GO Analysis Toolkit and Database for Agricultural Community

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GO Information					CM				☐ MS			☐ MP			☐ MO			☐ SL		
No	**☐ GO Term**	**Onto**	**Number**	**Description**	**1**	**2**	**3**	**4**	**Z-score**	**Mean**	**FDRnbsp;**	**Z-score**	**Mean**	**FDRnbsp;**	**Z-score**	**Mean**	**FDRnbsp;**	**Z-score**	**Mean**	**FDRnbsp;**
1	☐ GO:0006032	P	16	chitin catabolic process	🟥	▨	▨	▨	15	4.6e+02	0	-0.44	0.58	0.93	-1	12	0.54	-0.56	15	0.81
2	☐ GO:0006030	P	16	chitin metabolic process	🟥	▨	▨	▨	15	4.6e+02	0	-0.44	0.58	0.93	-1	12	0.54	-0.56	15	0.81
3	☐ GO:0006026	P	16	aminoglycan catabolic process	🟥	▨	▨	▨	15	4.6e+02	0	-0.44	0.58	0.93	-1	12	0.54	-0.56	15	0.81
4	☐ GO:0006022	P	18	aminoglycan metabolic process	🟥	▨	▨	▨	14	4.1e+02	0	-0.47	0.52	0.93	-1.1	12	0.48	-0.61	15	0.8
5	☐ GO:0000272	P	28	polysaccharide catabolic process	🟥	▨	▨	▨	11	2.6e+02	0	2.3	1.4e+02	0.27	-1.1	14	0.51	-0.65	17	0.79
6	☐ GO:0010876	P	49	lipid localization	🟥	▨	▨	▨	7.9	1.5e+02	3e-13	0.3	40	0.93	0.054	23	0.99	0.79	33	0.75
7	☐ GO:0006869	P	49	lipid transport	🟥	▨	▨	▨	7.9	1.5e+02	3e-13	0.3	40	0.93	0.054	23	0.99	0.79	33	0.75
8	☐ GO:0009057	P	315	macromolecule catabolic process	🟧	▨	🟥	🟥	5.9	63	3.5e-07	-0.34	24	0.93	6.7	38	3.7e-10	6.5	50	7.9e-10
9	☐ GO:0016052	P	159	carbohydrate catabolic process	🟧	▨	🟨	🟥	5.8	78	3.9e-07	0.58	41	0.93	3.8	35	0.00083	7.2	64	6.7e-12
10	☐ GO:0016998	P	30	cell wall macromolecule catabolic process	🟧	▨	▨	▨	5.7	1.4e+02	6.4e-07	-0.47	6.8	0.93	-1.3	13	0.41	-1.3	9.1	0.45
11	☐ GO:0009056	P	423	catabolic process	🟧	▨	🟧	🟥	5.5	55	1.9e-06	-0.75	20	0.93	5.3	33	1.1e-06	6.6	46	4.9e-10
12	☐ GO:0044036	P	32	cell wall macromolecule metabolic process	🟧	▨	▨	▨	5.5	1.4e+02	2.2e-06	-0.5	6.4	0.93	-1.4	13	0.36	-1.3	9.4	0.44
13	☐ GO:0009074	P	10	aromatic amino acid family catabolic process	🟨	▨	▨	▨	4.2	1.8e+02	0.0011	-0.35	0.14	0.93	-0.17	21	0.94	1.6	60	0.28
14	☐ GO:0006559	P	10	L-phenylalanine catabolic process	🟨	▨	▨	▨	4.2	1.8e+02	0.0011	-0.35	0.14	0.93	-0.17	21	0.94	1.6	60	0.28
15	☐ GO:0005976	P	164	polysaccharide metabolic process	🟨	▨	🟨	▨	4.2	62	0.0011	0.56	41	0.93	2.7	31	0.027	0.94	30	0.65
16	☐ GO:0006633	P	77	fatty acid biosynthetic process	🟨	▨	▨	▨	3.8	75	0.0049	-0.54	13	0.93	-0.21	22	0.93	0.76	31	0.75
17	☐ GO:0009308	P	389	amine metabolic process	🟨	▨	🟨	🟧	3.8	47	0.0049	-0.44	23	0.93	3.6	30	0.0016	5	42	3e-06
18	☐ GO:0006631	P	95	fatty acid metabolic process	🟨	▨	▨	▨	3.8	70	0.0049	-0.67	11	0.93	-0.052	23	0.99	0.81	31	0.73
19	☐ GO:0033036	P	427	macromolecule localization	🟨	▨	🟧	▨	3.8	45	0.0057	-0.68	21	0.93	4.1	31	0.00021	1.4	30	0.36
20	☐ GO:0006414	P	44	translational elongation	🟨	▨	🟥	🟥	3.8	89	0.0059	-0.38	14	0.93	13	1e+02	0	14	1.7e+02	0
21	☐ GO:0032787	P	121	monocarboxylic acid metabolic process	🟨	▨	▨	▨	3.5	61	0.014	-0.79	11	0.93	-0.099	22	0.97	1.4	34	0.38
22	☐ GO:0051258	P	38	protein polymerization	🟨	🟨	🟥	🟥	3.5	89	0.015	3.9	1.9e+02	0.0038	13	1.1e+02	0	6.1	92	8.4e-09
23	☐ GO:0006558	P	16	L-phenylalanine metabolic process	🟨	▨	▨	▨	3.2	1.2e+02	0.044	-0.45	0.3	0.93	-0.47	18	0.81	0.99	42	0.62
24	☐ GO:0004568	F	16	chitinase activity	🟥	▨	▨	▨	15	4.6e+02	0	-0.44	0.58	0.93	-1	12	0.64	-0.56	15	0.8
25	☐ GO:0008289	F	88	lipid binding	🟧	▨	▨	▨	6.2	1e+02	1.3e-07	0.53	44	0.93	0.63	26	0.81	0.71	30	0.77
26	☐ GO:0005199	F	82	structural constituent of cell wall	🟧	▨	🟧	▨	5.9	1e+02	5e-07	1.1	60	0.93	4.8	45	3.2e-05	0.44	28	0.84
27	☐ GO:0042923	F	16	neuropeptide binding	🟧	▨	▨	▨	4.8	1.6e+02	0.00016	-0.44	0.92	0.93	1.2	35	0.54	0.32	30	0.88
28	☐ GO:0008188	F	16	neuropeptide receptor activity	🟧	▨	▨	▨	4.8	1.6e+02	0.00016	-0.44	0.92	0.93	1.2	35	0.54	0.32	30	0.88
29	☐ GO:0042165	F	19	neurotransmitter binding	🟨	▨	▨	▨	4.5	1.4e+02	0.00059	-0.47	1.1	0.93	1.3	35	0.54	0.3	30	0.89
30	☐ GO:0030594	F	19	neurotransmitter receptor activity	🟨	▨	▨	▨	4.5	1.4e+02	0.00059	-0.47	1.1	0.93	1.3	35	0.54	0.3	30	0.89
31	☐ GO:0005198	F	741	structural molecule activity	🟨	▨	🟥	🟥	4.3	43	0.00095	-0.29	27	0.93	15	46	0	19	73	0
32	☐ GO:0016841	F	11	ammonia-lyase activity	🟨	▨	▨	▨	3.9	1.6e+02	0.0059	-0.37	0.46	0.93	0.073	24	0.99	1.6	58	0.41
33	☐ GO:0003746	F	30	translation elongation factor activity	🟨	▨	🟥	🟥	3.5	97	0.026	-0.3	15	0.93	13	1.2e+02	0	12	1.7e+02	0
34	☐ GO:0005737	C	1440	cytoplasm	🟨	▨	🟥	🟥	4.1	37	0.0062	-1.8	17	0.59	17	41	0	20	60	0
35	☐ GO:0005576	C	230	extracellular region	🟨	🟥	▨	▨	3.6	52	0.028	13	2.5e+02	0	-0.7	21	0.6	-1.4	18	0.37
36	☐ GO:0019953	P	49	sexual reproduction	▨	🟥	▨	▨	-0.22	21	1	16	6.3e+02	0	-1.5	14	0.3	-1.4	12	0.39
37	☐ GO:0071555	P	65	cell wall organization	▨	🟥	▨	▨	-0.98	11	1	13	4.4e+02	0	0.18	24	0.94	-1.1	16	0.55
38	☐ GO:0000003	P	76	reproduction	▨	🟥	▨	▨	-0.42	19	1	13	4e+02	0	-2.2	12	0.088	-1.9	10	0.18
39	☐ GO:0030036	P	42	actin cytoskeleton organization	▨	🟥	▨	▨	-0.53	15	1	12	5.2e+02	0	-0.62	19	0.76	-1.1	14	0.59
40	☐ GO:0030029	P	42	actin filament-based process	▨	🟥	▨	▨	-0.53	15	1	12	5.2e+02	0	-0.62	19	0.76	-1.1	14	0.59
41	☐ GO:0042545	P	30	cell wall modification	▨	🟥	▨	▨	-1	2.6	1	11	5.5e+02	0	-1.2	14	0.46	-1.6	5.2	0.3
42	☐ GO:0007010	P	64	cytoskeleton organization	▨	🟥	▨	▨	-0.64	15	1	10	3.6e+02	0	-0.56	20	0.79	-1.3	14	0.46
43	☐ GO:0071554	P	102	cell wall organization or biogenesis	▨	🟥	▨	▨	2.2	50	0.3	9.9	2.8e+02	0	-0.85	19	0.63	-1.8	13	0.22
44	☐ GO:0071669	P	30	plant-type cell wall organization or biogenesis	▨	🟥	▨	▨	-0.77	8.4	1	8	4.1e+02	9.1e-14	-0.47	19	0.81	-1.5	6.7	0.34
45	☐ GO:0009664	P	30	plant-type cell wall organization	▨	🟥	▨	▨	-0.77	8.4	1	8	4.1e+02	9.1e-14	-0.47	19	0.81	-1.5	6.7	0.34
46	☐ GO:0009415	P	17	response to water	▨	🟧	▨	▨	1.5	67	0.82	6	4.1e+02	1.1e-07	2.3	46	0.066	0.5	33	0.82
47	☐ GO:0006996	P	278	organelle organization	▨	🟧	🟥	🟧	0.42	27	1	4.6	1e+02	0.00024	14	57	0	5.2	46	1.5e-06
48	☐ GO:0016043	P	488	cellular component organization	▨	🟨	🟥	🟥	1.5	32	0.82	4.1	78	0.0019	15	52	0	6.3	44	2.7e-09
49	☐ GO:0009075	P	12	histidine family amino acid metabolic process	▨	🟨	▨	▨	-0.32	14	1	4	3.3e+02	0.0034	-0.17	21	0.94	0.019	25	1

50	☐ GO:0006547		P	12	histidine metabolic process	⬛	🟧	⬛	⬛	-0.32	14	1	4	3.3e+02	0.0034	-0.17	21	0.94	0.019	25	1
51	☐ GO:0009628		P	756	response to abiotic stimulus	⬛	🟨	⬛	⬛	-0.56	22	1	3.8	66	0.0054	-3	18	0.011	-0.19	24	0.97
52	☐ GO:0006950		P	1237	response to stress	⬛	🟨	⬛	⬛	2.1	31	0.36	3.7	57	0.0083	-3.3	19	0.0043	-0.37	24	0.89
53	☐ GO:0050896		P	1404	response to stimulus	⬛	🟨	⬛	⬛	1.7	30	0.67	3.5	53	0.018	-3.6	19	0.0016	-1.1	23	0.55
54	☐ GO:0042221		P	258	response to chemical stimulus	⬛	🟨	⬛	⬛	0.48	28	1	3.4	85	0.019	-1.2	20	0.46	-0.44	23	0.85
55	☐ GO:0050826		P	705	response to freezing	⬛	🟨	⬛	⬛	-0.78	21	1	3.2	60	0.032	-3	18	0.0088	-0.038	25	0.99
56	☐ GO:0048871		P	705	multicellular organismal homeostasis	⬛	🟨	⬛	⬛	-0.78	21	1	3.2	60	0.032	-3	18	0.0088	-0.038	25	0.99
57	☐ GO:0042309		P	705	homoiothermy	⬛	🟨	⬛	⬛	-0.78	21	1	3.2	60	0.032	-3	18	0.0088	-0.038	25	0.99
58	☐ GO:0009409		P	705	response to cold	⬛	🟨	⬛	⬛	-0.78	21	1	3.2	60	0.032	-3	18	0.0088	-0.038	25	0.99
59	☐ GO:0001659		P	705	temperature homeostasis	⬛	🟨	⬛	⬛	-0.78	21	1	3.2	60	0.032	-3	18	0.0088	-0.038	25	0.99
60	☐ GO:0009266		P	711	response to temperature stimulus	⬛	🟨	⬛	⬛	-0.8	21	1	3.1	60	0.036	-3.1	18	0.0083	-0.044	25	0.99
61	☐ GO:0005975		P	775	carbohydrate metabolic process	⬛	🟨	🟧	🟥	2.3	34	0.26	3.1	58	0.041	4.5	29	3.9e-05	7.6	43	2.8e-13
62	☐ GO:0043623	0043623	P	60	cellular protein complex assembly	⬛	🟨	🟥	🟧	2.6	63	0.15	3	1.3e+02	0.047	9.8	75	0	4.6	65	1.9e-05
63	☐ GO:0030599		F	55	pectinesterase activity	⬛	🟥	⬛	⬛	-1.1	7.9	1	21	7.7e+02	0	-2.5	8.8	0.071	-2.3	3.7	0.1
64	☐ GO:0004091		F	106	carboxylesterase activity	⬛	🟥	⬛	⬛	-1.2	11	1	15	4e+02	0	-2.7	12	0.045	-2.6	7.9	0.053
65	☐ GO:0004857		F	87	enzyme inhibitor activity	⬛	🟥	⬛	⬛	0.81	35	1	14	4.2e+02	0	-2.7	11	0.044	-1	17	0.68
66	☐ GO:0003779		F	79	actin binding	⬛	🟥	⬛	⬛	-0.41	19	1	12	3.9e+02	0	0.48	25	0.85	-0.81	19	0.75
67	☐ GO:0008092		F	82	cytoskeletal protein binding	⬛	🟥	⬛	⬛	-0.46	19	1	12	3.7e+02	0	0.57	25	0.85	-0.84	19	0.75
68	☐ GO:0004650		F	35	polygalacturonase activity	⬛	🟥	⬛	⬛	-1.1	3.5	1	12	5.5e+02	0	-1.9	9.3	0.23	-1.7	5.6	0.35
69	☐ GO:0030234		F	229	enzyme regulator activity	⬛	🟥	⬛	⬛	0.42	28	1	9.4	1.9e+02	0	-0.53	21	0.85	-1.4	19	0.52
70	☐ GO:0005507		F	73	copper ion binding	⬛	🟥	⬛	⬛	-1.2	8.6	1	6.2	2.2e+02	2.7e-08	-3	8.2	0.018	0.9	32	0.75
71	☐ GO:0016788		F	597	hydrolase activity, acting on ester bonds	⬛	🟧	⬛	⬛	-0.5	22	1	5.8	91	4.4e-07	-3.1	18	0.016	-3.2	16	0.011
72	☐ GO:0016835		F	72	carbon-oxygen lyase activity	⬛	🟧	⬛	🟧	0.37	30	1	4.9	1.8e+02	4.1e-05	1.1	28	0.6	4.5	61	9.4e-05
73	☐ GO:0004553		F	312	hydrolase activity, hydrolyzing O-glycosyl compounds	⬛	🟧	⬛	⬛	2.4	40	0.33	4.6	97	0.00017	-0.12	22	0.99	0.28	26	0.89
74	☐ GO:0016798		F	330	hydrolase activity, acting on glycosyl bonds	⬛	🟧	⬛	⬛	2.2	38	0.39	4.4	92	0.00048	-0.38	22	0.9	0.12	25	0.95
75	☐ GO:0016161		F	12	beta-amylase activity	⬛	🟧	⬛	⬛	-0.46	9.1	1	4	3.3e+02	0.0025	-0.48	17	0.86	-0.34	18	0.88
76	☐ GO:0016160		F	16	amylase activity	⬛	🟨	⬛	⬛	-0.42	13	1	3.4	2.5e+02	0.026	-0.61	16	0.83	-0.5	17	0.82
77	☐ GO:0005337		F	10	nucleoside transmembrane transporter activity	⬛	🟨	⬛	⬛	-0.21	17	1	3.3	3e+02	0.035	-0.51	16	0.85	0.87	43	0.75
78	☐ GO:0050825		F	705	ice binding	⬛	🟨	⬛	⬛	-0.78	21	1	3.2	60	0.043	-3	18	0.017	-0.038	25	0.98
79	☐ GO:0050824		F	705	water binding	⬛	🟨	⬛	⬛	-0.78	21	1	3.2	60	0.043	-3	18	0.017	-0.038	25	0.98
80	☐ GO:0044421		C	17	extracellular region part	⬛	🟥	⬛	⬛	-0.49	11	1	8.2	5.5e+02	2e-14	-1.5	7.7	0.23	-1.1	7	0.58
81	☐ GO:0005618		C	66	cell wall	⬛	🟥	⬛	⬛	-1	9.8	1	7.1	2.6e+02	1e-10	1.3	29	0.3	-0.36	22	0.83
82	☐ GO:0015629		C	116	actin cytoskeleton	⬛	🟥	⬛	⬛	-0.097	23	1	6.8	1.9e+02	6.3e-10	-0.023	23	0.98	-0.67	21	0.74
83	☐ GO:0005856		C	208	cytoskeleton	⬛	🟥	🟧	⬛	1.1	34	1	6.7	1.5e+02	6.6e-10	5	37	3.8e-06	1.5	32	0.33
84	☐ GO:0030312		C	84	external encapsulating structure	⬛	🟥	⬛	⬛	-1.2	9.8	1	6	2e+02	4.7e-08	0.73	26	0.59	-0.61	20	0.74
85	☐ GO:0046821		C	12	extrachromosomal DNA	⬛	🟧	⬛	⬛	-0.51	7.6	1	4.3	3.5e+02	0.00042	-1.3	7.6	0.32	-0.64	12	0.74
86	☐ GO:0005727		C	12	extrachromosomal circular DNA	⬛	🟧	⬛	⬛	-0.51	7.6	1	4.3	3.5e+02	0.00042	-1.3	7.6	0.32	-0.64	12	0.74
87	☐ GO:0005874		C	50	microtubule	⬛	🟨	🟥	🟧	2.9	72	0.087	3.5	1.6e+02	0.0098	10	84	0	5.4	77	2.8e-07
88	☐ GO:0034621		P	204	cellular macromolecular complex subunit organization	⬛	⬛	🟥	🟥	2.9	48	0.088	1.8	63	0.54	22	87	0	10	74	0
89	☐ GO:0034622		P	188	cellular macromolecular complex assembly	⬛	⬛	🟥	🟥	2.7	47	0.13	2	68	0.36	22	89	0	10	74	0
90	☐ GO:0065004		P	126	protein-DNA complex assembly	⬛	⬛	🟥	🟥	1.5	39	0.86	0.43	39	0.93	20	96	0	8.9	79	0
91	☐ GO:0034728		P	126	nucleosome organization	⬛	⬛	🟥	🟥	1.5	39	0.86	0.43	39	0.93	20	96	0	8.9	79	0
92	☐ GO:0031497		P	126	chromatin assembly	⬛	⬛	🟥	🟥	1.5	39	0.86	0.43	39	0.93	20	96	0	8.9	79	0
93	☐ GO:0006334		P	126	nucleosome assembly	⬛	⬛	🟥	🟥	1.5	39	0.86	0.43	39	0.93	20	96	0	8.9	79	0
94	☐ GO:0006323		P	127	DNA packaging	⬛	⬛	🟥	🟥	1.4	39	0.86	0.42	39	0.93	20	95	0	8.9	78	0
95	☐ GO:0006333		P	140	chromatin assembly or disassembly	⬛	⬛	🟥	🟥	1.3	37	0.98	0.29	36	0.93	19	89	0	8.4	73	0
96	☐ GO:0043933	0043933	P	319	macromolecular complex subunit organization	⬛	⬛	🟥	🟥	2.4	40	0.19	0.95	43	0.93	18	65	0	8.2	56	3.5e-15
97	☐ GO:0065003		P	303	macromolecular complex assembly	⬛	⬛	🟥	🟥	2.2	39	0.3	1.1	45	0.93	18	66	0	7.8	55	8.9e-14
98	☐ GO:0022607		P	315	cellular component assembly	⬛	⬛	🟥	🟥	2.1	38	0.36	0.97	44	0.93	18	64	0	7.5	54	6.6e-13
99	☐ GO:0051276		P	179	chromosome organization	⬛	⬛	🟥	🟥	0.88	32	1	-0.053	28	0.98	17	77	0	6.9	60	4.2e-11
100	☐ GO:0071103		P	174	DNA conformation change	⬛	⬛	🟥	🟥	1.1	34	1	0.02	30	0.99	17	77	0	8.7	70	0
101	☐ GO:0006325		P	173	chromatin organization	⬛	⬛	🟥	🟥	0.94	33	1	-0.003	29	1	17	78	0	7.1	61	1.8e-11
102	☐ GO:0044085		P	368	cellular component biogenesis	⬛	⬛	🟥	🟥	1.9	36	0.47	0.62	38	0.93	17	59	0	7.9	53	5.7e-14
103	☐ GO:0006412		P	681	translation	⬛	⬛	🟥	🟥	2.5	36	0.17	-2.1	7.9	0.34	15	47	0	22	83	0
104	☐ GO:0009987		P	7194	cellular process	⬛	⬛	🟥	🟥	1.1	26	1	-2.1	23	0.35	11	28	0	11	34	0
105	☐ GO:0044237		P	5578	cellular metabolic process	⬛	⬛	🟥	🟥	1.2	26	1	-3.5	17	0.018	9.4	28	0	12	36	0
106	☐ GO:0044267		P	2363	cellular protein metabolic process	⬛	⬛	🟥	🟥	0.67	26	1	-1.2	23	0.93	9.3	31	0	9.6	38	0
107	☐ GO:0044249		P	2873	cellular biosynthetic process	⬛	⬛	🟥	🟥	1.1	27	1	-3.2	14	0.032	9	30	0	10	38	0
108	☐ GO:0009058		P	3025	biosynthetic process	⬛	⬛	🟥	🟥	1.1	27	1	-3.2	14	0.032	8.8	29	0	11	38	0
109	☐ GO:0034645		P	2180	cellular macromolecule biosynthetic process	⬛	⬛	🟥	🟥	0.023	25	1	-3.2	12	0.032	8.5	30	0	8.2	37	3.5e-15

110	☐ GO:0007018	P	98	microtubule-based movement	▨	▨	🟥	🟨	1.2	39	1	2.1	84	0.36	8.5	58	0	3.1	46	0.0072
111	☐ GO:0010467	P	2144	gene expression	▨	▨	🟥	🟥	0.22	25	1	-3.3	11	0.026	8.5	30	0	8.2	37	3.5e-15
112	☐ GO:0009059	P	2183	macromolecule biosynthetic process	▨	▨	🟥	🟥	0.017	25	1	-3.2	12	0.032	8.5	30	0	8.2	37	6.9e-15
113	☐ GO:0019538	P	2787	protein metabolic process	▨	▨	🟥	🟥	1	27	1	-1.6	21	0.79	8.4	29	0	8.8	36	0
114	☐ GO:0044260	P	4281	cellular macromolecule metabolic process	▨	▨	🟥	🟧	-0.28	24	1	-3	17	0.052	8.3	28	0	5.7	31	1e-07
115	☐ GO:0044238	P	6051	primary metabolic process	▨	▨	🟥	🟥	1.8	27	0.58	-2.1	22	0.35	8.2	27	4.6e-15	8.1	32	1e-14
116	☐ GO:0006457	P	235	protein folding	▨	▨	🟥	🟥	2.4	43	0.19	-0.49	21	0.93	8.2	45	8.9e-15	6.5	54	6.3e-10
117	☐ GO:0070271	P	189	protein complex biogenesis	▨	▨	🟥	🟨	1.5	37	0.84	0.91	47	0.93	8	47	1.7e-14	3.2	41	0.0053
118	☐ GO:0006461	P	189	protein complex assembly	▨	▨	🟥	🟨	1.5	37	0.84	0.91	47	0.93	8	47	1.7e-14	3.2	41	0.0053
119	☐ GO:0043170	P	4738	macromolecule metabolic process	▨	▨	🟥	🟧	0.92	26	1	-3	18	0.047	7.7	27	2e-13	5.2	30	9.3e-07
120	☐ GO:0015986	P	64	ATP synthesis coupled proton transport	▨	▨	🟥	🟥	2.8	65	0.094	-0.47	14	0.93	7.5	61	1.4e-12	10	1.1e+02	0
121	☐ GO:0015985	P	64	energy coupled proton transport, down electrochemical gradient	▨	▨	🟥	🟥	2.8	65	0.094	-0.47	14	0.93	7.5	61	1.4e-12	10	1.1e+02	0
122	☐ GO:0006091	P	249	generation of precursor metabolites and energy	▨	▨	🟥	🟥	2.4	42	0.19	-0.46	22	0.93	7.4	42	1.6e-12	15	87	0
123	☐ GO:0034220	P	66	ion transmembrane transport	▨	▨	🟥	🟥	2.9	65	0.094	-0.48	14	0.93	7.4	61	1.7e-12	10	1.1e+02	0
124	☐ GO:0006596	P	12	polyamine biosynthetic process	▨	▨	🟥	🟧	1.6	78	0.72	1.7	1.6e+02	0.72	7.4	1.1e+02	1.8e-12	6.1	1.4e+02	7.2e-09
125	☐ GO:0006595	P	12	polyamine metabolic process	▨	▨	🟥	🟧	1.6	78	0.72	1.7	1.6e+02	0.72	7.4	1.1e+02	1.8e-12	6.1	1.4e+02	7.2e-09
126	☐ GO:0015992	P	76	proton transport	▨	▨	🟥	🟥	2.9	62	0.092	-0.34	19	0.93	7.4	58	2.2e-12	10	1e+02	0
127	☐ GO:0006818	P	76	hydrogen transport	▨	▨	🟥	🟥	2.9	62	0.092	-0.34	19	0.93	7.4	58	2.2e-12	10	1e+02	0
128	☐ GO:0007017	P	128	microtubule-based process	▨	▨	🟥	▨	0.79	33	1	1.7	68	0.72	7	48	4.6e-11	2.4	39	0.062
129	☐ GO:0044281	P	1146	small molecule metabolic process	▨	▨	🟥	🟥	2.9	34	0.09	-1.3	20	0.93	6.9	31	6.3e-11	11	48	0
130	☐ GO:0042401	P	15	cellular biogenic amine biosynthetic process	▨	▨	🟥	🟧	1.4	67	0.86	1.4	1.2e+02	0.93	6.9	96	6.8e-11	5.7	1.2e+02	1e-07
131	☐ GO:0006119	P	79	oxidative phosphorylation	▨	▨	🟥	🟥	2.6	59	0.15	-0.56	13	0.93	6.7	54	3e-10	9.5	97	0
132	☐ GO:0051246	P	85	regulation of protein metabolic process	▨	▨	🟥	🟨	3	61	0.086	-0.47	16	0.93	6.7	53	3.1e-10	2.9	46	0.016
133	☐ GO:0060348	P	15	bone development	▨	▨	🟥	🟨	0.6	42	1	-0.4	2.4	0.93	6.6	93	4.7e-10	3.6	88	0.0015
134	☐ GO:0001503	P	15	ossification	▨	▨	🟥	🟨	0.6	42	1	-0.4	2.4	0.93	6.6	93	4.7e-10	3.6	88	0.0015
135	☐ GO:0001501	P	15	skeletal system development	▨	▨	🟥	🟨	0.6	42	1	-0.4	2.4	0.93	6.6	93	4.7e-10	3.6	88	0.0015
136	☐ GO:0044262	P	440	cellular carbohydrate metabolic process	▨	▨	🟥	🟥	0.62	28	1	-0.47	24	0.93	6.4	35	1.8e-09	8.7	53	0
137	☐ GO:0048731	P	19	system development	▨	▨	🟥	🟨	0.5	38	1	-0.46	1.9	0.93	6.2	82	5.3e-09	3.1	73	0.0087
138	☐ GO:0044265	P	254	cellular macromolecule catabolic process	▨	▨	🟥	🟥	2.4	42	0.19	-0.92	14	0.93	6	38	2.3e-08	6.4	52	1.6e-09
139	☐ GO:0048856	P	20	anatomical structure development	▨	▨	🟥	🟨	0.45	36	1	-0.47	1.8	0.93	6	78	2.3e-08	3	70	0.012
140	☐ GO:0006006	P	169	glucose metabolic process	▨	▨	🟥	🟥	1.4	37	0.91	-0.18	26	0.93	5.9	41	4.1e-08	11	83	0
141	☐ GO:0030163	P	141	protein catabolic process	▨	▨	🟥	▨	1.1	35	1	-1	7.5	0.93	5.9	43	4.3e-08	1.5	33	0.33
142	☐ GO:0005996	P	213	monosaccharide metabolic process	▨	▨	🟧	🟥	1.2	34	1	-0.45	21	0.93	5.6	39	2.5e-07	10	71	0
143	☐ GO:0031325	P	11	positive regulation of cellular metabolic process	▨	▨	🟧	🟨	1.6	81	0.71	-0.32	4.5	0.93	5.6	92	2.5e-07	2.9	84	0.014
144	☐ GO:0010604	P	11	positive regulation of macromolecule metabolic process	▨	▨	🟧	🟨	1.6	81	0.71	-0.32	4.5	0.93	5.6	92	2.5e-07	2.9	84	0.014
145	☐ GO:0009893	P	11	positive regulation of metabolic process	▨	▨	🟧	🟨	1.6	81	0.71	-0.32	4.5	0.93	5.6	92	2.5e-07	2.9	84	0.014
146	☐ GO:0009141	P	141	nucleoside triphosphate metabolic process	▨	▨	🟧	🟥	1.9	43	0.47	-0.59	16	0.93	5.5	42	4.1e-07	7	65	3.4e-11
147	☐ GO:0009206	P	140	purine ribonucleoside triphosphate biosynthetic process	▨	▨	🟧	🟥	1.9	43	0.47	-0.59	16	0.93	5.5	42	4.5e-07	7	65	2.8e-11
148	☐ GO:0009205	P	140	purine ribonucleoside triphosphate metabolic process	▨	▨	🟧	🟥	1.9	43	0.47	-0.59	16	0.93	5.5	42	4.5e-07	7	65	2.8e-11
149	☐ GO:0009201	P	140	ribonucleoside triphosphate biosynthetic process	▨	▨	🟧	🟥	1.9	43	0.47	-0.59	16	0.93	5.5	42	4.5e-07	7	65	2.8e-11
150	☐ GO:0009199	P	140	ribonucleoside triphosphate metabolic process	▨	▨	🟧	🟥	1.9	43	0.47	-0.59	16	0.93	5.5	42	4.5e-07	7	65	2.8e-11
151	☐ GO:0009145	P	140	purine nucleoside triphosphate biosynthetic process	▨	▨	🟧	🟥	1.9	43	0.47	-0.59	16	0.93	5.5	42	4.5e-07	7	65	2.8e-11
152	☐ GO:0009144	P	140	purine nucleoside triphosphate metabolic process	▨	▨	🟧	🟥	1.9	43	0.47	-0.59	16	0.93	5.5	42	4.5e-07	7	65	2.8e-11
153	☐ GO:0009142	P	140	nucleoside triphosphate biosynthetic process	▨	▨	🟧	🟥	1.9	43	0.47	-0.59	16	0.93	5.5	42	4.5e-07	7	65	2.8e-11
154	☐ GO:0019318	P	190	hexose metabolic process	▨	▨	🟧	🟥	1.3	36	0.94	-0.3	24	0.93	5.4	39	5.3e-07	10	76	0
155	☐ GO:0046034	P	133	ATP metabolic process	▨	▨	🟧	🟥	1.8	43	0.52	-0.58	16	0.93	5.4	42	7.9e-07	6.7	64	1.7e-10
156	☐ GO:0006754	P	133	ATP biosynthetic process	▨	▨	🟧	🟥	1.8	43	0.52	-0.58	16	0.93	5.4	42	7.9e-07	6.7	64	1.7e-10
157	☐ GO:0008152	P	7584	metabolic process	▨	▨	🟧	🟥	1.8	27	0.53	-1.9	24	0.48	5.3	25	9.1e-07	11	33	0
158	☐ GO:0018193	P	12	peptidyl-amino acid modification	▨	▨	🟧	🟨	1.4	72	0.86	-0.35	3.4	0.93	5.3	85	1.3e-06	3.3	90	0.0037
159	☐ GO:0009309	P	143	amine biosynthetic process	▨	▨	🟧	🟧	0.7	31	1	0.91	49	0.93	5.2	41	2.2e-06	4.8	52	1e-05
160	☐ GO:0044248	P	329	cellular catabolic process	▨	▨	🟧	🟥	2.8	42	0.11	-1.2	13	0.93	5.1	34	2.5e-06	7.2	52	8.9e-12
161	☐ GO:0042026	P	25	protein refolding	▨	▨	🟧	🟧	0.58	38	1	-0.55	0.96	0.93	5.1	65	3.2e-06	4.1	80	0.00021
162	☐ GO:0009260	P	163	ribonucleotide biosynthetic process	▨	▨	🟧	🟥	1.7	40	0.64	-0.68	15	0.93	5	39	4.7e-06	6.5	59	7.9e-10
163	☐ GO:0009259	P	163	ribonucleotide metabolic process	▨	▨	🟧	🟥	1.7	40	0.64	-0.68	15	0.93	5	39	4.7e-06	6.5	59	7.9e-10
164	☐ GO:0009152	P	157	purine ribonucleotide biosynthetic process	▨	▨	🟧	🟥	1.7	40	0.63	-0.69	15	0.93	5	39	5e-06	6.5	60	6.3e-10
165	☐ GO:0009150	P	157	purine ribonucleotide metabolic process	▨	▨	🟧	🟥	1.7	40	0.63	-0.69	15	0.93	5	39	5e-06	6.5	60	6.3e-10
166	☐ GO:0048522	P	13	positive regulation of cellular process	▨	▨	🟧	🟨	1.4	70	0.86	-0.35	3.8	0.93	4.9	79	6.8e-06	2.5	71	0.045
167	☐ GO:0048518	P	13	positive regulation of biological process	▨	▨	🟧	🟨	1.4	70	0.86	-0.35	3.8	0.93	4.9	79	6.8e-06	2.5	71	0.045
168	☐ GO:0046365	P	125	monosaccharide catabolic process	▨	▨	🟧	🟥	1.3	38	0.98	-0.36	21	0.93	4.9	41	7.6e-06	8.4	76	0
169	☐ GO:0019320	P	125	hexose catabolic process	▨	▨	🟧	🟥	1.3	38	0.98	-0.36	21	0.93	4.9	41	7.6e-06	8.4	76	0

170	☐ GO:0006007		P	125	glucose catabolic process	▨	▨	🟧	🟥	1.3	38	0.98	-0.36	21	0.93	4.9	41	7.6e-06	8.4	76	0
171	☐ GO:0006164		P	162	purine nucleotide biosynthetic process	▨	▨	🟧	🟥	1.7	40	0.67	-0.72	15	0.93	4.8	38	9.3e-06	6.4	59	1.5e-09
172	☐ GO:0042398		P	28	cellular amino acid derivative biosynthetic process	▨	▨	🟧	🟧	0.99	46	1	1.4	97	0.93	4.8	60	1e-05	4.1	77	0.0002
173	☐ GO:0006163		P	165	purine nucleotide metabolic process	▨	▨	🟧	🟥	1.6	39	0.71	-0.74	14	0.93	4.8	38	1.2e-05	6.3	58	2.7e-09
174	☐ GO:0046164		P	130	alcohol catabolic process	▨	▨	🟧	🟥	1.3	38	0.94	-0.4	20	0.93	4.7	40	1.7e-05	8.3	74	0
175	☐ GO:0044275		P	130	cellular carbohydrate catabolic process	▨	▨	🟧	🟥	1.3	38	0.94	-0.4	20	0.93	4.7	40	1.7e-05	8.3	74	0
176	☐ GO:0046907		P	306	intracellular transport	▨	▨	🟧	▨	1.2	32	1	-0.84	17	0.93	4.7	34	1.9e-05	1.5	31	0.35
177	☐ GO:0045184		P	362	establishment of protein localization	▨	▨	🟧	▨	1.3	32	0.98	-0.76	19	0.93	4.5	33	3.7e-05	1.3	30	0.44
178	☐ GO:0015031		P	362	protein transport	▨	▨	🟧	▨	1.3	32	0.98	-0.76	19	0.93	4.5	33	3.7e-05	1.3	30	0.44
179	☐ GO:0006886		P	256	intracellular protein transport	▨	▨	🟧	▨	1.3	34	0.98	-0.67	18	0.93	4.5	34	3.7e-05	1.4	31	0.36
180	☐ GO:0015672		P	219	monovalent inorganic cation transport	▨	▨	🟧	🟥	1.7	38	0.64	-0.76	16	0.93	4.5	35	3.8e-05	7.7	60	1.3e-13
181	☐ GO:0070727		P	261	cellular macromolecule localization	▨	▨	🟧	▨	1.3	34	0.98	-0.7	18	0.93	4.5	34	4.5e-05	1.5	31	0.33
182	☐ GO:0034613		P	261	cellular protein localization	▨	▨	🟧	▨	1.3	34	0.98	-0.7	18	0.93	4.5	34	4.5e-05	1.5	31	0.33
183	☐ GO:0006096		P	102	glycolysis	▨	▨	🟧	🟥	1.2	38	1	-0.2	24	0.93	4.5	41	5.5e-05	8.3	80	3.5e-15
184	☐ GO:0009165		P	188	nucleotide biosynthetic process	▨	▨	🟧	🟥	1.4	36	0.87	-0.83	14	0.93	4.4	36	6.1e-05	5.8	54	4.3e-08
185	☐ GO:0006519		P	386	cellular amino acid and derivative metabolic process	▨	▨	🟧	🟥	1.1	31	1	-0.32	25	0.93	4.4	32	6.1e-05	5.8	45	4.1e-08
186	☐ GO:0008104		P	377	protein localization	▨	▨	🟧	▨	1.2	32	1	-0.82	18	0.93	4.4	32	6.8e-05	1.3	29	0.46
187	☐ GO:0055086		P	264	nucleobase, nucleoside and nucleotide metabolic process	▨	▨	🟧	🟧	1.2	33	1	-1.1	12	0.93	4.2	33	0.00014	5.3	47	6.3e-07
188	☐ GO:0006415		P	13	translational termination	▨	▨	🟧	🟨	1.4	68	0.91	-0.36	3.3	0.93	4.2	71	0.00017	2.8	77	0.02
189	☐ GO:0006575		P	65	cellular amino acid derivative metabolic process	▨	▨	🟧	🟧	1.1	40	1	0.51	46	0.93	4.2	44	0.00019	4.2	60	0.00011
190	☐ GO:0044106		P	360	cellular amine metabolic process	▨	▨	🟧	🟧	0.91	30	1	-0.36	24	0.93	4.2	32	0.0002	5.5	44	2.6e-07
191	☐ GO:0009117		P	236	nucleotide metabolic process	▨	▨	🟧	🟧	1.3	34	0.98	-1	12	0.93	4.1	34	0.00022	5.4	49	3.4e-07
192	☐ GO:0006753		P	236	nucleoside phosphate metabolic process	▨	▨	🟧	🟧	1.3	34	0.98	-1	12	0.93	4.1	34	0.00022	5.4	49	3.4e-07
193	☐ GO:0051649		P	360	establishment of localization in cell	▨	▨	🟧	▨	0.98	30	1	-1	15	0.93	4.1	32	0.00022	1	29	0.59
194	☐ GO:0006576		P	37	cellular biogenic amine metabolic process	▨	▨	🟧	🟧	0.85	40	1	0.63	56	0.93	4	50	0.00036	4.1	71	0.00018
195	☐ GO:0051641		P	375	cellular localization	▨	▨	🟧	▨	0.9	30	1	-1.1	14	0.93	4	31	0.00039	1	28	0.61
196	☐ GO:0010608		P	11	posttranscriptional regulation of gene expression	▨	▨	🟧	🟨	1.3	68	0.99	-0.28	7.3	0.93	4	72	0.00039	2.8	82	0.02
197	☐ GO:0006417		P	11	regulation of translation	▨	▨	🟧	🟨	1.3	68	0.99	-0.28	7.3	0.93	4	72	0.00039	2.8	82	0.02
198	☐ GO:0044042		P	98	glucan metabolic process	▨	▨	🟧	▨	-0.59	18	1	-0.29	22	0.93	3.9	39	0.00044	1.2	33	0.48
199	☐ GO:0006073		P	98	cellular glucan metabolic process	▨	▨	🟧	▨	-0.59	18	1	-0.29	22	0.93	3.9	39	0.00044	1.2	33	0.48
200	☐ GO:0051128		P	12	regulation of cellular component organization	▨	▨	🟨	▨	1.1	62	1	-0.35	3.1	0.93	3.9	69	0.00055	2.2	68	0.089
201	☐ GO:0006066		P	316	alcohol metabolic process	▨	▨	🟨	🟥	0.86	30	1	-0.27	25	0.93	3.9	32	0.00055	8	55	2.3e-14
202	☐ GO:0009250		P	74	glucan biosynthetic process	▨	▨	🟨	▨	-0.27	21	1	-0.17	24	0.94	3.9	41	0.00058	1.5	37	0.34
203	☐ GO:0051603		P	119	proteolysis involved in cellular protein catabolic process	▨	▨	🟨	▨	0.59	31	1	-0.88	8.4	0.93	3.9	37	0.00058	0.52	28	0.82
204	☐ GO:0044257		P	119	cellular protein catabolic process	▨	▨	🟨	▨	0.59	31	1	-0.88	8.4	0.93	3.9	37	0.00058	0.52	28	0.82
205	☐ GO:0032268		P	12	regulation of cellular protein metabolic process	▨	▨	🟨	🟨	1.2	64	1	-0.3	6.7	0.93	3.8	68	0.00072	2.6	76	0.03
206	☐ GO:0009082		P	16	branched chain family amino acid biosynthetic process	▨	▨	🟨	▨	0.4	36	1	-0.43	1.1	0.93	3.8	62	0.00084	1.9	56	0.19
207	☐ GO:0043624	0043624	P	16	cellular protein complex disassembly	▨	▨	🟨	🟨	1.1	57	1	-0.4	3.1	0.93	3.7	61	0.001	2.6	69	0.033
208	☐ GO:0043241	0043241	P	16	protein complex disassembly	▨	▨	🟨	🟨	1.1	57	1	-0.4	3.1	0.93	3.7	61	0.001	2.6	69	0.033
209	☐ GO:0034623		P	16	cellular macromolecular complex disassembly	▨	▨	🟨	🟨	1.1	57	1	-0.4	3.1	0.93	3.7	61	0.001	2.6	69	0.033
210	☐ GO:0032984		P	16	macromolecular complex disassembly	▨	▨	🟨	🟨	1.1	57	1	-0.4	3.1	0.93	3.7	61	0.001	2.6	69	0.033
211	☐ GO:0022411		P	16	cellular component disassembly	▨	▨	🟨	🟨	1.1	57	1	-0.4	3.1	0.93	3.7	61	0.001	2.6	69	0.033
212	☐ GO:0044282		P	167	small molecule catabolic process	▨	▨	🟨	🟥	2.1	43	0.36	-0.65	16	0.93	3.6	34	0.0014	7.9	66	3.9e-14
213	☐ GO:0006397		P	27	mRNA processing	▨	▨	🟨	▨	0.49	35	1	-0.45	6.9	0.93	3.6	51	0.0017	0.52	32	0.82
214	☐ GO:0016071		P	29	mRNA metabolic process	▨	▨	🟨	▨	0.46	34	1	-0.47	6.5	0.93	3.6	50	0.0017	0.48	31	0.83
215	☐ GO:0044271		P	248	cellular nitrogen compound biosynthetic process	▨	▨	🟨	🟧	0.1	25	1	0.027	30	0.99	3.5	32	0.002	5.3	47	8.9e-07
216	☐ GO:0044264		P	130	cellular polysaccharide metabolic process	▨	▨	🟨	▨	-0.4	20	1	-0.37	21	0.93	3.5	35	0.0022	1.4	33	0.38
217	☐ GO:0034641		P	486	cellular nitrogen compound metabolic process	▨	▨	🟨	🟥	0.57	27	1	-0.88	19	0.93	3.5	29	0.0022	6.2	44	3.9e-09
218	☐ GO:0007264		P	173	small GTPase mediated signal transduction	▨	▨	🟨	▨	1.2	35	1	0.74	44	0.93	3.5	34	0.0023	0.79	29	0.75
219	☐ GO:0010033		P	34	response to organic substance	▨	▨	🟨	▨	-0.22	20	1	-0.65	0.27	0.93	3.4	47	0.003	-0.57	18	0.81
220	☐ GO:0009725		P	34	response to hormone stimulus	▨	▨	🟨	▨	-0.22	20	1	-0.65	0.27	0.93	3.4	47	0.003	-0.57	18	0.81
221	☐ GO:0009719		P	34	response to endogenous stimulus	▨	▨	🟨	▨	-0.22	20	1	-0.65	0.27	0.93	3.4	47	0.003	-0.57	18	0.81
222	☐ GO:0007275		P	49	multicellular organismal development	▨	▨	🟨	▨	-0.02	24	1	-0.29	19	0.93	3.4	43	0.003	1	35	0.6
223	☐ GO:0044283		P	322	small molecule biosynthetic process	▨	▨	🟨	🟨	2.2	38	0.33	0.032	30	0.98	3.4	31	0.0032	3.9	39	0.00055
224	☐ GO:0006555		P	11	methionine metabolic process	▨	▨	🟨	🟨	0.82	53	1	-0.32	4.4	0.93	3.4	65	0.0035	3.4	95	0.0026
225	☐ GO:0030244		P	32	cellulose biosynthetic process	▨	▨	🟨	▨	0.21	29	1	-0.43	9.6	0.93	3.3	47	0.0038	2.4	53	0.059
226	☐ GO:0030243		P	32	cellulose metabolic process	▨	▨	🟨	▨	0.21	29	1	-0.43	9.6	0.93	3.3	47	0.0038	2.4	53	0.059
227	☐ GO:0033692		P	106	cellular polysaccharide biosynthetic process	▨	▨	🟨	▨	-0.099	23	1	-0.27	23	0.93	3.3	36	0.004	1.6	36	0.28
228	☐ GO:0032502		P	50	developmental process	▨	▨	🟨	▨	-0.045	24	1	-0.3	18	0.93	3.3	42	0.004	1	35	0.61
229	☐ GO:0043436	0043436	P	495	oxoacid metabolic process	▨	▨	🟨	🟥	2.6	38	0.15	-1	17	0.93	3.3	29	0.0041	6.5	45	6.1e-10

230	☐ GO:0019752		P	495	carboxylic acid metabolic process	⬛	⬛	🟨	🟥	2.6	38	0.15	-1	17	0.93	3.3	29	0.0041	6.5	45	6.1e-10
231	☐ GO:0006082		P	496	organic acid metabolic process	⬛	⬛	🟨	🟥	2.6	38	0.15	-1.1	17	0.93	3.3	29	0.0042	6.5	45	6e-10
232	☐ GO:0007242		P	185	intracellular signaling cascade	⬛	⬛	🟨	⬛	1.2	34	1	0.61	41	0.93	3.3	33	0.0043	0.58	28	0.81
233	☐ GO:0009081		P	26	branched chain family amino acid metabolic process	⬛	⬛	🟨	⬛	0.32	32	1	-0.54	2	0.93	3.3	49	0.0047	1.6	47	0.28
234	☐ GO:0042180		P	502	cellular ketone metabolic process	⬛	⬛	🟨	🟥	2.5	37	0.17	-1.1	17	0.93	3.2	29	0.006	6.4	44	1.1e-09
235	☐ GO:0000271		P	109	polysaccharide biosynthetic process	⬛	⬛	🟨	⬛	-0.13	23	1	-0.3	22	0.93	3.2	35	0.006	1.5	35	0.32
236	☐ GO:0022610		P	132	biological adhesion	⬛	⬛	🟨	⬛	0.4	28	1	0.22	34	0.93	3.1	34	0.0068	0.86	30	0.7
237	☐ GO:0007155		P	132	cell adhesion	⬛	⬛	🟨	⬛	0.4	28	1	0.22	34	0.93	3.1	34	0.0068	0.86	30	0.7
238	☐ GO:0008652		P	133	cellular amino acid biosynthetic process	⬛	⬛	🟨	🟨	0.23	27	1	0.42	39	0.93	3.1	34	0.0073	3.1	43	0.0079
239	☐ GO:0051274		P	11	beta-glucan biosynthetic process	⬛	⬛	🟨	⬛	0.24	33	1	-0.27	8.3	0.93	3.1	61	0.008	0.087	27	0.99
240	☐ GO:0051273		P	11	beta-glucan metabolic process	⬛	⬛	🟨	⬛	0.24	33	1	-0.27	8.3	0.93	3.1	61	0.008	0.087	27	0.99
241	☐ GO:0006075		P	11	1,3-beta-glucan biosynthetic process	⬛	⬛	🟨	⬛	0.24	33	1	-0.27	8.3	0.93	3.1	61	0.008	0.087	27	0.99
242	☐ GO:0006074		P	11	1,3-beta-glucan metabolic process	⬛	⬛	🟨	⬛	0.24	33	1	-0.27	8.3	0.93	3.1	61	0.008	0.087	27	0.99
243	☐ GO:0006520		P	337	cellular amino acid metabolic process	⬛	⬛	🟨	🟧	0.61	28	1	-0.66	20	0.93	3	30	0.0092	4.8	43	7.4e-06
244	☐ GO:0006413		P	45	translational initiation	⬛	⬛	🟨	⬛	0.97	41	1	-0.41	13	0.93	3	41	0.0097	1.9	44	0.16
245	☐ GO:0006812		P	397	cation transport	⬛	⬛	🟨	🟧	1.2	32	1	-1.2	14	0.93	3	29	0.011	4.9	41	6.3e-06
246	☐ GO:0006352		P	69	transcription initiation	⬛	⬛	🟨	⬛	-0.4	19	1	-0.79	4.5	0.93	3	37	0.011	0.56	29	0.81
247	☐ GO:0042254		P	51	ribosome biogenesis	⬛	⬛	🟨	🟨	0.24	28	1	-0.75	2.2	0.93	2.9	39	0.015	3	53	0.01
248	☐ GO:0022613		P	51	ribonucleoprotein complex biogenesis	⬛	⬛	🟨	🟨	0.24	28	1	-0.75	2.2	0.93	2.9	39	0.015	3	53	0.01
249	☐ GO:0043632	0043632	P	102	modification-dependent macromolecule catabolic process	⬛	⬛	🟨	⬛	0.29	28	1	-0.79	8.9	0.93	2.9	34	0.015	-0.022	25	1
250	☐ GO:0019941		P	102	modification-dependent protein catabolic process	⬛	⬛	🟨	⬛	0.29	28	1	-0.79	8.9	0.93	2.9	34	0.015	-0.022	25	1
251	☐ GO:0006511		P	102	ubiquitin-dependent protein catabolic process	⬛	⬛	🟨	⬛	0.29	28	1	-0.79	8.9	0.93	2.9	34	0.015	-0.022	25	1
252	☐ GO:0006108		P	20	malate metabolic process	⬛	⬛	🟨	🟥	0.88	47	1	-0.21	17	0.93	2.8	49	0.016	8.4	1.5e+02	0
253	☐ GO:0051169		P	61	nuclear transport	⬛	⬛	🟨	⬛	0.81	36	1	0.073	32	0.98	2.8	38	0.016	0.97	33	0.62
254	☐ GO:0006913		P	61	nucleocytoplasmic transport	⬛	⬛	🟨	⬛	0.81	36	1	0.073	32	0.98	2.8	38	0.016	0.97	33	0.62
255	☐ GO:0034637		P	143	cellular carbohydrate biosynthetic process	⬛	⬛	🟨	⬛	-0.14	23	1	-0.4	21	0.93	2.8	32	0.017	1.6	34	0.28
256	☐ GO:0016051		P	148	carbohydrate biosynthetic process	⬛	⬛	🟨	⬛	-0.17	23	1	-0.44	20	0.93	2.8	32	0.019	1.5	33	0.33
257	☐ GO:0043648	0043648	P	56	dicarboxylic acid metabolic process	⬛	⬛	🟨	🟧	0.41	31	1	-0.5	12	0.93	2.8	38	0.019	5.3	73	7.3e-07
258	☐ GO:0046483		P	347	heterocycle metabolic process	⬛	⬛	🟨	🟥	0.43	27	1	-0.69	20	0.93	2.7	29	0.022	6	47	1.3e-08
259	☐ GO:0006811		P	483	ion transport	⬛	⬛	🟨	🟧	1.1	30	1	-1	17	0.93	2.6	28	0.028	4.3	38	8.9e-05
260	☐ GO:0009086		P	10	methionine biosynthetic process	⬛	⬛	🟨	🟨	0.67	49	1	-0.31	3.7	0.93	2.5	55	0.04	2.5	79	0.041
261	☐ GO:0006807		P	2524	nitrogen compound metabolic process	⬛	⬛	🟨	⬛	0.46	26	1	-3.3	12	0.026	2.5	25	0.044	-0.077	25	0.99
262	☐ GO:0043094	0043094	P	17	cellular metabolic compound salvage	⬛	⬛	🟨	⬛	0.25	32	1	-0.34	7.9	0.93	2.4	47	0.047	1.4	48	0.37
263	☐ GO:0006396		P	188	RNA processing	⬛	⬛	🟨	⬛	-0.23	23	1	-1.4	3.2	0.93	2.4	30	0.049	0.27	26	0.96
264	☐ GO:0003735		F	484	structural constituent of ribosome	⬛	⬛	🟥	🟥	2	35	0.57	-1.8	8.5	0.86	14	48	0	23	94	0
265	☐ GO:0003924		F	154	GTPase activity	⬛	⬛	🟥	🟥	3	52	0.14	1.8	67	0.85	11	60	0	7	63	4.7e-11
266	☐ GO:0003676		F	2585	nucleic acid binding	⬛	⬛	🟥	⬛	0.13	25	1	-3.3	13	0.035	11	31	0	1.7	27	0.33
267	☐ GO:0008135		F	87	translation factor activity, nucleic acid binding	⬛	⬛	🟥	🟥	2.8	59	0.19	-0.61	12	0.93	9.9	66	0	8.7	88	0
268	☐ GO:0032561		F	289	guanyl ribonucleotide binding	⬛	⬛	🟥	🟧	2.4	41	0.33	1.5	52	0.93	9.1	45	0	5.6	47	4.4e-07
269	☐ GO:0005525		F	289	GTP binding	⬛	⬛	🟥	🟧	2.4	41	0.33	1.5	52	0.93	9.1	45	0	5.6	47	4.4e-07
270	☐ GO:0019001		F	299	guanyl nucleotide binding	⬛	⬛	🟥	🟧	2.3	40	0.36	1.4	51	0.93	9	44	0	5.4	46	1e-06
271	☐ GO:0003723		F	404	RNA binding	⬛	⬛	🟥	🟥	1.2	31	1	-2	3.4	0.64	8	39	7.7e-14	7	49	4.8e-11
272	☐ GO:0051082		F	150	unfolded protein binding	⬛	⬛	🟥	🟧	2.3	46	0.34	-1.1	5.9	0.93	7.2	47	2.4e-11	4.5	50	9.4e-05
273	☐ GO:0016462		F	886	pyrophosphatase activity	⬛	⬛	🟥	🟨	1.1	29	1	-1	20	0.93	7.2	33	3e-11	3.5	33	0.0042
274	☐ GO:0016817		F	908	hydrolase activity, acting on acid anhydrides	⬛	⬛	🟥	🟨	1	28	1	-1.1	20	0.93	7.1	32	5.8e-11	3.4	32	0.0066
275	☐ GO:0005488		F	8563	binding	⬛	⬛	🟥	⬛	1.3	26	1	0.57	31	0.93	7	26	7.2e-11	2.2	27	0.12
276	☐ GO:0016818		F	903	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	⬛	⬛	🟥	🟨	0.98	28	1	-1.1	20	0.93	7	32	8e-11	3.3	32	0.0076
277	☐ GO:0019843		F	20	rRNA binding	⬛	⬛	🟥	🟥	1	51	1	-0.47	2.1	0.93	7	87	1.1e-10	9.2	1.6e+02	0
278	☐ GO:0046961		F	29	proton-transporting ATPase activity, rotational mechanism	⬛	⬛	🟥	🟥	2.2	72	0.38	-0.18	21	0.93	6.6	74	9.6e-10	7.5	1.2e+02	2.2e-12
279	☐ GO:0017111		F	856	nucleoside-triphosphatase activity	⬛	⬛	🟥	🟨	0.91	28	1	-1	20	0.93	6.6	32	9.6e-10	3	32	0.016
280	☐ GO:0015078		F	105	hydrogen ion transmembrane transporter activity	⬛	⬛	🟥	🟥	2.6	53	0.25	-0.41	19	0.93	6.5	49	1.8e-09	10	93	0
281	☐ GO:0046933		F	26	hydrogen ion transporting ATP synthase activity, rotational mechanism	⬛	⬛	🟥	🟥	1.9	66	0.76	-0.19	20	0.93	6.2	73	1.5e-08	7.5	1.2e+02	1.4e-12
282	☐ GO:0019829		F	42	cation-transporting ATPase activity	⬛	⬛	🟧	🟧	1.7	54	0.97	-0.35	15	0.93	5.8	59	2.1e-07	5.9	87	6.2e-08
283	☐ GO:0015077		F	128	monovalent inorganic cation transmembrane transporter activity	⬛	⬛	🟧	🟥	2.2	47	0.38	-0.55	17	0.93	5.6	43	4.1e-07	9.1	79	0
284	☐ GO:0016620		F	23	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	⬛	⬛	🟧	🟥	1.7	66	0.93	-0.22	17	0.93	5.2	68	3.9e-06	11	1.7e+02	0
285	☐ GO:0051287		F	55	NAD or NADH binding	⬛	⬛	🟧	🟥	1.7	51	0.97	1.9	97	0.69	5	50	1.4e-05	11	1.2e+02	0
286	☐ GO:0016903		F	32	oxidoreductase activity, acting on the aldehyde or oxo group of donors	⬛	⬛	🟧	🟥	1.6	57	1	-0.27	17	0.93	4.8	58	2.9e-05	9.5	1.4e+02	0
287	☐ GO:0003677		F	1585	DNA binding	⬛	⬛	🟧	⬛	-1.5	20	1	-2.3	14	0.41	4.8	28	3.4e-05	-2.8	20	0.033
288	☐ GO:0019904		F	12	protein domain specific binding	⬛	⬛	🟧	⬛	1.9	86	0.76	2.1	1.9e+02	0.48	4.8	79	3.4e-05	2.4	71	0.088
289	☐ GO:0022890		F	174	inorganic cation transmembrane transporter activity	⬛	⬛	🟧	🟥	1.7	39	0.97	-0.82	13	0.93	4.7	37	4.8e-05	7.4	63	4.5e-12

290	☐ GO:0035251		F	56	UDP-glucosyltransferase activity	■	■	🟧	🟧	0.31	29	1	-0.6	8.5	0.93	4.5	47	0.00011	5.1	71	4.4e-06
291	☐ GO:0000166		F	2664	nucleotide binding	■	■	🟧	■	-0.099	24	1	0.52	32	0.93	4.4	26	0.00017	2.3	28	0.1
292	☐ GO:0046527		F	68	glucosyltransferase activity	■	■	🟧	🟧	0.079	26	1	-0.7	7.3	0.93	4.4	45	0.00018	4.7	63	4e-05
293	☐ GO:0032555		F	2410	purine ribonucleotide binding	■	■	🟧	■	-0.31	24	1	0.64	33	0.93	4.3	26	0.00021	0.73	26	0.77
294	☐ GO:0032553		F	2410	ribonucleotide binding	■	■	🟧	■	-0.31	24	1	0.64	33	0.93	4.3	26	0.00021	0.73	26	0.77
295	☐ GO:0004634		F	12	phosphopyruvate hydratase activity	■	■	🟧	🟨	0.92	55	1	0.22	46	0.93	4.2	73	0.00033	2.9	82	0.021
296	☐ GO:0070003		F	29	threonine-type peptidase activity	■	■	🟧	■	1.3	52	1	-0.53	3.9	0.93	4.1	54	0.00043	1.9	49	0.24
297	☐ GO:0004298		F	29	threonine-type endopeptidase activity	■	■	🟧	■	1.3	52	1	-0.53	3.9	0.93	4.1	54	0.00043	1.9	49	0.24
298	☐ GO:0017076		F	2530	purine nucleotide binding	■	■	🟨	■	-0.35	24	1	0.4	31	0.93	3.9	26	0.0012	0.82	26	0.75
299	☐ GO:0042625		F	98	ATPase activity, coupled to transmembrane movement of ions	■	■	🟨	🟨	1.1	37	1	-0.39	19	0.93	3.8	39	0.0016	3.5	49	0.0039
300	☐ GO:0004427		F	28	inorganic diphosphatase activity	■	■	🟨	🟨	1	46	1	0.014	30	1	3.6	51	0.0037	2.8	60	0.033
301	☐ GO:0016859		F	27	cis-trans isomerase activity	■	■	🟨	🟨	0.76	41	1	1.9	1.3e+02	0.68	3.5	50	0.0052	3.2	66	0.012
302	☐ GO:0003755		F	27	peptidyl-prolyl cis-trans isomerase activity	■	■	🟨	🟨	0.76	41	1	1.9	1.3e+02	0.68	3.5	50	0.0052	3.2	66	0.012
303	☐ GO:0016831		F	48	carboxy-lyase activity	■	■	🟨	🟥	0.79	38	1	0.48	47	0.93	3.4	43	0.0056	10	1.2e+02	0
304	☐ GO:0015405		F	168	P-P-bond-hydrolysis-driven transmembrane transporter activity	■	■	🟨	🟨	0.84	32	1	-0.7	15	0.93	3.4	34	0.006	3.2	42	0.0099
305	☐ GO:0015399		F	168	primary active transmembrane transporter activity	■	■	🟨	🟨	0.84	32	1	-0.7	15	0.93	3.4	34	0.006	3.2	42	0.0099
306	☐ GO:0016986		F	29	transcription initiation factor activity	■	■	🟨	■	-0.44	15	1	-0.56	2.4	0.93	3.3	48	0.0071	1.6	45	0.41
307	☐ GO:0016830		F	85	carbon-carbon lyase activity	■	■	🟨	🟥	0.61	32	1	0.32	38	0.93	3.3	38	0.0076	10	1e+02	0
308	☐ GO:0004576		F	10	oligosaccharyl transferase activity	■	■	🟨	■	0.46	41	1	-0.34	1.3	0.93	3.2	65	0.011	0.8	42	0.75
309	☐ GO:0003743		F	47	translation initiation factor activity	■	■	🟨	■	0.97	41	1	-0.44	13	0.93	3.2	42	0.011	2	45	0.2
310	☐ GO:0003843		F	11	1,3-beta-glucan synthase activity	■	■	🟨	■	0.24	33	1	-0.27	8.3	0.93	3.1	61	0.016	0.087	27	0.96
311	☐ GO:0000287		F	111	magnesium ion binding	■	■	🟨	■	1.2	37	1	-0.59	15	0.93	3.1	35	0.017	2.4	40	0.095
312	☐ GO:0008194		F	86	UDP-glycosyltransferase activity	■	■	🟨	🟨	0.17	27	1	-0.52	15	0.93	3.1	36	0.017	3.6	51	0.0035
313	☐ GO:0016820		F	138	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	■	■	🟨	🟨	0.78	32	1	-0.7	14	0.93	3	33	0.018	2.8	41	0.027
314	☐ GO:0008483		F	28	transaminase activity	■	■	🟨	■	0.62	38	1	-0.5	4.7	0.93	2.9	45	0.029	2.1	51	0.18
315	☐ GO:0043492	0043492	F	133	ATPase activity, coupled to movement of substances	■	■	🟨	🟨	0.74	32	1	-0.67	14	0.93	2.9	33	0.029	2.7	41	0.035
316	☐ GO:0042626		F	133	ATPase activity, coupled to transmembrane movement of substances	■	■	🟨	🟨	0.74	32	1	-0.67	14	0.93	2.9	33	0.029	2.7	41	0.035
317	☐ GO:0016615		F	20	malate dehydrogenase activity	■	■	🟨	🟥	0.88	47	1	-0.21	17	0.93	2.8	49	0.03	8.4	1.5e+02	0
318	☐ GO:0016832		F	10	aldehyde-lyase activity	■	■	🟨	🟥	0.96	59	1	0.79	94	0.93	2.8	60	0.03	8.8	2.1e+02	0
319	☐ GO:0016853		F	234	isomerase activity	■	■	🟨	🟨	1.7	37	0.97	-0.22	26	0.93	2.8	30	0.033	3.8	42	0.0014
320	☐ GO:0042623		F	270	ATPase activity, coupled	■	■	🟨	■	0.53	28	1	-1.3	8	0.93	2.8	30	0.035	1.6	31	0.41
321	☐ GO:0032991		C	1357	macromolecular complex	■	■	🟥	🟥	2.8	33	0.12	-1.2	21	0.87	20	45	0	23	67	0
322	☐ GO:0043232	0043232	C	936	intracellular non-membrane-bounded organelle	■	■	🟥	🟥	2.2	33	0.39	1.7	44	0.61	19	49	0	20	69	0
323	☐ GO:0043228	0043228	C	936	non-membrane-bounded organelle	■	■	🟥	🟥	2.2	33	0.39	1.7	44	0.61	19	49	0	20	69	0
324	☐ GO:0032993		C	123	protein-DNA complex	■	■	🟥	🟥	1.3	38	1	0.47	40	0.87	19	93	0	8.4	76	0
325	☐ GO:0000786		C	123	nucleosome	■	■	🟥	🟥	1.3	38	1	0.47	40	0.87	19	93	0	8.4	76	0
326	☐ GO:0044424		C	3090	intracellular part	■	■	🟥	🟥	2.4	30	0.29	-1	24	0.87	17	35	0	16	44	0
327	☐ GO:0000785		C	169	chromatin	■	■	🟥	🟥	0.85	32	1	0.096	31	0.94	16	75	0	7.3	63	1.6e-12
328	☐ GO:0044427		C	181	chromosomal part	■	■	🟥	🟥	0.72	31	1	-0.002	29	1	16	72	0	6.9	60	2.3e-11
329	☐ GO:0005622		C	3688	intracellular	■	■	🟥	🟥	2	28	0.46	-0.85	26	0.87	16	33	0	14	40	0
330	☐ GO:0005694		C	233	chromosome	■	■	🟥	🟥	0.5	28	1	-0.33	24	0.87	15	64	0	7.2	57	4.3e-12
331	☐ GO:0043229	0043229	C	2373	intracellular organelle	■	■	🟥	🟥	1.9	29	0.46	-0.67	26	0.87	15	36	0	13	43	0
332	☐ GO:0043226	0043226	C	2373	organelle	■	■	🟥	🟥	1.9	29	0.46	-0.67	26	0.87	15	36	0	13	43	0
333	☐ GO:0044446		C	682	intracellular organelle part	■	■	🟥	🟥	1.4	31	1	-0.46	25	0.87	15	46	0	12	56	0
334	☐ GO:0044422		C	682	organelle part	■	■	🟥	🟥	1.4	31	1	-0.46	25	0.87	15	46	0	12	56	0
335	☐ GO:0005840		C	489	ribosome	■	■	🟥	🟥	2.1	35	0.39	-1.8	8.5	0.59	14	48	0	23	94	0
336	☐ GO:0030529		C	534	ribonucleoprotein complex	■	■	🟥	🟥	2.1	35	0.39	-1.9	8.5	0.57	14	47	0	22	88	0
337	☐ GO:0044444		C	1059	cytoplasmic part	■	■	🟥	🟥	3	35	0.087	-2.2	11	0.26	13	40	0	18	63	0
338	☐ GO:0044464		C	5557	cell part	■	■	🟥	🟥	1.7	27	0.67	-0.092	29	0.94	11	29	0	9.6	34	0
339	☐ GO:0005623		C	5557	cell	■	■	🟥	🟥	1.7	27	0.67	-0.092	29	0.94	11	29	0	9.6	34	0
340	☐ GO:0015630		C	65	microtubule cytoskeleton	■	■	🟥	🟧	2.4	59	0.29	2.9	1.2e+02	0.076	9	69	0	4.3	61	5.9e-05
341	☐ GO:0043234	0043234	C	718	protein complex	■	■	🟥	🟥	1.6	31	0.74	-0.34	26	0.87	8.6	36	0	10	50	0
342	☐ GO:0043231	0043231	C	1596	intracellular membrane-bounded organelle	■	■	🟥	■	0.82	27	1	-2.1	16	0.35	8.1	31	4.9e-15	0.066	25	0.97
343	☐ GO:0043227	0043227	C	1610	membrane-bounded organelle	■	■	🟥	■	0.79	27	1	-2.1	16	0.34	8	31	1.3e-14	1.1	27	0.57
344	☐ GO:0044430		C	83	cytoskeletal part	■	■	🟥	🟨	2	49	0.46	2.3	96	0.26	7.8	58	3.5e-14	3.4	50	0.0022
345	☐ GO:0016469		C	67	proton-transporting two-sector ATPase complex	■	■	🟥	🟥	2.9	66	0.087	-0.49	14	0.87	7.5	60	6.1e-13	10	1.1e+02	0
346	☐ GO:0033178		C	36	proton-transporting two-sector ATPase complex, catalytic domain	■	■	🟥	🟥	2.1	65	0.39	-0.24	19	0.89	6.7	69	9.9e-11	7.9	1.1e+02	2.2e-14
347	☐ GO:0005634		C	1190	nucleus	■	■	🟥	■	-0.49	23	1	-1.6	17	0.79	6.6	31	2.2e-10	-2.2	21	0.078
348	☐ GO:0033279		C	67	ribosomal subunit	■	■	🟧	🟥	1	39	1	-0.75	5.5	0.87	5.9	52	2.3e-08	9.4	1e+02	0
349	☐ GO:0033180		C	11	proton-transporting V-type ATPase, V1 domain	■	■	🟧	🟧	1.8	88	0.54	-0.26	9.2	0.89	5.5	91	2.4e-07	4.1	1.1e+02	0.00019

350	☐ GO:0033176	C	29	proton-transporting V-type ATPase complex	▨	▨	🟧	🟧	2.1	70	0.39	-0.41	9.3	0.87	5.4	64	3.2e-07	4.1	77	0.00014
351	☐ GO:0015935	C	39	small ribosomal subunit	▨	▨	🟧	🟥	1.2	46	1	-0.54	6.9	0.87	5	56	3.1e-06	7.7	1.1e+02	1.1e-13
352	☐ GO:0000502	C	35	proteasome complex	▨	▨	🟧	▨	1.4	52	1	-0.59	3.4	0.87	4.8	56	8.7e-06	2.1	49	0.11
353	☐ GO:0045259	C	29	proton-transporting ATP synthase complex	▨	▨	🟧	🟥	1.5	57	0.88	-0.26	17	0.89	4.3	56	9.2e-05	10	1.5e+02	0
354	☐ GO:0000015	C	12	phosphopyruvate hydratase complex	▨	▨	🟧	🟨	0.92	55	1	0.22	46	0.89	4.2	73	0.00013	2.9	82	0.012
355	☐ GO:0005839	C	29	proteasome core complex	▨	▨	🟧	▨	1.3	52	1	-0.53	3.9	0.87	4.1	54	0.00017	1.9	49	0.16
356	☐ GO:0045261	C	19	proton-transporting ATP synthase complex, catalytic core F(1)	▨	▨	🟨	🟥	0.94	49	1	-0.1	23	0.94	3.8	59	0.00064	6.3	1.2e+02	1.5e-09
357	☐ GO:0005783	C	112	endoplasmic reticulum	▨	▨	🟨	▨	3.2	59	0.058	-0.83	9	0.87	3.8	37	0.00071	1.4	34	0.39
358	☐ GO:0033177	C	29	proton-transporting two-sector ATPase complex, proton-transporting domain	▨	▨	🟨	🟥	2	67	0.46	-0.44	8.3	0.87	3.7	51	0.00092	6.9	1.1e+02	2.1e-11
359	☐ GO:0044455	C	17	mitochondrial membrane part	▨	▨	🟨	🟨	1.2	57	1	-0.025	28	0.99	3.4	57	0.003	3.3	80	0.0031
360	☐ GO:0005794	C	55	Golgi apparatus	▨	▨	🟨	▨	0.63	34	1	-0.63	7.1	0.87	3.4	41	0.0031	1.2	36	0.48
361	☐ GO:0046930	C	11	pore complex	▨	▨	🟨	▨	0.56	44	1	-0.34	2.6	0.87	3.4	65	0.0031	1	45	0.64
362	☐ GO:0005643	C	11	nuclear pore	▨	▨	🟨	▨	0.56	44	1	-0.34	2.6	0.87	3.4	65	0.0031	1	45	0.64
363	☐ GO:0015934	C	28	large ribosomal subunit	▨	▨	🟨	🟧	0.19	29	1	-0.53	3.4	0.87	3.2	48	0.0052	5.5	95	2.1e-07
364	☐ GO:0005635	C	12	nuclear envelope	▨	▨	🟨	▨	0.53	42	1	-0.35	2.9	0.87	3.2	60	0.0061	0.91	43	0.7
365	☐ GO:0048475	C	56	coated membrane	▨	▨	🟨	▨	0.51	32	1	-0.69	5.3	0.87	3.1	40	0.0063	0.93	33	0.69
366	☐ GO:0030117	C	56	membrane coat	▨	▨	🟨	▨	0.51	32	1	-0.69	5.3	0.87	3.1	40	0.0063	0.93	33	0.69
367	☐ GO:0000148	C	11	1,3-beta-glucan synthase complex	▨	▨	🟨	▨	0.24	33	1	-0.27	8.3	0.89	3.1	61	0.0072	0.087	27	0.97
368	☐ GO:0044459	C	58	plasma membrane part	▨	▨	🟨	▨	1.1	41	1	0.9	60	0.87	3	39	0.0085	0.87	33	0.73
369	☐ GO:0044445	C	59	cytosolic part	▨	▨	🟨	▨	0.36	30	1	-0.49	13	0.87	3	39	0.0092	2.3	45	0.076
370	☐ GO:0005829	C	59	cytosol	▨	▨	🟨	▨	0.36	30	1	-0.49	13	0.87	3	39	0.0092	2.3	45	0.076
371	☐ GO:0031967	C	148	organelle envelope	▨	▨	🟨	🟨	0.27	27	1	-0.54	18	0.87	3	33	0.0099	2.5	39	0.038
372	☐ GO:0005886	C	68	plasma membrane	▨	▨	🟨	▨	0.95	38	1	0.73	52	0.87	3	38	0.01	1.5	37	0.37
373	☐ GO:0031988	C	37	membrane-bounded vesicle	▨	▨	🟨	▨	0.33	31	1	-0.57	4.8	0.87	2.8	42	0.016	0.62	32	0.74
374	☐ GO:0016023	C	37	cytoplasmic membrane-bounded vesicle	▨	▨	🟨	▨	0.33	31	1	-0.57	4.8	0.87	2.8	42	0.016	0.62	32	0.74
375	☐ GO:0033179	C	16	proton-transporting V-type ATPase, V0 domain	▨	▨	🟨	▨	1.2	60	1	-0.3	10	0.88	2.6	50	0.026	2	59	0.13
376	☐ GO:0019773	C	12	proteasome core complex, alpha-subunit complex	▨	▨	🟨	▨	1	58	1	-0.37	1.7	0.87	2.6	54	0.028	1.3	49	0.47
377	☐ GO:0044429	C	146	mitochondrial part	▨	▨	🟨	🟨	0.2	26	1	-0.53	18	0.87	2.5	31	0.034	2.5	39	0.042
378	☐ GO:0030118	C	21	clathrin coat	▨	▨	🟨	▨	0.44	36	1	-0.45	4	0.87	2.5	45	0.037	0.84	37	0.74
379	☐ GO:0012505	C	84	endomembrane system	▨	▨	🟨	▨	0.19	27	1	-0.86	5	0.87	2.5	34	0.037	0.072	25	0.97
380	☐ GO:0005798	C	14	Golgi-associated vesicle	▨	▨	🟨	▨	0.35	35	1	-0.29	9.3	0.88	2.5	50	0.037	1	43	0.64
381	☐ GO:0031975	C	167	envelope	▨	▨	🟨	▨	0.06	25	1	-0.67	16	0.87	2.5	31	0.037	2.2	36	0.085
382	☐ GO:0031982	C	41	vesicle	▨	▨	🟨	▨	0.28	30	1	-0.61	4.4	0.87	2.4	38	0.039	0.5	30	0.75
383	☐ GO:0031410	C	41	cytoplasmic vesicle	▨	▨	🟨	▨	0.28	30	1	-0.61	4.4	0.87	2.4	38	0.039	0.5	30	0.75
384	☐ GO:0005739	C	167	mitochondrion	▨	▨	🟨	🟨	0.088	25	1	-0.63	17	0.87	2.4	30	0.041	2.8	39	0.019
385	☐ GO:0031966	C	120	mitochondrial membrane	▨	▨	🟨	🟨	0.25	27	1	-0.34	21	0.87	2.4	32	0.041	2.5	40	0.046
386	☐ GO:0030135	C	33	coated vesicle	▨	▨	🟨	▨	0.27	30	1	-0.54	4.8	0.87	2.3	40	0.047	0.47	30	0.76
387	☐ GO:0015979	P	54	photosynthesis	▨	▨	▨	🟥	-0.58	15	1	-0.81	0.63	0.93	-3.1	5.3	0.008	21	2.2e+02	0
388	☐ GO:0071704	P	11	organic substance metabolic process	▨	▨	▨	🟥	0.025	25	1	-0.34	2.8	0.93	0.038	23	0.99	13	3e+02	0
389	☐ GO:0015977	P	11	carbon fixation	▨	▨	▨	🟥	0.025	25	1	-0.34	2.8	0.93	0.038	23	0.99	13	3e+02	0
390	☐ GO:0005985	P	14	sucrose metabolic process	▨	▨	▨	🟥	0.15	29	1	-0.29	9.5	0.93	1.3	37	0.4	6.6	1.4e+02	3.6e-10
391	☐ GO:0055114	P	994	oxidation reduction	▨	▨	▨	🟥	2.7	34	0.13	0.47	33	0.93	-1.4	21	0.33	6.3	38	2.2e-09
392	☐ GO:0046356	P	21	acetyl-CoA catabolic process	▨	▨	▨	🟧	0.39	34	1	-0.18	19	0.93	1.6	37	0.25	5.4	1e+02	3.4e-07
393	☐ GO:0009109	P	21	coenzyme catabolic process	▨	▨	▨	🟧	0.39	34	1	-0.18	19	0.93	1.6	37	0.25	5.4	1e+02	3.4e-07
394	☐ GO:0006099	P	21	tricarboxylic acid cycle	▨	▨	▨	🟧	0.39	34	1	-0.18	19	0.93	1.6	37	0.25	5.4	1e+02	3.4e-07
395	☐ GO:0006084	P	21	acetyl-CoA metabolic process	▨	▨	▨	🟧	0.39	34	1	-0.18	19	0.93	1.6	37	0.25	5.4	1e+02	3.4e-07
396	☐ GO:0015995	P	11	chlorophyll biosynthetic process	▨	▨	▨	🟧	-0.36	12	1	-0.37	0.44	0.93	-0.86	12	0.63	5.3	1.3e+02	8.5e-07
397	☐ GO:0015994	P	11	chlorophyll metabolic process	▨	▨	▨	🟧	-0.36	12	1	-0.37	0.44	0.93	-0.86	12	0.63	5.3	1.3e+02	8.5e-07
398	☐ GO:0051187	P	23	cofactor catabolic process	▨	▨	▨	🟧	0.35	33	1	-0.22	17	0.93	1.4	35	0.34	5.2	98	1.1e-06
399	☐ GO:0009060	P	25	aerobic respiration	▨	▨	▨	🟧	0.57	38	1	-0.25	17	0.93	2.3	42	0.06	4.9	91	6.2e-06
400	☐ GO:0045333	P	43	cellular respiration	▨	▨	▨	🟧	0.68	36	1	-0.38	14	0.93	2.2	36	0.089	4.1	67	0.00018
401	☐ GO:0033014	P	40	tetrapyrrole biosynthetic process	▨	▨	▨	🟨	-0.68	12	1	-0.69	1.1	0.93	-1.4	13	0.33	3.9	67	0.00038
402	☐ GO:0033013	P	42	tetrapyrrole metabolic process	▨	▨	▨	🟨	-0.68	12	1	-0.7	1	0.93	-1.5	13	0.3	3.9	65	0.00054
403	☐ GO:0016137	P	37	glycoside metabolic process	▨	▨	▨	🟨	-0.15	22	1	-0.51	7.5	0.93	0.17	24	0.94	3.4	63	0.0029
404	☐ GO:0005984	P	37	disaccharide metabolic process	▨	▨	▨	🟨	-0.15	22	1	-0.51	7.5	0.93	0.17	24	0.94	3.4	63	0.0029
405	☐ GO:0051186	P	211	cofactor metabolic process	▨	▨	▨	🟨	-0.17	23	1	-1.3	5.5	0.93	-1.4	19	0.33	3.3	40	0.0046
406	☐ GO:0009311	P	39	oligosaccharide metabolic process	▨	▨	▨	🟨	-0.17	21	1	-0.53	7.2	0.93	0.14	24	0.95	3.3	60	0.0049
407	☐ GO:0015980	P	65	energy derivation by oxidation of organic compounds	▨	▨	▨	🟨	0.21	27	1	0.04	31	0.98	2	33	0.13	3.2	52	0.0053
408	☐ GO:0006779	P	32	porphyrin biosynthetic process	▨	▨	▨	🟨	-0.6	12	1	-0.62	0.96	0.93	-1.3	13	0.4	3.2	63	0.0063
409	☐ GO:0000096	P	23	sulfur amino acid metabolic process	▨	▨	▨	🟨	1.1	52	1	-0.48	3.2	0.93	2.1	41	0.096	3.2	70	0.0064

410	☐ GO:0006778	P	34	porphyrin metabolic process	▨	▨	▨	🟨	-0.6	13	1	-0.64	0.95	0.93	-1.4	13	0.36	3.1	61	0.0082
411	☐ GO:0022900	P	35	electron transport chain	▨	▨	▨	🟨	0.54	35	1	-0.48	8.1	0.93	0.35	25	0.87	3.1	60	0.0087
412	☐ GO:0046148	P	32	pigment biosynthetic process	▨	▨	▨	🟨	-0.36	17	1	0.037	31	0.98	-0.51	19	0.8	2.9	60	0.014
413	☐ GO:0042440	P	34	pigment metabolic process	▨	▨	▨	🟨	-0.36	17	1	-0.0018	29	1	-0.6	18	0.77	2.8	58	0.018
414	☐ GO:0046394	P	219	carboxylic acid biosynthetic process	▨	▨	▨	🟨	2.4	43	0.19	-0.059	28	0.98	2.1	29	0.096	2.8	38	0.019
415	☐ GO:0016053	P	219	organic acid biosynthetic process	▨	▨	▨	🟨	2.4	43	0.19	-0.059	28	0.98	2.1	29	0.096	2.8	38	0.019
416	☐ GO:0018130	P	100	heterocycle biosynthetic process	▨	▨	▨	🟨	-0.56	18	1	0.48	42	0.93	-0.16	22	0.94	2.8	44	0.02
417	☐ GO:0006732	P	108	coenzyme metabolic process	▨	▨	▨	🟨	0.17	26	1	-0.87	7.4	0.93	0.49	25	0.8	2.8	43	0.022
418	☐ GO:0009084	P	29	glutamine family amino acid biosynthetic process	▨	▨	▨	🟨	-0.033	24	1	-0.46	6.9	0.93	1.2	32	0.45	2.7	59	0.026
419	☐ GO:0055085	P	595	transmembrane transport	▨	▨	▨	🟨	-0.3	23	1	-1.2	16	0.93	-0.66	22	0.73	2.6	32	0.031
420	☐ GO:0006730	P	47	one-carbon metabolic process	▨	▨	▨	🟨	0.74	37	1	-0.49	11	0.93	2.2	36	0.086	2.6	50	0.033
421	☐ GO:0009069	P	32	serine family amino acid metabolic process	▨	▨	▨	🟨	0.34	31	1	-0.16	22	0.94	0.92	29	0.59	2.6	56	0.033
422	☐ GO:0000097	P	20	sulfur amino acid biosynthetic process	▨	▨	▨	🟨	1.1	52	1	-0.45	2.9	0.93	1.6	38	0.25	2.6	63	0.037
423	☐ GO:0006541	P	21	glutamine metabolic process	▨	▨	▨	🟨	0.14	28	1	-0.31	12	0.93	0.79	30	0.66	2.6	62	0.037
424	☐ GO:0006544	P	14	glycine metabolic process	▨	▨	▨	🟨	-0.063	23	1	-0.35	5.2	0.93	1.6	40	0.26	2.5	69	0.048
425	☐ GO:0016829	F	229	lyase activity	▨	▨	▨	🟥	1.6	37	1	3.1	82	0.052	2.3	29	0.12	9.1	66	0
426	☐ GO:0004618	F	10	phosphoglycerate kinase activity	▨	▨	▨	🟥	0.25	33	1	-0.32	2.6	0.93	1	36	0.65	6.5	1.6e+02	1.8e-09
427	☐ GO:0048037	F	434	cofactor binding	▨	▨	▨	🟥	1.3	32	1	-0.24	26	0.93	1.9	27	0.23	6.5	46	1.8e-09
428	☐ GO:0004470	F	11	malic enzyme activity	▨	▨	▨	🟥	0.52	42	1	-0.067	24	0.98	1.9	46	0.26	6.2	1.5e+02	1.2e-08
429	☐ GO:0051537	F	23	2 iron, 2 sulfur cluster binding	▨	▨	▨	🟧	0.18	29	1	-0.38	8.8	0.93	-1	14	0.65	5.9	1.1e+02	8e-08
430	☐ GO:0016491	F	1202	oxidoreductase activity	▨	▨	▨	🟧	2.2	32	0.39	0.47	33	0.93	-1.8	21	0.27	5.8	36	9.9e-08
431	☐ GO:0050662	F	320	coenzyme binding	▨	▨	▨	🟧	1.1	32	1	-0.49	22	0.93	0.94	25	0.69	5.5	46	4.4e-07
432	☐ GO:0016616	F	184	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	▨	▨	▨	🟧	0.75	31	1	0.17	33	0.94	1.7	28	0.32	4.7	48	4e-05
433	☐ GO:0016836	F	54	hydro-lyase activity	▨	▨	▨	🟧	0.14	27	1	-0.43	14	0.93	1.4	30	0.49	4.6	67	6.1e-05
434	☐ GO:0008324	F	447	cation transmembrane transporter activity	▨	▨	▨	🟧	0.64	28	1	-1.3	13	0.93	1.8	26	0.27	4.4	39	0.00011
435	☐ GO:0016614	F	202	oxidoreductase activity, acting on CH-OH group of donors	▨	▨	▨	🟧	0.59	29	1	0.28	34	0.93	1.2	26	0.56	4.3	45	0.00023
436	☐ GO:0016165	F	11	lipoxygenase activity	▨	▨	▨	🟧	2	94	0.59	-0.37	0.35	0.93	1.7	43	0.36	4.3	1.1e+02	0.00024
437	☐ GO:0005215	F	1049	transporter activity	▨	▨	▨	🟧	0.41	26	1	-0.88	22	0.93	0.79	24	0.73	4	33	0.00072
438	☐ GO:0051540	F	95	metal cluster binding	▨	▨	▨	🟧	1	36	1	-0.82	7.4	0.93	0.5	25	0.85	3.9	52	0.00094
439	☐ GO:0051536	F	95	iron-sulfur cluster binding	▨	▨	▨	🟧	1	36	1	-0.82	7.4	0.93	0.5	25	0.85	3.9	52	0.00094
440	☐ GO:0015075	F	575	ion transmembrane transporter activity	▨	▨	▨	🟧	0.56	27	1	-1.2	17	0.93	1.6	26	0.36	3.7	35	0.0017
441	☐ GO:0016774	F	28	phosphotransferase activity, carboxyl group as acceptor	▨	▨	▨	🟧	-0.27	19	1	-0.54	2.9	0.93	0.87	30	0.71	3.5	70	0.0042
442	☐ GO:0022891	F	659	substrate-specific transmembrane transporter activity	▨	▨	▨	🟨	0.51	27	1	-0.73	22	0.93	1.2	25	0.56	3.3	34	0.0073
443	☐ GO:0022892	F	737	substrate-specific transporter activity	▨	▨	▨	🟨	0.48	27	1	-0.91	21	0.93	1.5	25	0.45	3.3	33	0.0073
444	☐ GO:0016681	F	15	oxidoreductase activity, acting on diphenols and related substances as donors, cytochrome as acceptor	▨	▨	▨	🟨	0.15	29	1	-0.16	18	0.94	0.057	23	0.99	3.2	81	0.0099
445	☐ GO:0008121	F	15	ubiquinol-cytochrome-c reductase activity	▨	▨	▨	🟨	0.15	29	1	-0.16	18	0.94	0.057	23	0.99	3.2	81	0.0099
446	☐ GO:0022857	F	731	transmembrane transporter activity	▨	▨	▨	🟨	0.47	26	1	-0.78	22	0.93	0.78	24	0.73	3.1	33	0.016
447	☐ GO:0003918	F	34	DNA topoisomerase (ATP-hydrolyzing) activity	▨	▨	▨	🟨	-0.034	24	1	-0.53	5.8	0.93	1.1	30	0.6	3	60	0.018
448	☐ GO:0016776	F	25	phosphotransferase activity, phosphate group as acceptor	▨	▨	▨	🟨	0.095	27	1	-0.27	15	0.93	0.73	29	0.76	3	65	0.018
449	☐ GO:0016676	F	11	oxidoreductase activity, acting on heme group of donors, oxygen as acceptor	▨	▨	▨	🟨	0.95	57	1	0.24	48	0.93	2.5	54	0.073	3	86	0.018
450	☐ GO:0016675	F	11	oxidoreductase activity, acting on heme group of donors	▨	▨	▨	🟨	0.95	57	1	0.24	48	0.93	2.5	54	0.073	3	86	0.018
451	☐ GO:0015002	F	11	heme-copper terminal oxidase activity	▨	▨	▨	🟨	0.95	57	1	0.24	48	0.93	2.5	54	0.073	3	86	0.018
452	☐ GO:0004129	F	11	cytochrome-c oxidase activity	▨	▨	▨	🟨	0.95	57	1	0.24	48	0.93	2.5	54	0.073	3	86	0.018
453	☐ GO:0051213	F	22	dioxygenase activity	▨	▨	▨	🟨	1.5	60	1	-0.47	3.2	0.93	1.2	34	0.55	3	67	0.02
454	☐ GO:0003824	F	6876	catalytic activity	▨	▨	▨	🟨	0.85	26	1	1.2	33	0.93	-0.68	22	0.78	2.9	27	0.02
455	☐ GO:0016702	F	20	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	▨	▨	▨	🟨	1.4	61	1	-0.45	3.4	0.93	1	32	0.64	2.9	69	0.023
456	☐ GO:0016701	F	27	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	▨	▨	▨	🟨	1.2	51	1	-0.45	7	0.93	0.35	26	0.92	2.8	61	0.033
457	☐ GO:0009521	C	33	photosystem	▨	▨	▨	🟥	-0.32	18	1	-0.63	0.62	0.87	-2.8	2.3	0.014	25	3.2e+02	0
458	☐ GO:0009579	C	45	thylakoid	▨	▨	▨	🟥	-0.43	17	1	-0.74	0.53	0.87	-2.8	5.4	0.015	24	2.7e+02	0
459	☐ GO:0034357	C	44	photosynthetic membrane	▨	▨	▨	🟥	-0.4	18	1	-0.73	0.54	0.87	-2.8	5.5	0.017	24	2.7e+02	0
460	☐ GO:0009522	C	14	photosystem I	▨	▨	▨	🟥	-0.058	23	1	-0.42	0.36	0.87	-2	1.1	0.1	21	4.1e+02	0
461	☐ GO:0044436	C	28	thylakoid part	▨	▨	▨	🟥	-0.46	15	1	-0.59	0.37	0.87	-1.9	8	0.12	17	2.4e+02	0
462	☐ GO:0009523	C	18	photosystem II	▨	▨	▨	🟥	-0.34	15	1	-0.46	0.85	0.87	-2	3.3	0.099	15	2.6e+02	0
463	☐ GO:0009654	C	14	oxygen evolving complex	▨	▨	▨	🟥	-0.35	14	1	-0.42	0.47	0.87	-1.7	4	0.17	14	2.8e+02	0
464	☐ GO:0019898	C	12	extrinsic to membrane	▨	▨	▨	🟥	-0.29	15	1	-0.39	0.13	0.87	-1.4	6.1	0.28	13	2.7e+02	0
465	☐ GO:0042651	C	14	thylakoid membrane	▨	▨	▨	🟥	-0.26	16	1	-0.42	0.28	0.87	-0.97	12	0.46	11	2.3e+02	0
466	☐ GO:0045263	C	10	proton-transporting ATP synthase complex, coupling factor F(o)	▨	▨	▨	🟥	1.3	72	1	-0.3	4.7	0.88	2	49	0.093	8.4	2e+02	0
467	☐ GO:0044425	C	1181	membrane part	▨	▨	▨	🟥	0.94	28	1	-0.63	25	0.87	1.8	25	0.15	7.3	39	1.8e-12
468	☐ GO:0031090	C	213	organelle membrane	▨	▨	▨	🟧	0.14	26	1	-0.87	14	0.87	2.3	29	0.051	4.6	46	1.5e-05

469	☐ GO:0016020	C	2254	membrane	▨	▨	▨	🟧	0.6	26	1	-1.2	23	0.87	-0.53	22	0.66	3.6	30	0.0014
470	☐ GO:0009536	C	33	plastid	▨	▨	▨	🟨	-0.63	12	1	-0.61	1.5	0.87	-2	8.2	0.097	2.5	55	0.04