

GO ID	GO term	Number of members
GO:0006412	translation	225
GO:0000786	nucleosome	50
GO:0005509	calcium ion binding	76
GO:0003735	structural constituent of ribosome	170
GO:0019861	flagellum	23
GO:0005840	ribosome	167
GO:0006334	nucleosome assembly	54
GO:0004722	protein serine/threonine phosphatase activity	26
GO:0006928	cellular component movement	22
GO:0022625	cytosolic large ribosomal subunit	16
GO:0005886	plasma membrane	26
GO:0051276	chromosome organization	50
GO:0016469	proton-transporting two-sector ATPase complex	23
GO:0007049	cell cycle	16
GO:0005200	structural constituent of cytoskeleton	21
GO:0005516	calmodulin binding	16
GO:0044267	cellular protein metabolic process	12
GO:0020037	heme binding	21
GO:0006470	protein dephosphorylation	42
GO:0009405	pathogenesis	12
GO:0015986	ATP synthesis coupled proton transport	14
GO:0008237	metallopeptidase activity	11
GO:0042254	ribosome biogenesis	24
GO:0004298	threonine-type endopeptidase activity	15
GO:0005839	proteasome core complex	15
GO:0004713	protein tyrosine kinase activity	150
GO:0004197	cysteine-type endopeptidase activity	18
GO:0004518	nuclease activity	12
GO:0006812	cation transport	18
GO:0009434	microtubule-based flagellum	17
GO:0005622	intracellular	360
GO:0016791	phosphatase activity	29
GO:0000226	microtubule cytoskeleton organization	11
GO:0004812	aminoacyl-tRNA ligase activity	24
GO:0005783	endoplasmic reticulum	12
GO:0005524	ATP binding	577
GO:0015992	proton transport	21
GO:0046034	ATP metabolic process	13
GO:0006508	proteolysis	107
GO:0007017	microtubule-based process	70
GO:0007155	cell adhesion	14
GO:0016311	dephosphorylation	27
GO:0004016	adenylate cyclase activity	58
GO:0005525	GTP binding	107
GO:0009190	cyclic nucleotide biosynthetic process	68
GO:0016849	phosphorus-oxygen lyase activity	68
GO:0006511	ubiquitin-dependent protein catabolic process	61
GO:0043234	protein complex	14
GO:0051258	protein polymerization	14
GO:0015031	protein transport	56
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic prc	39
GO:0015078	hydrogen ion transmembrane transporter activity	12
GO:0003824	catalytic activity	247
GO:0045454	cell redox homeostasis	36
GO:0046873	metal ion transmembrane transporter activity	11

GO:0009055	electron carrier activity	50
GO:0004222	metalloendopeptidase activity	28
GO:0009986	cell surface	26
GO:0016887	ATPase activity	64
GO:0003677	DNA binding	207
GO:0007264	small GTPase mediated signal transduction	40
GO:0016020	membrane	261
GO:0005874	microtubule	16
GO:0046914	transition metal ion binding	18
GO:0007165	signal transduction	45
GO:0043190	ATP-binding cassette (ABC) transporter complex	11
GO:0003777	microtubule motor activity	77
GO:0003924	GTPase activity	58
GO:0008026	ATP-dependent helicase activity	49
GO:0005875	microtubule associated complex	58
GO:0006913	nucleocytoplasmic transport	19
GO:0005337	nucleoside transmembrane transporter activity	14
GO:0005856	cytoskeleton	14
GO:0005506	iron ion binding	30
GO:0051726	regulation of cell cycle	14
GO:0006118	electron transport	35
GO:0004527	exonuclease activity	13
GO:0016787	hydrolase activity	81
GO:0005737	cytoplasm	181
GO:0007018	microtubule-based movement	79
GO:0005829	cytosol	15
GO:0006418	tRNA aminoacylation for protein translation	23
GO:0006468	protein phosphorylation	178
GO:0015934	large ribosomal subunit	12
GO:0006289	nucleotide-excision repair	11
GO:0050660	flavin adenine dinucleotide binding	20
GO:0004672	protein kinase activity	180
GO:0008234	cysteine-type peptidase activity	13
GO:0004674	protein serine/threonine kinase activity	172
GO:0006414	translational elongation	21
GO:0000166	nucleotide binding	161
GO:0004175	endopeptidase activity	24
GO:0016779	nucleotidyltransferase activity	12
GO:0005694	chromosome	15
GO:0003676	nucleic acid binding	265
GO:0009058	biosynthetic process	19
GO:0042626	ATPase activity, coupled to transmembrane movement of substar	18
GO:0005743	mitochondrial inner membrane	23
GO:0003746	translation elongation factor activity	14
GO:0008138	protein tyrosine/serine/threonine phosphatase activity	16
GO:0003887	DNA-directed DNA polymerase activity	14
GO:0006730	one-carbon metabolic process	12
GO:0006260	DNA replication	30
GO:0051536	iron-sulfur cluster binding	18
GO:0005198	structural molecule activity	27
GO:0006457	protein folding	124
GO:0016491	oxidoreductase activity	130
GO:0008152	metabolic process	226
GO:0005575	cellular_component	1409
GO:0030001	metal ion transport	12
GO:0005515	protein binding	372

GO:0006413	translational initiation	24
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GO:0005634	nucleus	350
GO:0020015	glycosome	17
GO:0005739	mitochondrion	139
GO:0051082	unfolded protein binding	84
GO:0022627	cytosolic small ribosomal subunit	19
GO:0006099	tricarboxylic acid cycle	11
GO:0006629	lipid metabolic process	24
GO:0006259	DNA metabolic process	17
GO:0003684	damaged DNA binding	14
GO:0006364	rRNA processing	23
GO:0017111	nucleoside-triphosphatase activity	107
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	28
GO:0003723	RNA binding	187
GO:0016740	transferase activity	16
GO:0008080	N-acetyltransferase activity	15
GO:0003743	translation initiation factor activity	27
GO:0006096	glycolysis	25
GO:0004221	ubiquitin thiolesterase activity	17
GO:0004386	helicase activity	75
GO:0008380	RNA splicing	16
GO:0006396	RNA processing	94
GO:0005838	proteasome regulatory particle	16
GO:0007010	cytoskeleton organization	14
GO:0003774	motor activity	49
GO:0016021	integral to membrane	501
GO:0008150	biological_process	964
GO:0006886	intracellular protein transport	76
GO:0045121	membrane raft	14
GO:0051287	NAD binding	13
GO:0006810	transport	132
GO:0004842	ubiquitin-protein ligase activity	23
GO:0005215	transporter activity	27
GO:0000287	magnesium ion binding	16
GO:0006888	ER to Golgi vesicle-mediated transport	14
GO:0006506	GPI anchor biosynthetic process	31
GO:0008270	zinc ion binding	281
GO:0030170	pyridoxal phosphate binding	13
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GO:0019538	protein metabolic process	12
GO:0006281	DNA repair	48
GO:0003674	molecular_function	869
GO:0006166	purine ribonucleoside salvage	14
GO:0009116	nucleoside metabolic process	13
GO:0030286	dynein complex	17
GO:0005488	binding	267
GO:0031072	heat shock protein binding	75
GO:0016049	cell growth	13
GO:0019787	small conjugating protein ligase activity	16
GO:0044237	cellular metabolic process	11
GO:0004871	signal transducer activity	11
GO:0005097	Rab GTPase activator activity	14
GO:0032313	regulation of Rab GTPase activity	14
GO:0004198	calcium-dependent cysteine-type endopeptidase activity	17

GO:0030117	membrane coat	15
GO:0008194	UDP-glycosyltransferase activity	24
GO:0051246	regulation of protein metabolic process	15
GO:0043687	post-translational protein modification	15
GO:0008033	tRNA processing	17
GO:0004519	endonuclease activity	11
GO:0001522	pseudouridine synthesis	15
GO:0009982	pseudouridine synthase activity	15
GO:0006310	DNA recombination	15
GO:0016881	acid-amino acid ligase activity	12
GO:0005730	nucleolus	13
GO:0006865	amino acid transport	44
GO:0005275	amine transmembrane transporter activity	42
GO:0005975	carbohydrate metabolic process	30
GO:0006512	ubiquitin cycle	21
GO:0030528	transcription regulator activity	14
GO:0003678	DNA helicase activity	11
GO:0016070	RNA metabolic process	14
GO:0008168	methyltransferase activity	30
GO:0016192	vesicle-mediated transport	65
GO:0008565	protein transporter activity	17
GO:0003700	sequence-specific DNA binding transcription factor activity	16
GO:0003899	DNA-directed RNA polymerase activity	37
GO:0006464	protein modification process	66

n distance (bp) of merr	With Sample Standard deviation	000) trials which were greater th	distance (bp) of i
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75278.47368	64415.68019	0.8474	48821
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Mean (log2) fold change of GO term group in response to heat shock

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