	dnaK-type molecular chaperone lhsA - <i>Aspergillus niger</i>	1	1000	13	64	82	40	20.2	22.1	0.09
An11g11140	strong similarity to nuclear pore membrane protein Pom152 - <i>Saccharomyces cerevisiae</i>	0	1255	6	22	32	16	5.9	7.0	0.09
An14g00180	strong similarity to proteasome 19S regulatory particle subunit Rpt6 - <i>Saccharomyces cerevisiae</i>	0	389	3	0	5	1	2.3	3.0	0.08
An08g06570	strong similarity to transketolase Tkl1 - <i>Saccharomyces cerevisiae</i>	0	684	48	34	93	17	31.4	29.1	0.08
An13g00710	strong similarity to copper amine oxidase AO-I - <i>Aspergillus niger</i>	0	688	8	11	27	5	7.4	8.5	0.08
An16g03640	similarity to phosphatidylcholine-sterol O-acyltransferase Lcat - <i>Mus musculus</i>	1	628	1	2	1	2	1.5	1.0	0.08
An07g02360	similarity to 6-hydroxy-D-nicotine oxidase 6-HDNO - <i>Arthrobacter oxidans</i>	0	551	8	8	16	4	7.8	6.7	0.08
An18g05210	similarity to multifunctional β -oxidation protein - <i>Neurospora crassa</i>	0	322	2	3	3	3	4.4	3.6	0.08
An12g04710	similarity to negative regulator of Cdc Fourty two Vtc1 - <i>Saccharomyces cerevisiae</i>	3	808	9	15	22	8	7.9	6.8	0.08
An15g06230	strong similarity to aminonitrophenyl propanediol resistance protein Anp1 - <i>Saccharomyces cerevisiae</i>	1	491	2	4	8	3	3.4	4.2	0.08
An04g05980	strong similarity to v-SNARE Vti1 - <i>Saccharomyces cerevisiae</i>	1	224	5	10	6	18	18.0	19.7	0.08
An02g09930	strong similarity to subunit VI of cytochrome c oxidase Cox6 - <i>Saccharomyces cerevisiae</i>	0	158	2	10	8	8	20.6	18.8	0.08
An08g00830	strong similarity to protein phosphatase type 2C Ptc2 - <i>Saccharomyces cerevisiae</i> -	0	424	2	1	6	0	2.1	2.8	0.08
An11g10200	strong similarity to subunit VIa of cytochrome c oxidase Cox13 - <i>Saccharomyces cerevisiae</i>	0	141	2	6	6	7	15.7	17.3	0.08
An09g03070	strong similarity to α -glucan synthase mok1p - <i>Schizosaccharomyces pombe</i>	13	2426	2	16	19	15	2.0	2.6	0.07
An04g05850	strong similarity to cytoplasmic ribosomal protein of the small subunit rps6p - <i>Schizosaccharomyces pombe</i>	0	237	6	9	13	11	17.0	18.6	0.07
An16g03370	strong similarity to sensor/transporter protein for cell wall integrity Cwh43 - <i>Saccharomyces cerevisiae</i>	16	911	10	23	25	17	9.6	8.4	0.07
An13g02980	strong similarity to hypothetical protein FG01228.1 - <i>Fusarium graminearum</i>	0	180	1	3	4	3	6.5	7.5	0.07

An06g00300	similarity to phosphate/phosphoenolpyruvate translocator TABPPT8 - <i>Nicotiana tabacum</i>	9	339	3	5	6	4	6.5	5.6	0.07
An18g01320	strong similarity to extracellular protease precursor Bar1 - <i>Saccharomyces cerevisiae</i>	0	456	0	3	4	2	2.0	2.6	0.07
An04g06320	strong similarity to hypothetical protein SPAC19A8.14 - <i>Schizosaccharomyces pombe</i>	1	215	2	2	5	0	5.4	4.6	0.07
An14g01960	strong similarity to aberrant X segregation Axs - <i>Drosophila melanogaster</i>	5	734	4	3	6	2	2.7	2.1	0.07
An18g02740	similarity to cytochrome P450 3A7 - <i>Homo sapiens</i>	2	590	5	8	13	9	6.0	6.9	0.07
An16g05090	strong similarity to endonuclease SceI 75 kDa subunit Ens1 - <i>Saccharomyces cerevisiae</i>	0	666	6	24	17	22	11.9	10.7	0.07
An17g00780	similarity to protease B processing protein Pbn1 - <i>Saccharomyces cerevisiae</i>	1	503	0	3	4	2	1.8	2.3	0.07
An07g09800	strong similarity to hypothetical polyphosphate synthase Vtc3 - <i>Saccharomyces cerevisiae</i>	3	794	8	23	29	11	10.3	9.2	0.06
An11g00510	strong similarity to ATP citrate lyase ACL1 - <i>Sordaria macrospora</i>	0	656	54	55	100	49	43.4	41.1	0.06
An02g09940	strong similarity to α -1 2-mannosyltransferase Ktr1 - <i>Saccharomyces cerevisiae</i>	1	398	8	10	21	8	12.1	13.4	0.06
An12g00130	strong similarity to mRNA processing protein of cytochrome c oxidase Mss51 - <i>Saccharomyces cerevisiae</i>	0	524	0	3	5	1	1.7	2.2	0.06
An04g00220	strong similarity to methionine-N-acetyltransferase Nat2 - <i>Saccharomyces cerevisiae</i>	0	288	0	2	1	3	2.3	2.8	0.06
124807	strong similarity to zinc binding enoyl reductase [<i>Aspergillus fumigatus</i> Af293]	0	357	3	4	6	6	5.5	6.3	0.06
An15g03900	strong similarity to heavy metal ion resistance protein Zrc1 - <i>Saccharomyces cerevisiae</i>	5	431	0	5	1	5	3.3	2.7	0.06
An11g03380	similarity to monoglyceride lipase mgll - <i>Mus musculus</i>	0	301	0	2	2	2	2.2	2.7	0.06
56745	strong similarity to pre-mRNA splicing factor (Srp1), putative [<i>Neosartorya fischeri</i> NRRL 181]	0	222	2	2	4	3	5.3	6.1	0.06
An12g03960	strong similarity to acyltransferase ataA - <i>Aspergillus nidulans</i>	2	293	3	7	6	7	9.3	8.3	0.06
An04g08480	strong similarity to cell division control protein SLY2 homolog YKL196c - <i>Saccharomyces cerevisiae</i>	0	196	4	2	5	5	8.6	9.7	0.06
53706	strong similarity to C-4 methyl sterol oxidase Erg25 [<i>Aspergillus fumigatus</i> Af293]	2	298	4	6	9	4	9.2	8.2	0.06
An12g03600	strong similarity to diacylglycerol acyltransferase DAGAT - <i>Arabidopsis thaliana</i>	9	456	5	0	4	2	3.1	2.6	0.06
211885	strong similarity to polyketide synthase [<i>Aspergillus fumigatus</i> Af293]	0	2443	115	77	146	111	20.5	19.0	0.06
An05g00540	strong similarity to cytoplasmic ribosomal protein of the large subunit L19 - <i>Saccharomyces cerevisiae</i>	0	201	5	12	11	12	22.7	21.1	0.06
An06g01730	strong similarity to mtRNA splice defect-suppressing mitochondrial carrier Mrs3 - <i>Saccharomyces cerevisiae</i>	0	319	0	2	1	3	2.0	2.5	0.06
An02g02340	strong similarity to chitin synthase with a myosin motor-like domain csmA - <i>Aspergillus nidulans</i>	6	1760	6	14	18	17	3.0	3.6	0.06
An04g05490	strong similarity to protein fragment SEQ ID NO:4306 from patent EP1033405-A2 - <i>Arabidopsis thaliana</i>	0	469	1	4	6	0	3.1	2.5	0.05
An18g03490	similarity to cation-dependent mannose 6-phosphate receptor precursor CD-MPR-Bos taurus	1	324	0	2	2	2	2.0	2.5	0.05
An12g01320	strong similarity to linoleate diol synthase - <i>Gaeumannomyces graminis</i>	0	1181	2	3	8	2	1.2	1.6	0.05
An16g01730	similarity to acid phosphatase precursor rPAP - <i>Rattus norvegicus</i>	1	476	2	3	3	3	3.0	2.5	0.05
An07g02170	similarity to transport protein Bos1 - <i>Saccharomyces cerevisiae</i>	1	244	1	3	1	6	4.8	5.5	0.05
An08g10060	strong similarity to small G-protein Gsp1 - <i>Candida albicans</i>	0	214	3	3	7	3	7.9	8.9	0.05
An07g05570	strong similarity to chitin synthase chs1 - <i>Aspergillus nidulans</i>	7	915	0	4	6	2	1.3	1.7	0.05
An02g07600	strong similarity to succinate dehydrogenase Sdh1 - <i>Saccharomyces cerevisiae</i>	0	656	3	6	4	7	3.8	3.2	0.05
An13g01220	strong similarity to hypothetical suppressor of bem1/bud5 bem46p - <i>Schizosaccharomyces pombe</i>	0	292	3	4	4	5	6.7	5.9	0.05
An08g03493	strong similarity to hypothetical protein AN1161.2 - <i>Aspergillus nidulans</i>	2	108	0	3	2	2	8.4	7.5	0.05
An07g03190	strong similarity to RNase III domain protein Afu5g09670 - <i>Aspergillus fumigatus</i> [putative sequencing error]	0	339	1	1	1	3	1.9	2.4	0.05
An04g03930	lysine aminopeptidase apsA - <i>Aspergillus niger</i>	0	881	14	19	41	2	9.9	8.9	0.05
An18g03810	strong similarity to cytoplasmic ribosomal protein of the large subunit L13a - <i>Saccharomyces cerevisiae</i>	0	202	9	7	14	11	21.3	22.8	0.05
54765	strong similarity to tetratricopeptide repeat domain protein [<i>Neosartorya fischeri</i> NRRL 181]	0	300	2	5	5	4	6.5	5.7	0.05
An09g00500	weak similarity to transcription factor Arg81 - <i>Saccharomyces cerevisiae</i>	1	874	4	9	9	7	4.0	3.4	0.05
An11g11250	strong similarity to interferon-induced dsRNA-activated protein kinase inhibitor P58 - <i>Homo sapiens</i>	0	507	4	7	8	6	5.9	5.2	0.05

An01g14250	strong similarity to δ subunit of the coatomer δ -coat protein CopD - Bos taurus [deleted ORF]	0	518	3	2	2	4	2.8	2.3	0.05
An02g00110	strong similarity to hypothetical protein encoded by An11g10340 - Aspergillus niger-	0	318	1	3	5	0	3.7	3.1	0.05
An12g01360	strong similarity to hypothetical cytochrome P450 protein 2E4.050 - Neurospora crassa	2	592	7	7	16	7	6.4	7.2	0.05
An03g03770	strong similarity to squalene monooxygenase - Rattus norvegicus	3	512	11	21	23	20	16.5	15.3	0.04
An07g03570	strong similarity to sorbitol utilization protein sou2 - Candida albicans	0	293	1	3	6	1	4.0	4.6	0.04
An01g02840	strong similarity to translation initiation factor IF2 - Homo sapiens	0	1061	5	4	13	3	2.3	2.8	0.04
An07g03880	serine proteinase pepC - Aspergillus niger	0	497	2	5	10	2	3.9	4.5	0.04
An16g08150	strong similarity to dipeptidyl-peptidase V DPP V - Aspergillus fumigatus	0	732	8	12	9	17	7.3	6.5	0.04
An12g00790	strong similarity to stress-induced protein Sti1 - Saccharomyces cerevisiae-	0	629	1	4	6	0	2.3	1.9	0.04
An07g09270	strong similarity to hypothetical protein SPAC1F12.09 - Schizosaccharomyces pombe	2	812	0	3	3	3	1.1	1.4	0.04
An01g14070	strong similarity to karyopherin β Kap95 - Saccharomyces cerevisiae-	0	880	4	11	19	0	4.6	4.0	0.04
An01g06560	strong similarity to argininosuccinate lyase ASAL - Candida albicans	0	464	16	10	30	5	14.9	13.8	0.04
An01g10000	strong similarity to ATP-binding cassette transporter abc1p - Schizosaccharomyces pombe	14	1501	0	1	2	1	0.3	0.4	0.04
An04g01950	strong similarity to zinc-metalloprotease Ste24 - Saccharomyces cerevisiae	5	456	9	14	20	16	13.4	14.4	0.04
An15g00980	strong similarity to maintaining mitochondrial morphology protein MMM1 - Neurospora crassa	1	484	2	0	2	2	1.3	1.7	0.04
An01g13920	strong similarity to adenylosuccinate synthase ade2p - Schizosaccharomyces pombe	0	424	5	2	4	5	4.6	4.0	0.04
An01g05510	strong similarity to GABA-A receptor ϵ -like subunit - Homo sapiens	0	320	4	2	6	4	5.3	5.9	0.04
An13g03940	strong similarity to long-chain-acyl-CoA dehydrogenase precursor LCAD - Rattus norvegicus	0	415	1	3	3	2	2.8	2.4	0.04
An07g06080	strong similarity to casein kinase-1 homolog hhp1p - Schizosaccharomyces pombe	0	370	3	1	2	5	3.2	3.7	0.04
An18g03200	strong similarity to actin like protein act2p - Schizosaccharomyces pombe	0	439	4	3	5	4	4.4	3.9	0.04
An04g07020	strong similarity to syntaxin Tlg2 - Saccharomyces cerevisiae	0	373	2	2	2	5	3.1	3.6	0.04
An07g06430	strong similarity to glycoprotein glucosyltransferase gpt1p - Schizosaccharomyces pombe	0	1495	12	40	53	29	9.1	10.0	0.03
An02g04250	similarity to protein p58 - Rattus norvegicus	1	324	8	14	16	18	18.1	19.2	0.03
An18g02720	strong similarity to hypothetical glutathione S-transferase CAA19067.1 - Schizosaccharomyces pombe	0	226	1	5	7	1	7.5	6.8	0.03
An08g01000	strong similarity to aspartate transaminase aspC - Methanobacterium thermoformicicum	0	386	2	2	6	1	3.0	3.5	0.03
An02g04880	strong similarity to arginine--tRNA ligase Msr1 - Saccharomyces cerevisiae	0	646	3	4	10	2	3.0	3.5	0.03
An05g00410	strong similarity to serine hydroxymethyl-transferase I Shm1 - Candida albicans	0	534	1	1	4	0	1.2	1.5	0.03
An18g06220	strong similarity to α -mannosidase Mns1 - Saccharomyces cerevisiae	1	663	0	7	10	2	2.9	3.4	0.03
An02g08670	strong similarity to hypothetical phosphate/PEP translocator protein At2g25520 - Arabidopsis thaliana	11	399	1	3	4	3	2.9	3.4	0.03
An07g03740	strong similarity to hypothetical protein SPAC25H1.07 - Schizosaccharomyces pombe	1	946	21	43	38	49	17.7	16.7	0.03
An15g01740	similarity to succinate-semialdehyde dehydrogenase NAD(P) ⁺ gabD - Escherichia coli	0	650	6	10	9	12	6.6	6.0	0.03
An09g05870	strong similarity to nucleoside-diphosphate kinase NDK-1 - Neurospora crassa	0	153	12	6	13	12	31.5	30.1	0.03
An18g05230	strong similarity to proteasome 19S regulatory particle subunit Rpt5 - Saccharomyces cerevisiae	0	464	3	1	3	2	2.5	2.1	0.03
An11g04370	strong similarity to cytochrome b5 - Mortierella alpina	1	138	5	6	9	8	21.7	22.9	0.03
An09g05880	strong similarity to α -glucosidase ModA - Dictyostelium discoideum	1	957	32	69	91	62	27.6	28.9	0.03
An16g07620	endoplasmic reticulum oxidising protein EroA - Aspergillus niger	0	600	4	7	12	6	5.0	5.6	0.03
An07g10100	strong similarity to adenylate kinase Adk1 - Saccharomyces cerevisiae	0	258	5	24	20	24	29.8	31.1	0.03
An18g05890	similarity to pyruvate dehydrogenase phosphatase isoenzyme 1 PDP1 - Rattus norvegicus	0	602	4	11	14	10	6.7	7.3	0.03
An03g05010	strong similarity to cell wall biosynthesis protein MNN9 - Candida albicans	1	392	2	4	2	8	4.3	4.8	0.03
An14g05510	strong similarity to dihydrosphingosine-1-phosphate phosphatase Ysr3 - Saccharomyces cerevisiae	5	533	3	4	3	6	3.7	3.2	0.03

An07g02960	strong similarity to cytoplasmic ribosomal protein of the small subunit S13.e - <i>Saccharomyces cerevisiae</i>	0	151	3	8	10	7	19.8	20.9	0.03
An07g09830	strong similarity to hypothetical protein encoded by B19C19.110 - <i>Neurospora crassa</i>	1	517	2	2	4	1	2.3	1.9	0.03
An18g06270	strong similarity to 14-3-3 protein homolog artA - <i>Aspergillus nidulans</i>	0	272	17	14	26	17	30.1	28.8	0.03
An01g08850	strong similarity to Gβ like protein cpcB - <i>Aspergillus nidulans</i>	0	316	11	8	14	12	16.1	15.1	0.03
An15g01860	strong similarity to malate synthase acuE - <i>Aspergillus nidulans</i> -	0	542	2	2	0	5	2.2	1.8	0.03
An13g00780	strong similarity to hypothetical protein CAD21419.1 - <i>Neurospora crassa</i>	1	286	4	2	2	6	5.9	5.4	0.03
An14g03910	strong similarity to α-1 2-mannosyltransferase kre2 - <i>Candida albicans</i>	1	392	5	11	16	9	11.0	11.7	0.03
An18g03010	strong similarity to 26S proteasome regulatory subunit S2 - <i>Homo sapiens</i>	0	906	11	16	25	11	7.9	7.3	0.03
An09g02540	similarity to hypothetical membrane protein YIL067c - <i>Saccharomyces cerevisiae</i>	7	681	0	2	3	1	1.0	1.2	0.03
An12g07570	strong similarity to synaptobrevin Snc2 - <i>Saccharomyces cerevisiae</i>	1	135	1	2	2	3	6.7	7.3	0.03
An11g06770	strong similarity to skin cell protein from patent WO9955865-A1 - <i>Rattus sp.</i> -	1	593	2	2	0	5	2.0	1.7	0.03
An02g08300	strong similarity to hypothetical protein EAL85123.1 - <i>Aspergillus fumigatus</i>	0	164	3	6	13	1	15.1	15.9	0.02
An10g00530	strong similarity to myo-inositol-1-phosphate synthase INO1 - <i>Arabidopsis thaliana</i>	0	533	44	25	65	31	33.9	32.7	0.02
An02g12640	strong similarity to RNA-binding protein 30 - <i>Nicotiana plumbaginifolia</i> -	0	538	3	1	7	0	2.2	2.5	0.02
An11g02590	strong similarity to peroxisomal membrane protein Pmp27 - <i>Saccharomyces cerevisiae</i>	0	235	1	2	2	2	3.9	3.5	0.02
An18g06050	strong similarity to casein kinase i homolog cki1p - <i>Schizosaccharomyces pombe</i>	1	567	1	3	3	4	2.1	2.4	0.02
An12g08030	strong similarity to NADH oxidoreductase complex I subunit Sub2 - <i>Saccharomyces cerevisiae</i>	0	440	7	2	3	9	5.6	5.1	0.02
225665	strong similarity to hypothetical protein AFUB 053450, putative Sec12 homologue - <i>Aspergillus fumigatus</i>	0	622	7	13	17	10	8.6	8.0	0.02
An08g04910	strong similarity to 22 kD subunit NADH:ubiquinone reductase - <i>Neurospora crassa</i>	0	159	0	3	2	3	5.7	6.2	0.02
An16g04170	strong similarity to acetolactate synthase protein from patent EP257993-A - <i>Saccharomyces cerevisiae</i> -	0	690	2	2	0	5	1.7	1.4	0.02
An02g02010	strong similarity to cytoplasmic tyrosine--tRNA ligase Tyrrs - <i>Saccharomyces cerevisiae</i>	0	382	2	4	6	2	4.4	4.0	0.02
An16g05260	strong similarity to eukaryotic translation initiation factor 3 subunit p42 - <i>Homo sapiens</i>	0	288	2	1	2	2	3.2	2.8	0.02
An07g02650	strong similarity to translation elongation factor 3 Yef3 - <i>Saccharomyces cerevisiae</i>	0	1064	55	48	99	44	25.3	24.3	0.02
An15g03780	strong similarity to ras pathway interacting protein moe1p - <i>Schizosaccharomyces pombe</i>	0	586	3	3	6	4	2.9	3.2	0.02
An07g03430	strong similarity to hypothetical protein CAD70902.1 - <i>Neurospora crassa</i>	0	294	2	1	2	2	3.1	2.8	0.02
An02g12420	strong similarity to trifunctional C1-tetrahydrofolate synthase Ade3 - <i>Saccharomyces cerevisiae</i>	0	930	1	1	3	1	0.7	0.9	0.02
An03g02525	similarity to hypothetical proteinase encoded by 2SC3B6.04c - <i>Streptomyces coelicolor</i>	0	199	1	6	9	2	9.8	10.4	0.02
An07g07760	strong similarity to DNA damage checkpoint protein rad24p - <i>Schizosaccharomyces pombe</i>	0	260	18	12	27	15	30.5	29.5	0.02
An08g08750	carboxypeptidase Y cpy from patent WO9609397-A1 - <i>Aspergillus niger</i> -	0	557	1	8	12	0	4.4	4.0	0.02
An15g00070	strong similarity to malate dehydrogenase precursor MDH - <i>Mus musculus</i>	0	330	8	11	19	10	15.4	16.1	0.02
An18g03980	strong similarity to glutamate carboxypeptidase II - <i>Rattus norvegicus</i> -	1	765	1	3	7	0	1.5	1.8	0.02
An01g04690	strong similarity to peroxisomal transporter Ant1 - <i>Saccharomyces cerevisiae</i>	3	335	1	2	2	2	2.7	2.4	0.02
An04g05880	strong similarity to linoleate diol synthase - <i>Gaeumannomyces graminis</i>	0	1080	7	16	29	7	5.7	6.1	0.02
An01g11960	similarity to brefeldin A resistance protein Bfr1 - <i>Saccharomyces cerevisiae</i> -	0	506	4	2	8	0	3.3	3.0	0.02
An14g04940	strong similarity to mRNA turnover 4 protein Mrt4 - <i>Saccharomyces cerevisiae</i>	0	234	3	2	5	3	6.1	6.6	0.01
An11g01550	strong similarity to cytochrome P450 52A4 - <i>Candida maltosa</i>	0	521	5	1	5	3	3.2	2.9	0.01
An08g07050	strong similarity to 189 kD subunit of DNA-directed RNA polymerase I rpa190p - <i>Schizosaccharomyces pombe</i>	0	1680	5	3	8	2	1.3	1.1	0.01
An01g06970	strong similarity to D-arabinose dehydrogenase Ara1 - <i>Saccharomyces cerevisiae</i>	0	325	6	7	16	4	10.8	11.4	0.01
An08g04250	strong similarity to dynamin-related protein msp1p - <i>Schizosaccharomyces pombe</i>	0	919	2	2	2	5	1.3	1.5	0.01
An18g05170	similarity to phosphoacetylglucosamine mutase AGM1 - <i>Candida albicans</i>	0	552	4	2	7	1	3.1	2.8	0.01

An18g03310	strong similarity to cytoplasmic ribosomal protein of the small subunit S3 - <i>Saccharomyces cerevisiae</i>	0	266	18	8	24	15	25.9	26.8	0.01
An07g03660	similarity to hypothetical protein CAD37045.1 - <i>Neurospora crassa</i>	0	263	0	5	1	7	5.4	5.8	0.01
An09g06680	citrate synthase citA - <i>Aspergillus niger</i>	0	474	19	19	27	30	21.1	21.9	0.01
An02g12010	strong similarity to inorganic pyrophosphatase Ipp1 - <i>Saccharomyces cerevisiae</i>	0	406	6	9	22	1	9.9	10.4	0.01
An11g03230	strong similarity to cytochrome P450 sterol δ 22-desaturase Erg5 - <i>Saccharomyces cerevisiae</i>	0	534	10	13	22	13	11.5	12.0	0.01
An02g13250	strong similarity to water channel protein aquaporin 3 AQP3 - <i>Rattus norvegicus</i>	6	285	2	1	4	1	3.2	3.5	0.01
An02g11720	strong similarity to α -mannosidase msd2 - <i>Aspergillus nidulans</i>	0	1089	1	3	3	4	1.1	1.2	0.01
53140	strong similarity to mitochondrial cytochrome b2, putative [<i>Aspergillus flavus</i> NRRL3357]	0	477	1	2	4	0	1.9	1.7	0.01
An02g09910	strong similarity to fatty acid elongase Fen1 - <i>Saccharomyces cerevisiae</i>	7	342	5	4	6	8	7.2	7.6	0.01
An01g07640	similarity to hypothetical membrane protein YPL087w - <i>Saccharomyces cerevisiae</i>	7	299	2	1	3	2	3.0	3.3	0.01
An07g09110	similarity to monooxygenase VioC - <i>Chromobacterium violaceum</i>	0	499	0	3	2	2	1.8	1.6	0.01
An17g02290	strong similarity to myosin Myo2 - <i>Saccharomyces cerevisiae</i>	0	1572	2	0	2	2	0.4	0.5	0.01
An15g01700	strong similarity to nascent polypeptide-associated complex α chain α -NAC - <i>Mus musculus</i>	0	202	3	2	6	1	7.1	6.7	0.01
An01g08780	strong similarity to high affinity hexose transporter Hxt1 - <i>Saccharomyces cerevisiae</i>	10	540	2	1	2	2	1.7	1.5	0.01
An01g14200	strong similarity to fatty acid hydroxylase Scs7 - <i>Saccharomyces cerevisiae</i>	3	372	4	3	8	3	5.2	5.6	0.01
An04g05380	strong similarity to cell wall antigen 6C5 from patent WO200048620-A1 - <i>Candida albicans</i>	0	348	2	1	3	2	2.6	2.9	0.01
An04g06310	strong similarity to hypothetical protein CAB91735.2 - <i>Neurospora crassa</i>	1	257	3	7	7	7	10.6	10.2	0.01
An08g10670	strong similarity to mitogen-activated protein kinase FsMAPK - <i>Fusarium solani</i>	0	354	0	3	3	2	2.6	2.8	0.01
An02g09470	strong similarity to hypothetical Ca ²⁺ -transporting ATPase Spf1 - <i>Saccharomyces cerevisiae</i>	0	1277	30	55	83	44	17.4	18.0	0.01
An11g10630	similarity to translation initiation factor 3 complex protein Prt1 - <i>Homo sapiens</i>	0	591	1	2	3	1	1.5	1.4	0.01
An03g04660	weak similarity to hypothetical protein YGR165w - <i>Saccharomyces cerevisiae</i> -	0	387	4	3	0	11	5.0	5.4	0.01
An02g01260	weak similarity to β transducin-like protein het-e1 - <i>Podospira anserina</i>	0	1404	2	2	1	6	0.8	1.0	0.01
An11g04650	similarity to α -complex protein 1 CP-1 - <i>Homo sapiens</i>	0	421	4	3	6	5	4.6	4.9	0.01
An02g07470	strong similarity to fructose-bisphosphate aldolase Fba1 - <i>Saccharomyces cerevisiae</i>	0	360	9	6	18	3	11.2	10.8	0.01
An07g09550	strong similarity to mitochondrial ribosomal protein Nam9 - <i>Saccharomyces cerevisiae</i>	0	436	3	0	1	4	2.1	2.3	0.01
An09g00260	α -galactosidase aglC - <i>Aspergillus niger</i>	0	748	1	2	2	2	1.2	1.1	0.01
An02g09260	strong similarity to nucleolar protein Nop5 - <i>Saccharomyces cerevisiae</i>	0	580	5	3	6	5	3.8	3.6	0.01
An07g09920	strong similarity to NADH-dependent glutamate synthase NADH-GOGAT - <i>Medicago sativa</i>	0	2126	38	12	66	10	6.2	6.5	0.01
An01g10750	strong similarity to hypothetical acid phosphatase CAB58405.1 - <i>Schizosaccharomyces pombe</i>	0	603	6	7	11	7	5.8	5.5	0.01
An14g02080	strong similarity to prolidase - <i>Aureobacterium anophageum</i>	0	480	2	3	6	2	3.0	3.2	0.01
An14g03110	strong similarity to cytochrome P450 monooxygenase TRI4 - <i>Myrothecium roridum</i>	0	521	2	1	3	2	1.7	1.9	0.01
An18g05820	strong similarity to hypothetical protein SPAC24C9.05c - <i>Schizosaccharomyces pombe</i>	1	609	0	9	4	10	4.1	4.3	0.01
An03g02770	strong similarity to hypothetical protein YLR361c - <i>Saccharomyces cerevisiae</i>	2	551	0	3	3	2	1.7	1.8	0.01
An02g13740	strong similarity to Gly-X carboxypeptidase precursor Yscs - <i>Saccharomyces cerevisiae</i> -	0	578	1	2	5	0	1.6	1.7	0.01
An09g02270	strong similarity to triacylglycerol lipase lipI - <i>Geotrichum candidum</i>	0	592	1	2	3	2	1.5	1.7	0.01
An03g00640	similarity to neutral amino acid permease mtr - <i>Neurospora crassa</i>	11	599	1	2	3	2	1.5	1.7	0.01
An06g00310	similarity to carboxypeptidase D - <i>Penicillium janthinellum</i>	0	605	0	3	4	1	1.5	1.6	0.01
An02g00210	strong similarity to nonribosomal peptide synthase MxA - <i>Stigmatella aurantiaca</i>	0	1276	14	12	26	10	5.4	5.2	0.01
An14g03280	strong similarity to dihydroxy-acid dehydratase Ilv3 - <i>Saccharomyces cerevisiae</i> -	0	615	1	2	5	0	1.5	1.6	0.01
An04g02850	similarity to X-Pro dipeptidyl-peptidase IV - <i>Xanthomonas maltophilia</i> -	0	663	3	4	11	0	2.9	3.1	0.01

An09g01240	strong similarity to phospholipase B - <i>Penicillium notatum</i>	0	638	0	3	2	3	1.4	1.6	0.01
An09g03940	strong similarity to ketol-acid reductoisomerase ilv-2 - <i>Neurospora crassa</i>	0	401	12	19	25	21	20.4	20.9	0.01
An04g00430	strong similarity to branched-chain-amino-acid aminotransferase Bat2 - <i>Saccharomyces cerevisiae</i>	0	412	1	4	6	1	3.5	3.3	0.01
An15g04140	strong similarity to polyketide synthase PKS1 - <i>Cochliobolus heterostrophus</i>	0	2565	21	4	20	14	2.6	2.4	0.01
An14g04400	strong similarity to succinate dehydrogenase iron-sulfur protein subunit Sdh2 - <i>Saccharomyces cerevisiae</i>	0	300	11	16	18	22	23.9	24.4	0.01
An03g06360	strong similarity to chitin synthase C chsC - <i>Aspergillus fumigatus</i>	6	873	0	1	2	0	0.4	0.5	0.01
An09g05480	strong similarity to ubiquitin specific protease HAUSP - <i>Homo sapiens</i>	0	1155	2	13	19	4	3.5	3.7	0.00
An12g07580	strong similarity to acetylglutamate kinase/N-acetyl- γ -glutamyl-phosphate reductase arg-6 - <i>Neurospora crassa</i>	0	903	1	2	0	5	1.0	1.1	0.00
An08g09010	strong similarity to spliceosomal protein SAPI30 - <i>Homo sapiens</i>	0	1209	3	6	13	1	2.0	2.2	0.00
An08g10650	strong similarity to transport protein Sec24 - <i>Saccharomyces cerevisiae</i>	0	919	10	12	10	23	6.4	6.6	0.00
An12g04020	strong similarity to acetyl-CoA carboxylase SPAC56E4.04c - <i>Schizosaccharomyces pombe</i>	0	2283	46	16	54	33	7.1	6.9	0.00
An01g03480	strong similarity to sorbitol dehydrogenase gutB - <i>Bacillus subtilis</i>	0	340	7	5	15	3	9.6	9.8	0.00
An04g08430	strong similarity to hypothetical protein AN1817.2 - <i>Aspergillus nidulans</i>	1	92	1	1	1	2	7.1	6.9	0.00
An01g04600	PDI related protein A prpA - <i>Aspergillus niger</i>	0	464	9	38	46	21	26.6	26.2	0.00
An02g05400	strong similarity to 146D nuclear protein - <i>Xenopus laevis</i>	0	1206	3	0	4	1	0.8	0.8	0.00
An08g06940	strong similarity to histone H4.1 - <i>Aspergillus nidulans</i>	0	103	1	1	1	2	6.3	6.1	0.00
An04g02030	strong similarity to ATP-dependent RNA helicase Ded1 - <i>Saccharomyces cerevisiae</i>	0	678	25	13	22	32	14.8	14.5	0.00
An16g05930	strong similarity to hypothetical protein EAA59446.1 - <i>Aspergillus nidulans</i>	0	300	5	9	10	10	12.6	12.3	0.00
An07g07430	strong similarity to cytoplasmic ribosomal protein of the large subunit L34.b - <i>Saccharomyces cerevisiae</i>	0	117	1	1	1	2	5.6	5.4	0.00
An08g04480	strong similarity to hypothetical protein B3E4.60 - <i>Neurospora crassa</i>	2	858	28	38	54	40	20.2	19.9	0.00
An16g08010	strong similarity to Casein kinase CK II - <i>Arabidopsis thaliana</i>	0	335	5	5	9	6	8.2	8.3	0.00
An01g06670	strong similarity to peptidyl-prolyl isomerase FKBP-21 - <i>Neurospora crassa</i>	0	135	1	1	2	1	4.8	4.7	0.00
An01g01830	strong similarity to catalase/peroxidase cpeB - <i>Streptomyces reticuli</i>	0	762	32	36	89	8	23.4	23.1	0.00
An13g00430	similarity to pre-induction sporulation gene acoB - <i>Aspergillus nidulans</i>	0	375	3	11	10	10	10.1	9.9	0.00
An03g05290	similarity to glucan 1,3- β -glucosidase Bgl2 - <i>Saccharomyces cerevisiae</i>	0	464	1	6	4	6	4.2	4.1	0.00
An02g10200	strong similarity to protein TRRAP - <i>Homo sapiens</i>	0	3911	2	1	2	2	0.2	0.2	0.00
An08g08840	strong similarity to glutamate decarboxylase GAD1 - <i>Arabidopsis thaliana</i>	0	515	6	4	11	4	5.3	5.4	0.00
An01g12370	similarity to hypothetical protein SPCC285.11 - <i>Schizosaccharomyces pombe</i>	0	525	2	8	8	7	5.2	5.3	0.00
An02g06030	strong similarity to urate oxidase uaz - <i>Aspergillus flavus</i>	0	302	4	4	5	7	7.3	7.5	0.00
An08g02470	strong similarity to cytoplasmic ribosomal protein of the large subunit L35 - <i>Rattus norvegicus</i>	0	121	2	4	5	4	14.0	14.2	0.00
An02g05900	similarity to hypothetical protein AA57718.1 - <i>Aspergillus nidulans</i>	1	124	0	6	4	5	13.6	13.8	0.00
An10g00480	similarity to hypothetical GPI-anchor biosynthesis PIG-F related protein CAD70892.1 - <i>Neurospora crassa</i>	3	259	1	1	1	2	2.5	2.4	0.00
An07g02820	strong similarity to hypothetical protein SPBC1539.04 - <i>Schizosaccharomyces pombe</i>	3	287	8	20	28	13	25.8	26.1	0.00
An04g05870	strong similarity to E3 ubiquitin ligase Tom1 - <i>Saccharomyces cerevisiae</i>	0	4068	4	7	14	3	0.7	0.8	0.00
An15g06260	strong similarity to GU4 nucleic-binding protein 1 Arc1 - <i>Saccharomyces cerevisiae</i>	0	448	2	6	9	3	4.9	5.0	0.00
211875	strong similarity to aldose 1-epimerase family protein, putative [<i>Aspergillus clavatus</i> NRRL 1]	0	398	4	12	11	12	10.8	10.7	0.00
An04g05220	strong similarity to subunit 6 of ubiquinol--cytochrome-c reductase Qcr6 - <i>Saccharomyces cerevisiae</i>	0	167	3	3	5	4	10.1	10.3	0.00
An14g02990	similarity to hypothetical protein KIAA1715 - <i>Homo sapiens</i>	2	430	1	1	2	1	1.5	1.5	0.00
An04g02090	pyruvate carboxylase pyc - <i>Aspergillus niger</i>	0	1192	53	37	80	49	19.8	19.6	0.00
An02g05210	strong similarity to synexin (annexin VII) - <i>Mus musculus</i>	0	449	2	0	1	2	1.4	1.4	0.00

An11g09880	similarity to hypothetical protein CAE76201.1 - Neurospora crassa	1	235	2	4	5	4	7.2	7.3	0.00
An17g01815	strong similarity to translation initiation factor Eif6 - Saccharomyces cerevisiae	0	247	3	3	6	3	6.8	6.9	0.00
An01g06480	strong similarity to TCP1 complex β chain TCP1 β - Saccharomyces cerevisiae	0	531	2	0	1	2	1.2	1.2	0.00
An02g05700	strong similarity to translation elongation factor eEF-2 - Cricetus griseus	0	844	62	57	123	48	36.8	36.7	0.00
An15g00570	strong similarity to bifunctional purine synthase ade1p - Schizosaccharomyces pombe-	0	808	4	4	12	0	2.7	2.8	0.00
An17g00240	strong similarity to hypothetical protein YER036c - Saccharomyces cerevisiae	0	613	2	0	1	2	1.1	1.0	0.00
An08g05160	strong similarity to oleate δ -12 desaturase odeA - Aspergillus nidulans	4	466	9	16	15	21	14.2	14.1	0.00
An02g10350	strong similarity to farnesyl-pyrophosphate synthase FPPS - Gibberella fujikuroi-	0	346	2	4	9	0	4.9	5.0	0.00
An17g01550	strong similarity to Na ⁺ -H ⁺ antiporter Nha2 - Saccharomyces cerevisiae	12	707	0	2	1	2	0.9	0.9	0.00
An07g07420	strong similarity to splicing factor PRP8 - Homo sapiens	0	2407	9	1	3	12	1.1	1.2	0.00
211733	strong similarity to PX domain protein [Aspergillus fumigatus Af293]	1	1024	2	0	1	2	0.6	0.6	0.00
An16g03090	strong similarity to small nucleolar RNP component Nop56 - Saccharomyces cerevisiae	0	519	2	4	7	2	3.3	3.3	0.00
An16g09260	strong similarity to dnaK-type molecular chaperone Ssb2 - Saccharomyces cerevisiae	0	614	11	15	21	17	11.2	11.3	0.00
An18g03290	strong similarity to regulator subunit of the protein phosphatase 2A PR65 - Xenopus laevis	0	616	4	2	8	1	2.7	2.8	0.00
An05g00530	strong similarity to translational regulator HsGCN1 - Homo sapiens	0	2589	8	0	10	2	0.9	0.9	0.00
An08g06560	strong similarity to spermidine synthase Spe3 - Saccharomyces cerevisiae	0	292	5	6	15	1	10.2	10.2	0.00
An14g03820	strong similarity to UDP-glucose 4-epimerase Gal10 - Saccharomyces cerevisiae	0	371	7	6	10	9	9.5	9.5	0.00
An17g01110	strong similarity to 17.2 kD subunit of NADH:ubiquinone reductase b17.2 - Bos taurus	0	140	1	3	2	4	8.4	8.4	0.00
An16g01570	strong similarity to Arp2/3 complex 21kDa subunit ARC21 - Homo sapiens	0	188	3	1	2	4	6.2	6.2	0.00
An02g07090	strong similarity to ASNA1 product arsenite translocating ATPase - Homo sapiens-	0	341	3	1	6	0	3.4	3.4	0.00
An18g05090	similarity to retinal short-chain dehydrogenase/reductase retSDR1 - Mus musculus	3	387	1	3	2	4	3.0	3.0	0.00
An07g05830	strong similarity to formamidase fmdS - Aspergillus nidulans-	0	413	2	2	6	0	2.8	2.8	0.00
An12g10590	strong similarity to hypothetical protein EAU36877, a novel DnaK-type chaperone - Aspergillus terreus	0	489	2	2	4	2	2.4	2.4	0.00
An04g02500	strong similarity to glycolipid N-tetradecanoyltransferase Nmt - Ajellomyces capsulatus	0	491	3	1	2	4	2.4	2.4	0.00
An16g01030	strong similarity to phenylacetate hydroxylase pahA - Penicillium chrysogenum	0	516	4	0	3	3	2.3	2.3	0.00
An15g06360	similarity to multifunctional glutamine-proline--tRNA ligase Aats-glupro - Drosophila melanogaster	0	604	4	0	5	1	1.9	1.9	0.00