

Collins et al. 2006, Molecular Function, Over-representation						
GOCCID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0003735	7.15E-50	8.75668401	60.6747113	164	217	structural constituent of ribosome
GO:0003723	1.58E-24	6.76077023	35.2304775	90	232	RNA binding
GO:0016251	8.41E-19	34.2943778	11.7434925	39	62	general RNA polymerase II transcription factor activity
GO:0003899	1.60E-15	40.6935889	9.22702982	31	33	DNA-directed RNA polymerase activity
GO:0005515	5.77E-12	2.05781138	117.155318	180	419	protein binding
GO:0016455	7.84E-12	Inf	5.59213929	20	20	RNA polymerase II transcription mediator activity
GO:0031202	4.08E-11	6.94479495	14.2599552	37	51	RNA splicing factor activity, transesterification mechanism
GO:0030515	1.72E-10	20.0225141	7.26978107	23	26	snoRNA binding
GO:0003743	2.75E-10	15.6758448	7.828995	24	28	translation initiation factor activity
GO:0045182	5.30E-10	5.54566498	15.65799	38	56	translation regulator activity
GO:0016796	3.51E-09	12.0077548	7.828995	23	28	exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters
GO:0016944	4.88E-09	44.2529595	5.03292536	17	18	RNA polymerase II transcription elongation factor activity
GO:0004532	5.54E-09	17.3782772	6.43096018	20	23	exoribonuclease activity
GO:0005198	3.29E-08	2.82592131	32.9936218	61	335	structural molecule activity
GO:0030528	4.13E-08	1.91172644	90.0334425	134	322	transcription regulator activity
GO:0000175	1.10E-07	20.8069738	5.03292536	16	18	3'-5'-exoribonuclease activity
GO:0004407	5.17E-07	13.867995	5.31253232	16	19	histone deacetylase activity
GO:0003729	7.13E-07	5.99668543	9.22702982	23	33	mRNA binding
GO:0003676	1.19E-06	1.9060288	69.6221341	104	481	nucleic acid binding
GO:0004722	5.48E-06	6.17974111	7.54938804	19	27	protein serine/threonine phosphatase activity
GO:0016887	8.26E-06	1.99206168	50.0496466	77	179	ATPase activity

Collins et al. 2006, Biological Process, Over-representation						
GOCCID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0009987	1.38E-45	2.46813148	1013.01603	1242	4243	cellular process
GO:0008152	1.48E-43	2.34950107	490.989829	712	2991	metabolism
GO:0044267	4.00E-43	3.87950385	131.135666	267	1033	cellular protein metabolism
GO:0051276	5.65E-42	3.85575446	128.339597	261	459	chromosome organization and biogenesis
GO:0006139	1.29E-40	2.77535117	243.537666	413	1345	nucleobase, nucleoside, nucleotide and nucleic acid metabolism
GO:0043037	7.21E-40	5.70764463	71.0201689	170	327	translation
GO:0016043	9.97E-39	2.46613207	322.946044	506	1701	cell organization and biogenesis
GO:0042254	5.65E-36	7.03102736	51.4476814	132	246	ribosome biogenesis and assembly
GO:0009059	5.55E-35	3.10992425	154.063437	284	551	macromolecule biosynthesis
GO:0006325	9.90E-31	10.9699638	31.036373	89	212	establishment and/or maintenance of chromatin architecture
GO:0006259	3.31E-30	3.06897787	132.533701	245	474	DNA metabolism
GO:0016071	8.53E-26	7.11947712	35.5100845	92	182	mRNA metabolism
GO:0000398	7.56E-23	8.7772434	26.2830546	72	94	nuclear mRNA splicing, via spliceosome
GO:0006365	1.62E-21	11.4276569	20.6909154	60	74	35S primary transcript processing
GO:0043283	2.57E-20	2.10820139	216.41579	327	1467	biopolymer metabolism
GO:0016569	1.82E-19	12.5498552	17.6152388	52	63	covalent chromatin modification
GO:0000375	2.35E-19	6.42425806	28.5199104	72	102	RNA splicing, via transesterification reactions
GO:0042255	5.50E-19	12.300677	17.3356318	51	62	ribosome assembly
GO:0006338	6.00E-19	15.5584921	15.378383	47	135	chromatin remodeling
GO:0050791	7.76E-19	2.16866637	178.109636	276	637	regulation of physiological process
GO:0051641	1.28E-17	2.21657863	152.665403	241	546	cellular localization
GO:0050794	1.93E-17	2.11958152	173.356318	266	620	regulation of cellular process
GO:0006333	8.10E-14	4.59854977	28.2403034	64	101	chromatin assembly or disassembly
GO:0006364	1.04E-13	8.10164661	15.937597	43	162	rRNA processing
GO:0000027	9.09E-13	12.377596	11.1842786	33	40	ribosomal large subunit assembly and maintenance
GO:0009892	9.42E-13	3.08477127	47.5331839	91	170	negative regulation of metabolism
GO:0006396	1.14E-12	3.31824085	41.3818307	82	332	RNA processing
GO:0030490	4.06E-12	9.9202351	12.0230995	34	43	processing of 20S pre-rRNA
GO:0006402	5.69E-12	7.01896334	15.378383	40	55	mRNA catabolism
GO:0031323	9.14E-12	2.12912448	103.17497	162	424	regulation of cellular metabolism
GO:0045045	1.02E-11	2.63407241	59.2766764	105	212	secretory pathway
GO:0007059	2.06E-11	3.69079645	30.7567661	64	110	chromosome segregation
GO:0006383	2.90E-11	10.1587838	10.9046716	31	39	transcription from RNA polymerase III promoter
GO:0045449	3.11E-11	2.1723473	91.7110843	146	328	regulation of transcription
GO:0009058	3.28E-11	1.66049969	253.603517	337	907	biosynthesis
GO:0006413	3.34E-11	9.32494759	11.4638855	32	41	translational initiation
GO:0045892	3.61E-11	3.31039397	35.7896914	71	128	negative regulation of transcription, DNA-dependent
GO:0048193	4.76E-11	3.05411841	40.8226168	78	146	Golgi vesicle transport
GO:0045934	6.01E-11	3.05872579	40.2634029	77	144	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism
GO:0000723	7.16E-11	2.32568288	72.9774177	121	261	telomere maintenance
GO:0031507	9.36E-11	4.39885496	22.3685571	50	80	heterochromatin formation
GO:0016458	9.36E-11	4.39885496	22.3685571	50	80	gene silencing
GO:0045814	9.36E-11	4.39885496	22.3685571	50	80	negative regulation of gene expression, epigenetic
GO:0051243	1.55E-10	2.64187223	51.7272884	92	185	negative regulation of cellular physiological process
GO:0006974	2.55E-10	2.49772049	57.3194277	99	205	response to DNA damage stimulus
GO:0006366	2.74E-10	2.43987952	60.3951043	103	288	transcription from RNA polymerase II promoter
GO:0006368	2.75E-10	15.6758448	7.828995	24	28	RNA elongation from RNA polymerase II promoter
GO:0051168	4.99E-10	3.75292025	25.7238407	54	92	nuclear export
GO:0044265	7.53E-10	3.05564645	35.5100845	68	264	cellular macromolecule catabolism
GO:0016573	8.53E-10	15.0132896	7.54938804	23	27	histone acetylation
GO:0006403	1.12E-09	3.87760066	23.486985	50	84	RNA localization
GO:0009056	1.16E-09	1.96731857	102.895363	155	368	catabolism
GO:0031123	1.75E-09	18.2585884	6.71056714	21	24	RNA 3'-end processing
GO:0006367	4.84E-09	5.98742138	12.8619204	32	46	transcription initiation from RNA polymerase II promoter
GO:0043285	7.40E-09	3.58492265	23.766592	49	246	biopolymer catabolism
GO:0050658	1.18E-08	3.85627376	20.6909154	44	74	RNA transport
GO:0046907	1.32E-08	1.88804729	101.776935	150	510	intracellular transport
GO:0043632	1.66E-08	2.68606303	38.3061541	69	137	modification-dependent macromolecule catabolism
GO:0006511	1.66E-08	2.68606303	38.3061541	69	137	ubiquitin-dependent protein catabolism
GO:0006351	2.26E-08	2.93540001	31.315598	59	446	transcription, DNA-dependent
GO:0006406	3.12E-08	4.09364498	17.840457	39	64	mRNA export from nucleus
GO:0051603	3.54E-08	2.60804894	38.865368	69	139	proteolysis during cellular protein catabolism
GO:0030163	4.49E-08	2.42961165	45.0167213	77	161	protein catabolism
GO:0019538	8.37E-08	2.83539695	30.7567661	57	1156	protein metabolism
GO:0043414	1.01E-07	6.17270449	10.3454577	26	37	biopolymer methylation
GO:0043543	1.06E-07	4.6524109	13.9803482	32	50	protein amino acid acylation
GO:0006378	1.10E-07	20.8069738	5.03292536	16	18	mRNA polyadenylation
GO:0006379	1.90E-07	36.3756219	4.19410446	14	15	mRNA cleavage
GO:0006301	1.90E-07	36.3756219	4.19410446	14	15	postreplication repair
GO:0051246	3.30E-07	4.11202014	15.0987761	33	54	regulation of protein metabolism
GO:0016571	3.55E-07	19.4943995	4.75331839	15	17	histone methylation
GO:0015931	1.12E-06	2.9599298	23.207378	44	83	nucleobase, nucleoside, nucleotide and nucleic acid transport
GO:0006348	1.29E-06	4.20830718	13.1415273	29	47	chromatin silencing at telomere
GO:0006464	1.30E-06	1.59341256	143.71798	191	564	protein modification
GO:0000278	1.36E-06	2.53820576	31.315598	55	235	mitotic cell cycle
GO:0007121	1.81E-06	5.732375	8.94742286	22	32	bipolar bud site selection
GO:0006298	2.21E-06	7.80486284	6.71056714	18	24	mismatch repair
GO:0031326	2.33E-06	3.63664206	15.378383	32	55	regulation of cellular biosynthesis
GO:0030846	2.86E-06	Inf	2.79606964	10	10	transcription termination from Pol II promoter, RNA polymerase(A) coupled
GO:0006445	3.01E-06	4.81293925	10.3454577	24	37	regulation of translation
GO:0007105	4.43E-06	3.13921816	18.4540596	36	66	cytokinesis, site selection
GO:0000154	4.74E-06	12.119403	4.75331839	14	17	rRNA modification
GO:0006360	5.02E-06	5.78443612	8.10860197	20	29	transcription from RNA polymerase I promoter
GO:0000080	5.84E-06	6.6882793	6.99017411	18	25	G1 phase of mitotic cell cycle
GO:0006609	5.84E-06	6.6882793	6.99017411	18	25	mRNA-binding (mRNP) protein import into nucleus
GO:0000054	5.95E-06	8.31681196	5.87174625	16	21	ribosome export from nucleus
GO:0019954	6.25E-06	2.75060127	22.9277711	42	82	asexual reproduction
GO:0042147	7.12E-06	28.5276226	3.35528357	11	12	retrograde transport, endosome to Golgi
GO:0000087	8.75E-06	2.2697357	34.3916566	57	123	M phase of mitotic cell cycle
GO:0006289	9.69E-06	4.97007552	8.94742286	21	32	nucleotide-excision repair

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GOCCID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0005622	3.06E-130	11.8969841	1262.42544	1567	4515	intracellular
GO:0043228	1.10E-103	5.26976361	238.784348	515	854	non-membrane-bound organelle
GO:0005623	4.46E-92	13.1624057	1374.82744	1591	4917	cell
GO:0031981	6.64E-90	14.2630209	82.2044475	243	517	nuclear lumen

GO:0043234	5.11E-50	3.81154751	161.333218	322	1407 protein complex
GO:0005730	7.15E-38	6.11375085	62.352353	153	223 nucleolus
GO:0043231	2.50E-32	2.05917971	943.393898	1140	3374 intracellular membrane-bound organelle
GO:0043229	4.31E-29	3.82128727	85.2801241	176	3679 intracellular organelle
GO:0005732	7.83E-27	47.9387755	15.937597	54	57 small nucleolar ribonucleoprotein complex
GO:0044422	7.13E-24	1.96242596	367.123944	514	2032 organelle part
GO:0005842	1.14E-21	9.6505031	23.207378	65	83 cytosolic large ribosomal subunit (sensu Eukaryota)
GO:0005667	1.44E-21	8.95990354	24.3258059	67	125 transcription factor complex
GO:0000313	2.76E-16	6.70098966	22.6481641	58	81 organellar ribosome
GO:0005694	1.70E-15	3.08359416	59.8358904	114	214 chromosome
GO:0005843	5.16E-15	8.28393651	17.3356318	47	62 cytosolic small ribosomal subunit (sensu Eukaryota)
GO:0046540	2.00E-14	70.7247649	7.828995	27	28 U4/U6 x US tri-snRNP complex
GO:0015935	4.39E-12	15.1972379	9.50663679	29	96 small ribosomal subunit
GO:0005763	4.39E-12	15.1972379	9.50663679	29	34 mitochondrial small ribosomal subunit
GO:0000119	7.84E-12	Inf	5.59213929	20	20 mediator complex
GO:0005759	2.23E-11	2.94611699	45.2963282	85	162 mitochondrial matrix
GO:0005840	3.68E-11	8.65808685	12.0230995	33	269 ribosome
GO:0008023	8.97E-11	28.716875	6.71056714	22	24 transcription elongation factor complex
GO:0044454	9.48E-11	3.19662547	36.3489054	71	146 nuclear chromosome part
GO:0048475	2.07E-10	10.4692597	9.78624375	28	35 coated membrane
GO:0005666	3.67E-10	Inf	4.75331839	17	17 DNA-directed RNA polymerase III complex
GO:0005685	3.67E-10	Inf	4.75331839	17	17 snRNP U1
GO:0005941	3.67E-10	Inf	4.75331839	17	17 unlocalized protein complex
GO:0016591	3.88E-10	13.068253	8.38820893	25	77 DNA-directed RNA polymerase II, holoenzyme
GO:0046695	1.32E-09	Inf	4.47371143	16	16 SLIK (SAGA-like) complex
GO:0000124	1.43E-09	46.8852868	5.31253232	18	19 SAGA complex
GO:0000502	1.47E-09	10.8876018	8.66781589	25	47 proteasome complex (sensu Eukaryota)
GO:0016585	3.51E-09	12.0077548	7.828995	23	73 chromatin remodeling complex
GO:0005847	4.76E-09	Inf	4.19410446	15	15 mRNA cleavage and polyadenylation specificity factor complex
GO:0005669	4.76E-09	Inf	4.19410446	15	15 transcription factor TFIID complex
GO:0030120	1.40E-08	8.95118899	8.66781589	24	31 vesicle coat
GO:0005736	1.71E-08	Inf	3.9144975	14	14 DNA-directed RNA polymerase I complex
GO:0043233	1.92E-08	2.27113722	56.4806068	93	719 organelle lumen
GO:0030659	4.12E-08	7.83041302	8.94742286	24	32 cytoplasmic vesicle membrane
GO:0030529	4.50E-08	3.64387424	20.6909154	43	440 ribonucleoprotein complex
GO:0005684	5.44E-08	15.6209476	5.87174625	18	45 major (U2-dependent) spliceosome
GO:0043601	5.64E-08	38.9981332	4.47371143	15	16 replisome (sensu Eukaryota)
GO:0005839	5.64E-08	38.9981332	4.47371143	15	16 proteasome core complex (sensu Eukaryota)
GO:0043189	6.17E-08	Inf	3.63489054	13	13 H4/H2A histone acetyltransferase complex
GO:0000812	6.17E-08	Inf	3.63489054	13	13 SWR1 complex
GO:0016586	1.90E-07	36.3756219	4.19410446	14	15 RSC complex
GO:0000176	2.22E-07	Inf	3.35528357	12	12 nuclear exosome (RNase complex)
GO:0016514	2.22E-07	Inf	3.35528357	12	12 SWI/SNF complex
GO:0044451	2.35E-07	5.65695489	10.6250646	26	301 nucleoplasm part
GO:0015934	3.94E-07	4.87628607	12.0230995	28	126 large ribosomal subunit
GO:0005762	3.94E-07	4.87628607	12.0230995	28	43 mitochondrial large ribosomal subunit
GO:0005682	6.40E-07	33.7563704	3.9144975	13	14 snRNP U5
GO:0031011	7.97E-07	Inf	3.07567661	11	11 INO80 complex
GO:0000243	7.97E-07	Inf	3.07567661	11	11 commitment complex
GO:0044445	1.44E-06	5.21526909	10.0658507	24	181 cytosolic part
GO:0030532	1.57E-06	12.9931549	5.03292536	15	59 small nuclear ribonucleoprotein complex
GO:0005665	2.14E-06	31.1403727	3.63489054	12	13 DNA-directed RNA polymerase II, core complex
GO:0030119	2.14E-06	31.1403727	3.63489054	12	13 membrane coat adaptor complex
GO:0008541	2.86E-06	Inf	2.79606964	10	10 proteasome regulatory particle, lid subcomplex (sensu Eukaryota)
GO:0030008	2.86E-06	Inf	2.79606964	10	10 TRAPP complex
GO:0043614	2.86E-06	Inf	2.79606964	10	10 multi-eIF complex
GO:0016282	2.86E-06	Inf	2.79606964	10	72 eukaryotic 43S preinitiation complex
GO:0000177	2.86E-06	Inf	2.79606964	10	10 cytoplasmic exosome (RNase complex)
GO:0044428	4.07E-06	1.96108342	56.4806068	86	902 nuclear part
GO:0000775	4.29E-06	3.29247131	17.0560248	34	61 chromosome, pericentric region
GO:0000785	5.06E-06	4.34564809	11.1842786	25	40 chromatin
GO:0000118	6.02E-06	7.36666667	6.43096018	17	23 histone deacetylase complex
GO:0005643	7.57E-06	3.60451977	13.9803482	29	50 nuclear pore
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GOCCID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0005554	5.41E-57	0.35449682	591.089123	337	2114 molecular function unknown
GO:0005215	6.32E-08	0.38294149	63.1911739	30	414 transporter activity
GO:0046943	9.69E-08	0	13.7007413	0	49 carboxylic acid transporter activity
GO:0005275	1.37E-06	0	11.4638855	0	41 amine transporter activity
GO:0015075	2.46E-06	0.34952043	41.3818307	18	148 ion transporter activity
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GOCCID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0000004	9.19E-113	0.14016221	406.828133	102	1455 biological process unknown
GO:0006629	4.61E-18	0.15743202	65.1484227	14	233 lipid metabolism
GO:0008610	4.87E-10	0.16910854	35.5100845	8	127 lipid biosynthesis
GO:0006811	2.46E-09	0.14840565	30.1975521	6	108 ion transport
GO:0006643	2.67E-08	0.19421409	31.31598	8	112 membrane lipid metabolism
GO:0015849	5.00E-08	0	14.2599552	0	51 organic acid transport
GO:0030001	3.34E-06	0.09610995	15.378383	2	55 metal ion transport
GO:0006650	3.66E-06	0.05542741	13.1415273	1	47 glycerophospholipid metabolism
GO:0008202	3.66E-06	0.05542741	13.1415273	1	47 steroid metabolism
GO:0006865	7.15E-06	0	10.0658507	0	36 amino acid transport
GO:0008654	8.11E-06	0.10195062	14.5395621	2	52 phospholipid biosynthesis
GO:0006767	9.91E-06	0.2148236	21.5297363	6	77 water-soluble vitamin metabolism
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GOCCID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0008372	4.39E-94	0.06910211	244.656094	28	875 cellular component unknown
GO:0005740	2.41E-14	0.27030777	79.1287709	28	283 mitochondrial envelope
GO:0005886	2.67E-14	0.23938326	69.6221341	22	249 plasma membrane
GO:0005783	4.25E-09	0.4329481	93.94794	50	336 endoplasmic reticulum
GO:0030312	4.61E-09	0.13437677	27.6810895	5	99 external encapsulating structure
GO:0009277	4.61E-09	0.13437677	27.6810895	5	99 cell wall (sensu Fungi)
GO:0005743	7.84E-08	0.30998702	45.8555421	18	164 mitochondrial inner membrane
GO:0016020	1.48E-07	0.63002391	226.761248	167	1060 membrane
GO:0031975	3.27E-07	0.51563484	105.691433	65	378 envelope
GO:0005773	4.02E-07	0.3760794	53.6845371	25	192 vacuole
GO:0005739	4.24E-07	0.66799221	277.649716	215	993 mitochondrion
GO:0019867	3.55E-06	0.20316832	22.6481641	6	81 outer membrane
GO:0005741	3.55E-06	0.20316832	22.6481641	6	81 mitochondrial outer membrane