

Supplemental Table 10 Gene Ontology classification of differentially associated *Arabidopsis* mRNAs. mRNAs showing differential transcript accumulation in the polysomal and total RNA fractions (FDR ≤ 5%) were selected for analysis. AgriGO ontologies are included if represented by 5 or more genes and at a 1% FDR cutoff. The first number in each column header represents the total number of probe sets meeting these criteria in the gene list, while the number below in parentheses represents the number of probe sets in this list with AgriGO annotation(s). Bgitem refers to total number of genes with the corresponding annotation in this genome. GO_acc is the Gene Ontology accession, hi refers to mRNAs that are significantly highly represented on polysomes, and lo refers to mRNAs that are significantly poorly represented on polysomes.

GO_acc	Term	bgitem	Turnv hi (1404)	Mock hi (1935)	Turnv lo (1936)	Mock lo (2753)
GO:0000003	reproduction	1186	32	53	120	176
GO:0000059	protein import into nucleus, docking	17	0	0	10	11
GO:0000148	1,3-beta-glucan synthase complex	13	0	0	6	8
GO:0000151	ubiquitin ligase complex	259	1	5	38	51
GO:0000166	nucleotide binding	2267	53	62	241	322
GO:0000271	polysaccharide biosynthetic process	112	1	1	22	24
GO:0000272	polysaccharide catabolic process	19	0	0	7	8
GO:0000302	response to reactive oxygen species	85	10	15	3	4
GO:0000418	DNA-directed RNA polymerase IV complex	12	5	5	0	0
GO:0000428	DNA-directed RNA polymerase complex	30	6	8	3	1
GO:0000785	chromatin	71	8	20	1	4
GO:0000786	nucleosome	37	7	16	0	1
GO:0000815	ESCRT III complex	13	0	5	0	0
GO:0000904	cell morphogenesis involved in differentiation	63	4	4	13	20
GO:0001882	nucleoside binding	1465	17	20	164	213
GO:0001883	purine nucleoside binding	1465	17	20	164	213
GO:0002376	immune system process	368	12	19	45	53
GO:0003006	reproductive developmental process	978	29	46	113	161
GO:0003677	DNA binding	2892	112	204	133	174
GO:0003724	RNA helicase activity	21	0	0	9	9
GO:0003735	structural constituent of ribosome	494	65	76	15	16
GO:0003743	translation initiation factor activity	115	13	18	9	15
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	68	13	12	5	7
GO:0003824	catalytic activity	9638	325	384	756	1139
GO:0003843	1,3-beta-glucan synthase activity	13	0	0	6	8
GO:0004175	endopeptidase activity	257	9	8	27	39
GO:0004176	ATP-dependent peptidase activity	29	0	0	8	12
GO:0004222	metalloendopeptidase activity	47	1	0	12	17
GO:0004364	glutathione transferase activity	57	7	14	1	1
GO:0004386	helicase activity	182	1	3	39	48
GO:0004602	glutathione peroxidase activity	10	5	0	0	0
GO:0004672	protein kinase activity	953	16	21	87	109
GO:0004674	protein serine/threonine kinase activity	681	10	12	65	74
GO:0004812	aminoacyl-tRNA ligase activity	80	1	0	11	18
GO:0004842	ubiquitin-protein ligase activity	324	17	24	42	46
GO:0004843	ubiquitin-specific protease activity	28	0	0	4	11
GO:0004857	enzyme inhibitor activity	173	20	24	3	3
GO:0004866	endopeptidase inhibitor activity	39	0	11	0	0
GO:0004871	signal transducer activity	422	4	13	45	51
GO:0004872	receptor activity	212	2	3	26	25
GO:0004888	transmembrane receptor activity	171	1	2	23	22
GO:0005198	structural molecule activity	659	74	90	31	36
GO:0005215	transporter activity	1477	60	76	132	234
GO:0005342	organic acid transmembrane transporter activity	78	2	2	8	25
GO:0005343	organic acid:sodium symporter activity	8	0	0	0	6
GO:0005388	calcium-transporting ATPase activity	18	0	0	2	8
GO:0005488	binding	11258	453	634	777	1047
GO:0005509	calcium ion binding	215	30	42	12	13
GO:0005515	protein binding	2944	125	175	241	305
GO:0005524	ATP binding	1377	16	19	160	205
GO:0005576	extracellular region	285	23	26	6	14
GO:0005618	cell wall	403	37	35	11	23
GO:0005622	intracellular	9671	600	762	783	1174
GO:0005623	cell	15217	789	1040	1042	1554
GO:0005634	nucleus	2621	137	217	214	264
GO:0005635	nuclear envelope	58	3	6	14	16
GO:0005643	nuclear pore	26	0	1	11	11
GO:0005665	DNA-directed RNA polymerase II, core complex	18	5	6	2	1
GO:0005694	chromosome	177	8	22	9	19
GO:0005730	nucleolus	209	26	30	18	21
GO:0005732	small nucleolar ribonucleoprotein complex	113	7	16	2	2
GO:0005737	cytoplasm	6822	478	570	551	886
GO:0005739	mitochondrion	1276	92	112	95	159
GO:0005740	mitochondrial envelope	223	31	38	16	27
GO:0005743	mitochondrial inner membrane	172	17	24	13	23
GO:0005746	mitochondrial respiratory chain	39	9	9	2	2
GO:0005750	mitochondrial respiratory chain complex III	23	8	8	2	2
GO:0005768	endosome	84	11	16	3	7
GO:0005773	vacuole	383	41	52	33	64
GO:0005774	vacuolar membrane	100	3	4	14	26
GO:0005783	endoplasmic reticulum	466	31	33	35	65
GO:0005794	Golgi apparatus	293	11	12	35	41
GO:0005802	trans-Golgi network	19	1	1	7	7
GO:0005829	cytosol	912	73	99	72	91
GO:0005840	ribosome	524	64	78	16	17
GO:0005886	plasma membrane	1456	105	139	148	204
GO:0005975	carbohydrate metabolic process	866	23	22	70	107
GO:0005976	polysaccharide metabolic process	152	2	2	29	34
GO:0005982	starch metabolic process	41	0	1	14	19
GO:0005983	starch catabolic process	15	0	0	7	8
GO:0005996	monosaccharide metabolic process	168	5	7	16	29
GO:0006066	alcohol metabolic process	270	6	8	27	46
GO:0006073	cellular glucan metabolic process	87	2	2	24	31
GO:0006074	1,3-beta-glucan metabolic process	13	0	0	6	8
GO:0006075	1,3-beta-glucan biosynthetic process	13	0	0	6	8
GO:0006082	organic acid metabolic process	860	25	36	83	114
GO:0006119	oxidative phosphorylation	69	16	18	0	0
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	3198	93	152	217	301
GO:0006323	DNA packaging	64	7	18	0	1
GO:0006325	chromatin organization	175	9	23	14	23

GO:0006333	chromatin assembly or disassembly	82	8	22	2	4
GO:0006334	nucleosome assembly	56	7	18	0	1
GO:0006396	RNA processing	453	6	5	55	77
GO:0006399	tRNA metabolic process	141	1	0	22	32
GO:0006413	translational initiation	90	12	18	5	10
GO:0006418	tRNA aminoacylation for protein translation	84	1	0	12	19
GO:0006457	protein folding	275	26	29	24	29
GO:0006461	protein complex assembly	134	12	9	22	37
GO:0006464	protein modification process	1474	35	38	119	165
GO:0006508	proteolysis	810	35	38	72	94
GO:0006519	cellular amino acid and derivative metabolic process	682	20	25	54	80
GO:0006520	cellular amino acid metabolic process	430	10	14	42	62
GO:0006605	protein targeting	155	20	25	23	34
GO:0006606	protein import into nucleus	41	0	3	12	13
GO:0006626	protein targeting to mitochondrion	20	4	8	1	3
GO:0006629	lipid metabolic process	841	21	26	76	116
GO:0006644	phospholipid metabolic process	121	3	2	15	26
GO:0006650	glycerophospholipid metabolic process	55	1	1	7	15
GO:0006694	steroid biosynthetic process	56	0	0	7	14
GO:0006720	isoprenoid metabolic process	168	4	4	16	27
GO:0006732	coenzyme metabolic process	188	0	1	15	31
GO:0006807	nitrogen compound metabolic process	3826	111	174	265	380
GO:0006810	transport	1846	117	145	137	233
GO:0006814	sodium ion transport	21	1	0	1	11
GO:0006818	hydrogen transport	59	10	12	0	2
GO:0006869	lipid transport	163	13	22	7	8
GO:0006873	cellular ion homeostasis	96	7	7	13	20
GO:0006886	intracellular protein transport	311	30	38	39	59
GO:0006913	nucleocytoplasmic transport	71	0	3	17	19
GO:0006914	autophagy	35	3	10	1	1
GO:0006950	response to stress	2320	154	210	172	230
GO:0006955	immune response	367	12	19	45	53
GO:0006970	response to osmotic stress	408	25	37	38	52
GO:0006979	response to oxidative stress	332	37	44	13	17
GO:0006996	organelle organization	640	35	57	61	94
GO:0007275	multicellular organismal development	2020	60	98	187	268
GO:0008017	microtubule binding	36	1	10	1	2
GO:0008026	ATP-dependent helicase activity	128	1	3	33	35
GO:0008028	monocarboxylic acid transmembrane transporter activity	8	0	0	0	5
GO:0008092	cytoskeletal protein binding	100	6	16	7	11
GO:0008104	protein localization	408	33	43	49	74
GO:0008121	ubiquinol-cytochrome-c reductase activity	10	5	6	0	0
GO:0008152	metabolic process	10614	416	528	704	1017
GO:0008173	RNA methyltransferase activity	25	1	1	5	9
GO:0008233	peptidase activity	646	23	25	55	85
GO:0008237	metallopeptidase activity	90	3	1	18	27
GO:0008299	isoprenoid biosynthetic process	135	3	2	13	23
GO:0008312	7S RNA binding	12	5	3	0	2
GO:0008320	protein transmembrane transporter activity	69	11	20	6	9
GO:0008324	cation transmembrane transporter activity	503	22	24	37	74
GO:0008361	regulation of cell size	274	12	16	22	38
GO:0008380	RNA splicing	115	1	2	17	21
GO:0008508	bile acid:sodium symporter activity	7	0	0	0	5
GO:0008565	protein transporter activity	159	17	27	22	29
GO:0008610	lipid biosynthetic process	439	12	13	40	69
GO:0008654	phospholipid biosynthetic process	88	3	2	10	18
GO:0008794	arsenate reductase (glutaredoxin) activity	15	0	8	0	0
GO:0009055	electron carrier activity	294	27	31	4	5
GO:0009110	vitamin biosynthetic process	78	2	3	10	17
GO:0009250	glucan biosynthetic process	54	1	1	17	22
GO:0009251	glucan catabolic process	15	0	0	7	8
GO:0009266	response to temperature stimulus	485	45	58	27	51
GO:0009308	amine metabolic process	521	11	17	45	69
GO:0009404	toxin metabolic process	53	6	13	1	1
GO:0009407	toxin catabolic process	53	6	13	1	1
GO:0009408	response to heat	161	15	26	11	18
GO:0009409	response to cold	328	35	37	17	34
GO:0009414	response to water deprivation	229	23	31	15	21
GO:0009415	response to water	240	23	32	16	22
GO:0009507	chloroplast	2740	207	205	244	416
GO:0009526	plastid envelope	331	32	29	38	69
GO:0009532	plastid stroma	322	37	21	33	57
GO:0009534	chloroplast thylakoid	290	52	39	23	38
GO:0009535	chloroplast thylakoid membrane	231	44	34	20	32
GO:0009536	plastid	2965	221	222	263	451
GO:0009543	chloroplast thylakoid lumen	89	15	12	7	11
GO:0009555	pollen development	148	2	3	16	26
GO:0009570	chloroplast stroma	249	34	19	28	48
GO:0009579	thylakoid	376	67	43	25	51
GO:0009607	response to biotic stimulus	638	44	59	54	77
GO:0009624	response to nematode	70	1	1	6	17
GO:0009628	response to abiotic stimulus	1471	92	125	115	159
GO:0009653	anatomical structure morphogenesis	637	18	26	51	75
GO:0009657	plastid organization	119	8	2	18	33
GO:0009658	chloroplast organization	73	6	1	9	20
GO:0009705	plant-type vacuole membrane	51	1	2	6	12
GO:0009719	response to endogenous stimulus	1068	62	101	62	86
GO:0009725	response to hormone stimulus	982	60	96	58	81
GO:0009733	response to auxin stimulus	360	26	41	22	29
GO:0009743	response to carbohydrate stimulus	240	20	36	10	20
GO:0009790	embryonic development	535	20	30	69	94
GO:0009791	post-embryonic development	705	36	56	122	173
GO:0009793	embryonic development ending in seed dormancy	465	15	23	61	87
GO:0009846	pollen germination	34	0	0	5	11
GO:0009886	post-embryonic morphogenesis	35	2	3	8	11
GO:0009932	cell tip growth	79	1	2	9	18
GO:0009941	chloroplast envelope	265	26	27	34	58
GO:0009987	cellular process	11684	520	677	820	1168
GO:0010014	meristem initiation	11	0	0	2	6
GO:0010033	response to organic substance	1342	78	130	83	114

GO:0010035	response to inorganic substance	279	27	36	25	32
GO:0010154	fruit development	557	18	27	69	98
GO:0010200	response to chitin	151	14	28	7	7
GO:0010876	lipid localization	24	13	22	8	9
GO:0015031	protein transport	381	33	43	46	67
GO:0015035	protein disulfide oxidoreductase activity	46	10	16	0	0
GO:0015036	disulfide oxidoreductase activity	60	10	17	0	1
GO:0015075	ion transmembrane transporter activity	655	24	28	52	99
GO:0015077	monovalent inorganic cation transmembrane transporter activity	156	19	20	8	19
GO:0015078	hydrogen ion transmembrane transporter activity	139	19	20	6	14
GO:0015079	potassium ion transmembrane transporter activity	26	1	0	6	11
GO:0015085	calcium ion transmembrane transporter activity	21	0	0	3	9
GO:0015125	bile acid transmembrane transporter activity	7	0	0	0	5
GO:0015171	amino acid transmembrane transporter activity	64	1	2	7	15
GO:0015291	secondary active transmembrane transporter activity	345	2	2	34	58
GO:0015297	antiporter activity	170	1	1	18	32
GO:0015298	solute:cation antiporter activity	67	1	0	9	15
GO:0015300	solute:solute antiporter activity	90	1	1	11	23
GO:0015370	solute:sodium symporter activity	9	0	0	0	6
GO:0015386	potassium:hydrogen antiporter activity	9	1	0	4	6
GO:0015399	primary active transmembrane transporter activity	244	15	22	25	55
GO:0015405	P-P-bond-hydrolysis-driven transmembrane transporter activity	243	15	22	25	55
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	59	10	17	6	9
GO:0015491	cation:cation antiporter activity	66	1	0	9	15
GO:0015631	tubulin binding	44	2	11	2	5
GO:0015662	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	49	0	0	7	16
GO:0015672	monovalent inorganic cation transport	115	11	12	6	21
GO:0015849	organic acid transport	81	0	1	6	17
GO:0015934	large ribosomal subunit	225	23	30	9	6
GO:0015935	small ribosomal subunit	164	25	26	2	2
GO:0015979	photosynthesis	162	21	11	9	22
GO:0015985	energy coupled proton transport, down electrochemical gradient	41	9	11	0	0
GO:0015986	ATP synthesis coupled proton transport	41	9	11	0	0
GO:0015992	proton transport	59	10	12	0	2
GO:0016020	membrane	4068	268	325	343	512
GO:0016021	integral to membrane	395	8	18	36	49
GO:0016043	cellular component organization	1179	57	77	98	162
GO:0016049	cell growth	265	12	16	22	38
GO:0016051	carbohydrate biosynthetic process	277	12	12	32	33
GO:0016052	carbohydrate catabolic process	128	1	2	13	23
GO:0016053	organic acid biosynthetic process	417	14	17	42	51
GO:0016070	RNA metabolic process	1657	35	66	130	176
GO:0016192	vesicle-mediated transport	272	33	38	24	30
GO:0016301	kinase activity	1641	36	44	143	204
GO:0016462	pyrophosphatase activity	832	21	21	120	181
GO:0016469	proton-transporting two-sector ATPase complex	27	6	0	0	0
GO:0016567	protein ubiquitination	121	2	4	14	22
GO:0016591	DNA-directed RNA polymerase II, holoenzyme	36	7	8	2	1
GO:0016667	oxidoreductase activity, acting on sulfur group of donors	109	16	24	2	4
GO:0016681	oxidoreductase activity, acting on diphenols and related substances as donors, cytochrome as acceptor	10	5	6	0	0
GO:0016740	transferase activity	3321	78	96	265	401
GO:0016758	transferase activity, transferring hexosyl groups	340	6	3	33	45
GO:0016772	transferase activity, transferring phosphorus-containing groups	1887	48	56	168	240
GO:0016773	phosphotransferase activity, alcohol group as acceptor	1154	19	26	109	142
GO:0016779	nucleotidyltransferase activity	207	13	12	24	33
GO:0016787	hydrolase activity	3468	101	111	308	449
GO:0016788	hydrolase activity, acting on ester bonds	1200	29	34	94	116
GO:0016817	hydrolase activity, acting on acid anhydrides	839	22	22	120	181
GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	837	22	22	120	181
GO:0016820	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	183	5	6	19	45
GO:0016853	isomerase activity	265	26	23	19	29
GO:0016859	cis-trans isomerase activity	69	13	12	5	8
GO:0016874	ligase activity	564	25	32	73	94
GO:0016875	ligase activity, forming carbon-oxygen bonds	80	1	0	11	18
GO:0016876	ligase activity, forming aminoacyl-tRNA and related compounds	80	1	0	11	18
GO:0016879	ligase activity, forming carbon-nitrogen bonds	423	21	29	55	68
GO:0016881	acid-amino acid ligase activity	364	18	26	47	54
GO:0016887	ATPase activity	482	9	13	79	121
GO:0016903	oxidoreductase activity, acting on the aldehyde or oxo group of donors	84	2	1	10	17
GO:0017038	protein import	86	8	14	19	27
GO:0017076	purine nucleotide binding	1713	34	40	182	244
GO:0017111	nucleoside-triphosphatase activity	792	15	17	117	178
GO:0018130	heterocycle biosynthetic process	123	6	4	14	23
GO:0019252	starch biosynthetic process	19		1	7	10
GO:0019318	hexose metabolic process	126	3	5	11	23
GO:0019637	organophosphate metabolic process	130	3	2	15	26
GO:0019725	cellular homeostasis	174	20	28	15	24
GO:0019752	carboxylic acid metabolic process	859	25	36	83	114
GO:0019783	small conjugating protein-specific protease activity	37	1	3	5	12
GO:0019787	small conjugating protein ligase activity	336	18	25	43	47
GO:0019866	organelle inner membrane	230	21	28	18	33
GO:0019867	outer membrane	80	11	12	6	12
GO:0022414	reproductive process	1161	32	53	119	175
GO:0022607	cellular component assembly	265	20	29	28	45
GO:0022613	ribonucleoprotein complex biogenesis	253	26	34	15	16
GO:0022622	root system development	255	8	13	27	36
GO:0022625	cytosolic large ribosomal subunit	162	19	27	9	6
GO:0022626	cytosolic ribosome	336	45	59	13	11
GO:0022627	cytosolic small ribosomal subunit	130	22	24	2	2
GO:0022804	active transmembrane transporter activity	664	18	26	65	126
GO:0022821	potassium ion antiporter activity	9	1	0	4	6
GO:0022857	transmembrane transporter activity	1128	41	52	93	170
GO:0022884	macromolecule transmembrane transporter activity	59	10	17	6	9
GO:0022890	inorganic cation transmembrane transporter activity	228	21	23	14	34
GO:0022891	substrate-specific transmembrane transporter activity	908	41	51	70	127
GO:0022892	substrate-specific transporter activity	1059	54	65	89	155
GO:0030001	metal ion transport	224	18	18	13	33
GO:0030003	cellular cation homeostasis	84	7	7	12	19
GO:0030154	cell differentiation	355	11	15	33	47
GO:0030312	external encapsulating structure	407	38	35	11	23

GO:0030384	phosphoinositide metabolic process	44	0	0	6	13
GO:0030414	peptidase inhibitor activity	44	0	14	0	0
GO:0030529	ribonucleoprotein complex	703	77	99	27	27
GO:0030554	adenyl nucleotide binding	1465	17	20	164	213
GO:0030611	arsenate reductase activity	16	4	8	0	1
GO:0030613	oxidoreductase activity, acting on phosphorus or arsenic in donors	15	0	8	0	0
GO:0030614	oxidoreductase activity, acting on phosphorus or arsenic in donors, with disulfide as acceptor	15	0	8	0	0
GO:0030880	RNA polymerase complex	30	6	8	3	1
GO:0030964	NADH dehydrogenase complex	72	15	19	4	4
GO:0031090	organelle membrane	842	94	98	75	123
GO:0031225	anchored to membrane	272	32	34	5	15
GO:0031461	cullin-RING ubiquitin ligase complex	192	0	4	33	41
GO:0031497	chromatin assembly	60	7	18	0	1
GO:0031966	mitochondrial membrane	210	28	36	15	26
GO:0031967	organelle envelope	595	65	71	67	109
GO:0031968	organelle outer membrane	77	11	12	6	12
GO:0031974	membrane-enclosed lumen	546	57	68	40	56
GO:0031975	envelope	595	65	71	67	109
GO:0031976	plastid thylakoid	293	52	39	23	38
GO:0031977	thylakoid lumen	95	17	13	7	11
GO:0031978	plastid thylakoid lumen	89	15	12	7	11
GO:0031981	nuclear lumen	374	35	44	29	35
GO:0031984	organelle subcompartment	295	52	39	23	38
GO:0032446	protein modification by small protein conjugation	136	6	8	16	24
GO:0032501	multicellular organismal process	2094	68	108	191	273
GO:0032502	developmental process	2304	71	111	195	281
GO:0032504	multicellular organism reproduction	41	2	2	10	14
GO:0032553	ribonucleotide binding	1631	33	40	179	239
GO:0032555	purine ribonucleotide binding	1631	33	40	179	239
GO:0032559	adenyl ribonucleotide binding	1384	16	20	161	208
GO:0032787	monocarboxylic acid metabolic process	408	15	22	38	52
GO:0032991	macromolecular complex	2180	175	223	155	215
GO:0032993	protein-DNA complex	44	7	16	0	1
GO:0033036	macromolecule localization	462	49	67	64	94
GO:0033279	ribosomal subunit	389	48	56	11	8
GO:0033365	protein localization in organelle	80	9	14	13	20
GO:0033692	cellular polysaccharide biosynthetic process	92	1	1	19	22
GO:0034220	ion transmembrane transport	59	11	13	1	2
GO:0034357	photosynthetic membrane	273	50	37	22	38
GO:0034504	protein localization in nucleus	45		3	12	14
GO:0034613	cellular protein localization	322	30	38	39	63
GO:0034621	cellular macromolecular complex subunit organization	224	19	30	22	34
GO:0034622	cellular macromolecular complex assembly	200	17	27	20	31
GO:0034637	cellular carbohydrate biosynthetic process	177	9	11	26	29
GO:0034641	cellular nitrogen compound metabolic process	506	19	23	62	102
GO:0034660	ncRNA metabolic process	254	3	0	28	40
GO:0034728	nucleosome organization	56	7	18	0	1
GO:0035196	production of miRNAs involved in gene silencing by miRNA	16	0	0	4	7
GO:0040007	growth	340	15	21	28	47
GO:0042180	cellular ketone metabolic process	882	25	36	85	118
GO:0042221	response to chemical stimulus	2085	138	203	125	173
GO:0042254	ribosome biogenesis	241	26	34	13	14
GO:0042440	pigment metabolic process	134	8	4	12	25
GO:0042578	phosphoric ester hydrolase activity	481	10	13	47	57
GO:0042592	homeostatic process	216	20	29	17	31
GO:0042623	ATPase activity, coupled	359	6	9	60	94
GO:0042625	ATPase activity, coupled to transmembrane movement of ions	68	5	5	7	17
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	181	5	6	19	45
GO:0042651	thylakoid membrane	244	45	35	22	36
GO:0043038	amino acid activation	84	1	0	12	19
GO:0043039	tRNA aminoacylation	84	1	0	12	19
GO:0043167	ion binding	2087	119	145	114	153
GO:0043169	cation binding	2087	119	145	114	153
GO:0043170	macromolecule metabolic process	7127	262	349	473	637
GO:0043226	organelle	8155	537	665	651	993
GO:0043227	membrane-bounded organelle	7622	496	607	628	963
GO:0043228	non-membrane-bounded organelle	1040	98	130	58	76
GO:0043229	intracellular organelle	8149	537	665	651	993
GO:0043231	intracellular membrane-bounded organelle	7615	495	606	627	961
GO:0043232	intracellular non-membrane-bounded organelle	1040	98	130	58	76
GO:0043233	organelle lumen	539	56	65	40	56
GO:0043234	protein complex	1443	91	108	130	189
GO:0043412	macromolecule modification	1636	37	40	129	182
GO:0043436	oxoacid metabolic process	859	25	36	83	114
GO:0043492	ATPase activity, coupled to movement of substances	181	5	6	19	45
GO:0043623	cellular protein complex assembly	124	10	8	17	26
GO:0043687	post-translational protein modification	1248	28	32	102	138
GO:0043933	macromolecular complex subunit organization	235	21	31	27	45
GO:0044042	glucan metabolic process	89	2	2	24	32
GO:0044085	cellular component biogenesis	571	51	65	47	64
GO:0044106	cellular amine metabolic process	438	10	15	42	63
GO:0044237	cellular metabolic process	8722	360	465	588	827
GO:0044238	primary metabolic process	8995	326	419	607	845
GO:0044247	cellular polysaccharide catabolic process	17	0	0	7	8
GO:0044248	cellular catabolic process	746	36	57	77	96
GO:0044255	cellular lipid metabolic process	618	16	19	53	84
GO:0044260	cellular macromolecule metabolic process	6447	242	326	426	567
GO:0044262	cellular carbohydrate metabolic process	417	15	17	55	82
GO:0044264	cellular polysaccharide metabolic process	127	2	2	26	31
GO:0044265	cellular macromolecule catabolic process	465	21	24	50	66
GO:0044271	cellular nitrogen compound biosynthetic process	394	14	15	39	60
GO:0044275	cellular carbohydrate catabolic process	125	1	2	13	23
GO:0044422	organelle part	2562	235	261	210	325
GO:0044424	intracellular part	9302	589	746	750	1142
GO:0044425	membrane part	1360	104	124	105	143
GO:0044427	chromosomal part	133	8	22	3	7
GO:0044428	nuclear part	543	40	54	52	64
GO:0044429	mitochondrial part	274	34	44	19	35
GO:0044431	Golgi apparatus part	118	7	6	17	16
GO:0044434	chloroplast part	746	90	69	75	136

GO:0044435	plastid part	867	95	73	82	152
GO:0044436	thylakoid part	307	52	40	25	41
GO:0044437	vacuolar part	104	0	6	14	27
GO:0044444	cytoplasmic part	6289	453	524	511	831
GO:0044445	cytosolic part	360	43	55	12	10
GO:0044446	intracellular organelle part	2561	235	261	210	325
GO:0044455	mitochondrial membrane part	94	16	21	7	7
GO:0044464	cell part	15217	789	1040	1042	1554
GO:0045036	protein targeting to chloroplast	33	4	2	5	11
GO:0045087	innate immune response	347	11	18	41	48
GO:0045184	establishment of protein localization	381	33	43	46	67
GO:0045271	respiratory chain complex I	72	15	19	4	4
GO:0045275	respiratory chain complex III	23	8	8	2	2
GO:0045454	cell redox homeostasis	72	13	20	2	4
GO:0046148	pigment biosynthetic process	112	7	3	10	22
GO:0046394	carboxylic acid biosynthetic process	417	14	17	42	51
GO:0046486	glycerolipid metabolic process	64	2	2	8	15
GO:0046527	glucosyltransferase activity	136	1	0	20	24
GO:0046872	metal ion binding	1997	115	143	113	147
GO:0046873	metal ion transmembrane transporter activity	168	3	3	18	34
GO:0046907	intracellular transport	463	45	53	61	87
GO:0046930	pore complex	26	0	1	11	11
GO:0046942	carboxylic acid transport	81	0	1	6	17
GO:0046943	carboxylic acid transmembrane transporter activity	78	2	2	8	25
GO:0048046	apoplast	182	18	17	5	11
GO:0048316	seed development	530	15	25	67	96
GO:0048364	root development	255	8	13	27	36
GO:0048500	signal recognition particle	16	5	3	1	3
GO:0048513	organ development	838	21	32	68	98
GO:0048519	negative regulation of biological process	442	8	14	34	56
GO:0048583	regulation of response to stimulus	188	3	10	22	31
GO:0048584	positive regulation of response to stimulus	62	2	4	10	14
GO:0048589	developmental growth	242	7	10	21	35
GO:0048608	reproductive structure development	978	28	44	106	147
GO:0048609	reproductive process in a multicellular organism	38	2	2	9	13
GO:0048731	system development	839	21	32	69	98
GO:0048856	anatomical structure development	1726	50	82	161	231
GO:0048869	cellular developmental process	520	17	23	39	63
GO:0048878	chemical homeostasis	136	7	8	13	25
GO:0050801	ion homeostasis	103	7	7	13	22
GO:0050896	response to stimulus	4057	238	336	291	398
GO:0051169	nuclear transport	71	0	3	17	19
GO:0051170	nuclear import	42	0	3	12	13
GO:0051179	localization	1922	120	147	144	247
GO:0051186	cofactor metabolic process	308	9	8	26	50
GO:0051188	cofactor biosynthetic process	191	8	6	17	34
GO:0051234	establishment of localization	1851	118	145	137	233
GO:0051273	beta-glucan metabolic process	13	0	0	6	8
GO:0051274	beta-glucan biosynthetic process	13	0	0	6	8
GO:0051641	cellular localization	569	49	57	69	104
GO:0051649	establishment of localization in cell	525	47	55	67	95
GO:0051704	multi-organism process	776	43	62	63	101
GO:0051707	response to other organism	599	40	55	49	75
GO:0051716	cellular response to stimulus	840	36	57	73	102
GO:0055029	nuclear DNA-directed RNA polymerase complex	30	6	8	3	1
GO:0055035	plastid thylakoid membrane	231	44	34	20	32
GO:0055046	microgametogenesis	12	0	0	4	6
GO:0055080	cation homeostasis	90	7	7	12	21
GO:0055082	cellular chemical homeostasis	97	7	7	13	20
GO:0060089	molecular transducer activity	422	4	13	45	51
GO:0065003	macromolecular complex assembly	210	19	28	25	42
GO:0065004	protein-DNA complex assembly	60	7	18	1	3
GO:0065008	regulation of biological quality	665	34	50	51	84
GO:0070011	peptidase activity, acting on L-amino acid peptides	579	17	17	54	83
GO:0070013	intracellular organelle lumen	539	56	65	40	56
GO:0070035	purine NTP-dependent helicase activity	128	1	3	33	35
GO:0070271	protein complex biogenesis	134	12	9	22	37
GO:0070469	respiratory chain	115	25	28	6	6
GO:0070585	protein localization in mitochondrion	20	4	8	1	3
GO:0070647	protein modification by small protein conjugation or removal	158	6	8	19	28
GO:0070727	cellular macromolecule localization	341	32	40	41	68
GO:0070838	divalent metal ion transport	21	0	0	3	9
GO:0070887	cellular response to chemical stimulus	452	20	36	37	59
GO:0080008	CUL4 RING ubiquitin ligase complex	150	0	2	26	35