

GO term	Description	Ratio in foreground list	Ratio in background list	P-value	FDR	Number in foregrou nd list
GO:0006886	intracellular protein transport	113/4193	620/58683	3.62E-20	6.36E-17	113
GO:0005802	trans-Golgi network	113/4527	759/63390	1.15E-13	2.36E-11	113
GO:0009737	response to abscisic acid	111/4193	1154/58683	0.00095	0.0164	111
GO:0009414	response to water deprivation	110/4193	885/58683	1.22E-08	2.11E-06	110
GO:0009409	response to cold	105/4193	969/58683	1.54E-05	0.00059	105
GO:0005516	calmodulin binding	105/4244	1058/61756	0.00011	0.00387	105
GO:0009651	response to salt stress	101/4193	1075/58683	0.00317	0.0389	101
GO:0004497	monooxygenase activity	94/4244	976/61756	0.00066	0.0147	94
GO:0005525	GTP binding	83/4244	777/61756	5.04E-05	0.00203	83
GO:0031969	chloroplast membrane	80/4527	474/63390	7.10E-13	9.72E-11	80
GO:0004675	transmembrane receptor protein serine/threonine kinase activity	76/4244	820/61756	0.00526	0.0477	76
GO:0012505	endomembrane system	64/4527	617/63390	0.00187	0.0183	64
GO:0071456	cellular response to hypoxia	61/4193	466/58683	3.89E-06	0.00022	61
GO:0003924	GTPase activity	58/4244	519/61756	2.00E-04	0.00622	58
GO:0009751	response to salicylic acid	57/4193	519/58683	0.00088	0.0157	57
GO:0030247	polysaccharide binding	57/4244	585/61756	0.0053	0.0477	57
GO:0035556	intracellular signal transduction	55/4193	375/58683	3.38E-07	3.29E-05	55
GO:0046686	response to cadmium ion	54/4193	504/58683	0.00204	0.0304	54
GO:0016192	vesicle-mediated transport	47/4193	339/58683	1.07E-05	0.00045	47
GO:0015297	antiporter activity	47/4244	380/61756	7.46E-05	0.00269	47
GO:0009534	chloroplast thylakoid	46/4527	290/63390	3.15E-07	1.18E-05	46
GO:0051082	unfolded protein binding	43/4244	411/61756	0.00421	0.0477	43
GO:0006891	intra-Golgi vesicle-mediated transport	42/4193	159/58683	7.48E-14	6.57E-11	42
GO:0009579	thylakoid	40/4527	281/63390	2.51E-05	0.0004	40
GO:0007623	circadian rhythm	39/4193	255/58683	5.90E-06	0.00032	39
GO:0030170	pyridoxal phosphate binding	39/4244	354/61756	0.00258	0.0328	39
GO:0008643	carbohydrate transport	36/4193	219/58683	2.49E-06	0.00017	36
GO:0005788	endoplasmic reticulum lumen	34/4527	155/63390	3.49E-09	2.39E-07	34
GO:0018105	peptidyl-serine phosphorylation	34/4193	224/58683	2.64E-05	0.00088	34
GO:0005198	structural molecule activity	33/4244	194/61756	1.30E-06	0.00012	33

GO:1900150	regulation of defense response to fungus	30/4193	201/58683	0.0001	0.00268	30
GO:0080167	response to karrikin	30/4193	241/58683	0.00221	0.0315	30
GO:0045454	cell redox homeostasis	29/4193	161/58683	3.63E-06	0.00022	29
GO:1901001	negative regulation of response to salt stress	29/4193	186/58683	6.08E-05	0.00172	29
GO:0032991	protein-containing complex	29/4527	211/63390	0.00055	0.00641	29
GO:0030126	COPI vesicle coat	28/4527	106/63390	9.90E-10	8.14E-08	28
GO:0019253	reductive pentose-phosphate cycle	27/4193	79/58683	2.72E-12	1.59E-09	27
GO:0008233	peptidase activity	26/4244	145/61756	6.19E-06	0.00041	26
GO:0009853	photorespiration	26/4193	146/58683	1.39E-05	0.00056	26
GO:0008061	chitin binding	25/4244	118/61756	3.84E-07	5.38E-05	25
GO:0030968	endoplasmic reticulum unfolded protein response	23/4193	73/58683	7.00E-10	1.54E-07	23
GO:0006487	protein N-linked glycosylation	23/4193	84/58683	1.44E-08	2.11E-06	23
GO:0015250	water channel activity	23/4244	90/61756	2.90E-08	1.08E-05	23
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	23/4244	165/61756	0.00097	0.019	23
GO:0009816	defense response to bacterium, incompatible interaction	22/4193	163/58683	0.00301	0.0376	22
GO:0010598	NAD(P)H dehydrogenase complex (plastoquinone)	21/4527	36/63390	1.58E-15	6.50E-13	21
GO:0016117	carotenoid biosynthetic process	21/4193	81/58683	1.68E-07	1.84E-05	21
GO:0007030	Golgi organization	21/4193	86/58683	5.00E-07	4.39E-05	21
GO:0009773	photosynthetic electron transport in photosystem I	20/4193	46/58683	1.05E-11	3.07E-09	20
GO:0010311	lateral root formation	20/4193	125/58683	0.00056	0.0116	20
GO:0009311	oligosaccharide metabolic process	20/4193	126/58683	0.00063	0.0126	20
GO:0006465	signal peptide processing	19/4193	67/58683	1.38E-07	1.84E-05	19
GO:0016998	cell wall macromolecule catabolic process	19/4193	87/58683	1.00E-05	0.00045	19
GO:0009625	response to insect	19/4193	88/58683	1.19E-05	0.00049	19
GO:0016984	ribulose-bisphosphate carboxylase activity	18/4244	35/61756	1.64E-12	1.84E-09	18
GO:0034599	cellular response to oxidative stress	18/4193	109/58683	0.00071	0.0137	18
GO:0048765	root hair cell differentiation	17/4193	44/58683	3.37E-09	6.58E-07	17
GO:0030173	integral component of Golgi membrane	17/4527	85/63390	9.32E-05	0.00128	17
GO:0010431	seed maturation	17/4193	83/58683	6.85E-05	0.00191	17
GO:0005758	mitochondrial intermembrane space	17/4527	102/63390	0.00088	0.00953	17
GO:0002221	pattern recognition receptor signaling pathway	16/4193	32/58683	8.92E-11	2.24E-08	16
GO:0042651	thylakoid membrane	16/4527	55/63390	9.01E-07	3.02E-05	16
GO:0009644	response to high light intensity	16/4193	89/58683	0.00053	0.0112	16
GO:0010193	response to ozone	16/4193	95/58683	0.0011	0.0186	16

GO:0005347	ATP transmembrane transporter activity	16/4244	104/61756	0.00196	0.0305	16
GO:0005484	SNAP receptor activity	16/4244	113/61756	0.00458	0.0477	16
GO:0030134	COPII-coated ER to Golgi transport vesicle	15/4527	49/63390	9.55E-07	3.02E-05	15
GO:0045492	xylan biosynthetic process	15/4193	83/58683	0.00074	0.0139	15
GO:0008250	oligosaccharyltransferase complex	14/4527	24/63390	8.69E-11	8.93E-09	14
GO:0046513	ceramide biosynthetic process	14/4193	38/58683	1.65E-07	1.84E-05	14
GO:0070588	calcium ion transmembrane transport	14/4193	38/58683	1.65E-07	1.84E-05	14
GO:0045047	protein targeting to ER	14/4193	42/58683	6.88E-07	5.76E-05	14
GO:0006874	cellular calcium ion homeostasis	14/4193	64/58683	0.00014	0.00342	14
GO:0004518	nuclease activity	14/4244	76/61756	0.00061	0.014	14
GO:0015079	potassium ion transmembrane transporter activity	14/4244	93/61756	0.00444	0.0477	14
GO:0072657	protein localization to membrane	13/4193	35/58683	4.10E-07	3.79E-05	13
GO:0055038	recycling endosome membrane	13/4527	39/63390	1.71E-06	4.39E-05	13
GO:0004715	non-membrane spanning protein tyrosine kinase activity	13/4244	36/61756	3.84E-07	5.38E-05	13
GO:0009657	plastid organization	13/4193	38/58683	1.23E-06	9.79E-05	13
GO:0003756	protein disulfide isomerase activity	13/4244	42/61756	2.87E-06	0.00023	13
GO:0048354	mucilage biosynthetic process involved in seed coat development	13/4193	49/58683	2.83E-05	0.00092	13
GO:0009864	induced systemic resistance, jasmonic acid mediated signaling pathway	13/4193	51/58683	4.48E-05	0.00143	13
GO:0080142	regulation of salicylic acid biosynthetic process	13/4193	61/58683	0.00032	0.0071	13
GO:0006012	galactose metabolic process	13/4193	76/58683	0.0027	0.0349	13
GO:0009504	cell plate	13/4527	84/63390	0.00648	0.05	13
GO:0010207	photosystem II assembly	12/4193	47/58683	8.59E-05	0.00231	12
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	12/4244	73/61756	0.00395	0.0471	12
GO:0016987	sigma factor activity	11/4244	18/61756	3.23E-09	1.81E-06	11
GO:0005779	integral component of peroxisomal membrane	11/4527	27/63390	1.08E-06	3.18E-05	11
GO:0004337	geranyltranstransferase activity	11/4244	24/61756	1.72E-07	3.20E-05	11
GO:0016559	peroxisome fission	11/4193	30/58683	3.73E-06	0.00022	11
GO:0006108	malate metabolic process	11/4193	44/58683	0.00021	0.00476	11
GO:0045927	positive regulation of growth	11/4193	49/58683	0.00056	0.0116	11
GO:0010026	trichome differentiation	11/4193	51/58683	0.00081	0.0144	11
GO:0005544	calcium-dependent phospholipid binding	11/4244	56/61756	0.00133	0.0243	11
GO:0052542	defense response by callose deposition	11/4193	57/58683	0.0021	0.031	11
GO:0051787	misfolded protein binding	11/4244	61/61756	0.00271	0.0338	11
GO:0006094	gluconeogenesis	11/4193	60/58683	0.0032	0.039	11

GO:0003978	UDP-glucose 4-epimerase activity	10/4244	18/61756	6.09E-08	1.70E-05	10
GO:0030388	fructose 1,6-bisphosphate metabolic process	10/4193	26/58683	6.27E-06	0.00033	10
GO:0004656	procollagen-proline 4-dioxygenase activity	10/4244	27/61756	6.60E-06	0.00041	10
GO:0005459	UDP-galactose transmembrane transporter activity	10/4244	27/61756	6.60E-06	0.00041	10
GO:0018401	peptidyl-proline hydroxylation to 4-hydroxy-L-proline	10/4193	27/58683	9.32E-06	0.00045	10
GO:0016671	oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	10/4244	34/61756	6.58E-05	0.00252	10
GO:0060178	regulation of exocyst localization	10/4193	35/58683	0.00012	0.00304	10
GO:0006636	unsaturated fatty acid biosynthetic process	10/4193	47/58683	0.00153	0.0243	10
GO:0010105	negative regulation of ethylene-activated signaling pathway	10/4193	47/58683	0.00153	0.0243	10
GO:0045491	xylan metabolic process	10/4193	51/58683	0.00292	0.0371	10
GO:0090114	COPII-coated vesicle budding	9/4193	20/58683	3.91E-06	0.00022	9
GO:0004332	fructose-bisphosphate aldolase activity	9/4244	20/61756	2.83E-06	0.00023	9
GO:0042732	D-xylose metabolic process	9/4193	22/58683	1.02E-05	0.00045	9
GO:0016688	L-ascorbate peroxidase activity	9/4244	27/61756	5.08E-05	0.00203	9
GO:0034051	negative regulation of plant-type hypersensitive response	9/4193	36/58683	0.00077	0.0141	9
GO:0071323	cellular response to chitin	9/4193	37/58683	0.00095	0.0164	9
GO:0080187	floral organ senescence	9/4193	45/58683	0.00405	0.0465	9
GO:0008889	glycerophosphodiester phosphodiesterase activity	9/4244	49/61756	0.00566	0.0484	9
GO:0033320	UDP-D-xylose biosynthetic process	8/4193	14/58683	1.37E-06	1.00E-04	8
GO:2001141	regulation of RNA biosynthetic process	8/4193	15/58683	2.75E-06	0.00018	8
GO:0010482	regulation of epidermal cell division	8/4193	19/58683	2.49E-05	0.00084	8
GO:0015976	carbon utilization	8/4193	19/58683	2.49E-05	0.00084	8
GO:0071277	cellular response to calcium ion	8/4193	19/58683	2.49E-05	0.00084	8
GO:0033384	geranyl diphosphate biosynthetic process	8/4193	21/58683	5.89E-05	0.00172	8
GO:0045337	farnesyl diphosphate biosynthetic process	8/4193	21/58683	5.89E-05	0.00172	8
GO:0051290	protein heterotetramerization	8/4193	22/58683	8.68E-05	0.00231	8
GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	8/4193	23/58683	0.00013	0.00308	8
GO:0070403	NAD+ binding	8/4244	29/61756	0.00057	0.0134	8
GO:0140326	ATPase-coupled intramembrane lipid transporter activity	8/4244	30/61756	0.00073	0.0158	8
GO:0045332	phospholipid translocation	8/4193	30/58683	0.00095	0.0164	8
GO:0015369	calcium:proton antiporter activity	8/4244	34/61756	0.00178	0.0305	8
GO:0031012	extracellular matrix	8/4527	36/63390	0.00333	0.0311	8
GO:0071483	cellular response to blue light	7/4193	9/58683	3.00E-07	3.09E-05	7
GO:0004470	malic enzyme activity	7/4244	10/61756	7.18E-07	8.94E-05	7

GO:0008460	dTDP-glucose 4,6-dehydratase activity	7/4244	12/61756	4.19E-06	0.00031	7
GO:0006090	pyruvate metabolic process	7/4193	14/58683	2.07E-05	0.00076	7
GO:2001142	nicotinate transport	7/4193	16/58683	6.08E-05	0.00172	7
GO:2001143	N-methylnicotinate transport	7/4193	16/58683	6.08E-05	0.00172	7
GO:0090416	nicotinate transmembrane transporter activity	7/4244	16/61756	4.73E-05	0.00203	7
GO:0090417	N-methylnicotinate transmembrane transporter activity	7/4244	16/61756	4.73E-05	0.00203	7
GO:0009051	pentose-phosphate shunt, oxidative branch	7/4193	17/58683	9.69E-05	0.00254	7
GO:0046512	sphingosine biosynthetic process	7/4193	18/58683	0.00015	0.00358	7
GO:0010236	plastoquinone biosynthetic process	7/4193	19/58683	0.00022	0.00504	7
GO:0033926	glycopeptide alpha-N-acetylgalactosaminidase activity	7/4244	21/61756	0.00035	0.00923	7
GO:0006796	phosphate-containing compound metabolic process	7/4193	25/58683	0.00144	0.0234	7
GO:0010117	photoprotection	7/4193	26/58683	0.00185	0.0278	7
GO:0005986	sucrose biosynthetic process	7/4193	27/58683	0.00235	0.0323	7
GO:0005987	sucrose catabolic process	7/4193	27/58683	0.00235	0.0323	7
GO:0009423	chorismate biosynthetic process	7/4193	29/58683	0.00364	0.0432	7
GO:2001070	starch binding	7/4244	31/61756	0.00437	0.0477	7
GO:0004758	serine C-palmitoyltransferase activity	6/4244	6/61756	1.05E-07	2.35E-05	6
GO:0005960	glycine cleavage complex	6/4527	9/63390	9.20E-06	0.00016	6
GO:0019464	glycine decarboxylation via glycine cleavage system	6/4193	9/58683	9.22E-06	0.00045	6
GO:0035102	PRC1 complex	6/4527	12/63390	8.38E-05	0.00119	6
GO:0048032	galacturonate binding	6/4244	11/61756	3.59E-05	0.00175	6
GO:0003987	acetate-CoA ligase activity	6/4244	12/61756	6.75E-05	0.00252	6
GO:0004615	phosphomannomutase activity	6/4244	14/61756	0.0002	0.00622	6
GO:1990381	ubiquitin-specific protease binding	6/4244	16/61756	0.00046	0.0115	6
GO:0008964	phosphoenolpyruvate carboxylase activity	6/4244	18/61756	0.00095	0.0189	6
GO:0015977	carbon fixation	6/4193	18/58683	0.00116	0.0194	6
GO:0044375	regulation of peroxisome size	6/4193	19/58683	0.0016	0.0244	6
GO:0051567	histone H3-K9 methylation	6/4193	19/58683	0.0016	0.0244	6
GO:0080186	developmental vegetative growth	6/4193	19/58683	0.0016	0.0244	6
GO:0005354	galactose transmembrane transporter activity	6/4244	21/61756	0.00232	0.0305	6
GO:0005365	myo-inositol transmembrane transporter activity	6/4244	21/61756	0.00232	0.0305	6
GO:0015148	D-xylose transmembrane transporter activity	6/4244	21/61756	0.00232	0.0305	6
GO:0015168	glycerol transmembrane transporter activity	6/4244	21/61756	0.00232	0.0305	6
GO:0015575	mannitol transmembrane transporter activity	6/4244	21/61756	0.00232	0.0305	6

GO:0015576	sorbitol transmembrane transporter activity	6/4244	21/61756	0.00232	0.0305	6
GO:0015591	D-ribose transmembrane transporter activity	6/4244	21/61756	0.00232	0.0305	6
GO:0033356	UDP-L-arabinose metabolic process	6/4193	20/58683	0.00214	0.031	6
GO:0070370	cellular heat acclimation	6/4193	21/58683	0.00282	0.0361	6
GO:0034975	protein folding in endoplasmic reticulum	5/4193	6/58683	1.05E-05	0.00045	5
GO:0042476	odontogenesis	5/4193	6/58683	1.05E-05	0.00045	5
GO:0071560	cellular response to transforming growth factor beta stimulus	5/4193	6/58683	1.05E-05	0.00045	5
GO:0090677	reversible differentiation	5/4193	6/58683	1.05E-05	0.00045	5
GO:1990931	RNA N6-methyladenosine dioxygenase activity	5/4244	6/61756	8.65E-06	0.00051	5
GO:1902479	positive regulation of defense response to bacterium, incompatible interaction	5/4193	9/58683	0.00018	0.00435	5
GO:0004579	dolichyl-diphosphooligosaccharide-protein glycotransferase activity	5/4244	9/61756	0.00015	0.00502	5
GO:0010148	transpiration	5/4193	10/58683	0.00035	0.00753	5
GO:0046923	ER retention sequence binding	5/4244	11/61756	0.0005	0.0118	5
GO:0036064	ciliary basal body	5/4527	13/63390	0.00147	0.0147	5
GO:0010475	galactose-1-phosphate guanylyltransferase (GDP) activity	5/4244	12/61756	0.0008	0.0164	5
GO:0080047	GDP-L-galactose phosphorylase activity	5/4244	12/61756	0.0008	0.0164	5
GO:0080048	GDP-D-glucose phosphorylase activity	5/4244	12/61756	0.0008	0.0164	5
GO:0032958	inositol phosphate biosynthetic process	5/4193	12/58683	0.00096	0.0164	5
GO:0032451	demethylase activity	5/4244	13/61756	0.00123	0.0232	5
GO:0072334	UDP-galactose transmembrane transport	5/4193	14/58683	0.00215	0.031	5
GO:0009882	blue light photoreceptor activity	5/4244	15/61756	0.00256	0.0328	5
GO:0047517	1,4-beta-D-xylan synthase activity	5/4244	15/61756	0.00256	0.0328	5
GO:0000256	allantoin catabolic process	5/4193	15/58683	0.00304	0.0376	5
GO:0006145	purine nucleobase catabolic process	5/4193	15/58683	0.00304	0.0376	5
GO:1905157	positive regulation of photosynthesis	5/4193	15/58683	0.00304	0.0376	5
GO:0090229	negative regulation of red or far-red light signaling pathway	5/4193	16/58683	0.00416	0.0471	5
GO:0042548	regulation of photosynthesis, light reaction	4/4193	5/58683	0.00012	0.00308	4
GO:0045962	positive regulation of development, heterochronic	4/4193	6/58683	0.00035	0.00753	4
GO:0004385	guanylate kinase activity	4/4244	6/61756	0.0003	0.00796	4
GO:0032051	clathrin light chain binding	4/4244	6/61756	0.0003	0.00796	4
GO:0033188	sphingomyelin synthase activity	4/4244	6/61756	0.0003	0.00796	4
GO:0045140	inositol phosphoceramide synthase activity	4/4244	6/61756	0.0003	0.00796	4
GO:0047493	ceramide cholinephosphotransferase activity	4/4244	6/61756	0.0003	0.00796	4
GO:1990482	sphingolipid alpha-glucuronosyltransferase activity	4/4244	6/61756	0.0003	0.00796	4

GO:0050347	trans-octaprenyltranstransferase activity	4/4244	8/61756	0.00124	0.0232	4
GO:0052923	all-trans-nonaprenyl-diphosphate synthase (geranyl-diphosphate specific) activity	4/4244	8/61756	0.00124	0.0232	4
GO:0042425	choline biosynthetic process	4/4193	8/58683	0.00144	0.0234	4
GO:0000234	phosphoethanolamine N-methyltransferase activity	4/4244	9/61756	0.00212	0.0305	4
GO:0000257	nitrilase activity	4/4244	9/61756	0.00212	0.0305	4
GO:0004751	ribose-5-phosphate isomerase activity	4/4244	9/61756	0.00212	0.0305	4
GO:0008883	glutamyl-tRNA reductase activity	4/4244	9/61756	0.00212	0.0305	4
GO:0047427	cyanoalanine nitrilase activity	4/4244	9/61756	0.00212	0.0305	4
GO:0009440	cyanate catabolic process	4/4193	9/58683	0.00245	0.0323	4
GO:0045227	capsule polysaccharide biosynthetic process	4/4193	9/58683	0.00245	0.0323	4
GO:0051410	detoxification of nitrogen compound	4/4193	9/58683	0.00245	0.0323	4
GO:0007507	heart development	4/4193	10/58683	0.00385	0.0445	4
GO:0010136	ureide catabolic process	4/4193	10/58683	0.00385	0.0445	4
GO:0045595	regulation of cell differentiation	4/4193	10/58683	0.00385	0.0445	4
GO:0048507	meristem development	4/4193	10/58683	0.00385	0.0445	4
GO:0047066	phospholipid-hydroperoxide glutathione peroxidase activity	4/4244	11/61756	0.00496	0.0477	4
GO:0080124	pheophytinase activity	4/4244	11/61756	0.00496	0.0477	4
GO:0000329	fungus-type vacuole membrane	4/4527	11/63390	0.0057	0.0488	4
GO:0005358	high-affinity glucose:proton symporter activity	3/4244	5/61756	0.00292	0.0359	3
GO:0008202	steroid metabolic process	3/4193	5/58683	0.00327	0.039	3
GO:0010124	phenylacetate catabolic process	3/4193	5/58683	0.00327	0.039	3
GO:0003868	4-hydroxyphenylpyruvate dioxygenase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0003871	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0003873	6-phosphofructo-2-kinase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0004048	anthranilate phosphoribosyltransferase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0004134	4-alpha-glucanotransferase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0004325	ferrochelatase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0004331	fructose-2,6-bisphosphate 2-phosphatase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0004360	glutamine-fructose-6-phosphate transaminase (isomerizing) activity	3/4244	6/61756	0.00554	0.0477	3
GO:0009703	nitrate reductase (NADH) activity	3/4244	6/61756	0.00554	0.0477	3
GO:0010297	heteropolysaccharide binding	3/4244	6/61756	0.00554	0.0477	3
GO:0015930	glutamate synthase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0018708	thiol S-methyltransferase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0033550	MAP kinase tyrosine phosphatase activity	3/4244	6/61756	0.00554	0.0477	3

GO:0046422	violaxanthin de-epoxidase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0047840	dCTP diphosphatase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0102092	5-diphosphoinositol pentakisphosphate 3-kinase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0102500	beta-maltose 4-alpha-glucanotransferase activity	3/4244	6/61756	0.00554	0.0477	3
GO:1990585	hydroxyproline O-arabinosyltransferase activity	3/4244	6/61756	0.00554	0.0477	3
GO:0043227	membrane-bounded organelle	3/4527	6/63390	0.00618	0.0488	3
GO:0044297	cell body	3/4527	6/63390	0.00618	0.0488	3
GO:0099080	supramolecular complex	3/4527	6/63390	0.00618	0.0488	3

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