

id	source	term_id	term_name	term_size	intersection_size	p_value
1	GO:MF	GO:0004866	endopeptidase inhibitor activity	69	15	2.0e-06
2	GO:MF	GO:0061135	endopeptidase regulator activity	70	15	2.0e-06
3	GO:MF	GO:0061134	peptidase regulator activity	71	15	2.0e-06
4	GO:MF	GO:0030414	peptidase inhibitor activity	69	15	2.0e-06
5	GO:BP	GO:0009611	response to wounding	48	12	4.0e-05
6	GO:BP	GO:0120254	olefinic compound metabolic process	25	9	4.0e-05
7	KEGG	KEGG:01110	Biosynthesis of secondary metabolites	729	54	6.8e-05
8	GO:BP	GO:0019752	carboxylic acid metabolic process	772	54	1.1e-04
9	GO:BP	GO:0043436	oxoacid metabolic process	792	54	1.2e-04
10	GO:BP	GO:0006082	organic acid metabolic process	793	54	1.2e-04
11	GO:BP	GO:0120255	olefinic compound biosynthetic process	23	8	1.2e-04
12	GO:BP	GO:0006629	lipid metabolic process	815	55	1.2e-04
13	GO:BP	GO:0044550	secondary metabolite biosynthetic process	52	11	1.5e-04
14	GO:BP	GO:0009063	amino acid catabolic process	64	12	1.7e-04
15	GO:BP	GO:0009072	aromatic amino acid metabolic process	67	12	2.5e-04
16	KEGG	KEGG:01100	Metabolic pathways	1235	74	2.9e-04
17	GO:BP	GO:0031407	oxylipin metabolic process	21	7	3.6e-04
18	GO:BP	GO:0031408	oxylipin biosynthetic process	21	7	3.6e-04
19	GO:BP	GO:0008295	spermidine biosynthetic process	9	5	4.1e-04
20	GO:BP	GO:0008216	spermidine metabolic process	9	5	4.1e-04
21	GO:BP	GO:0046395	carboxylic acid catabolic process	99	14	4.3e-04
22	GO:BP	GO:0016054	organic acid catabolic process	99	14	4.3e-04
23	GO:MF	GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	70	12	4.6e-04
24	GO:MF	GO:0043565	sequence-specific DNA binding	687	47	5.2e-04
25	GO:BP	GO:0006520	amino acid metabolic process	352	29	6.5e-04
26	GO:BP	GO:0032787	monocarboxylic acid metabolic process	353	29	6.5e-04
27	GO:MF	GO:0051213	dioxygenase activity	145	17	8.1e-04
28	GO:BP	GO:0044255	cellular lipid metabolic process	598	41	8.1e-04
29	GO:BP	GO:1901605	alpha-amino acid metabolic process	215	21	8.1e-04
30	GO:BP	GO:1902221	erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process	18	6	9.9e-04
31	GO:BP	GO:0006558	L-phenylalanine metabolic process	18	6	9.9e-04
32	GO:BP	GO:0009699	phenylpropanoid biosynthetic process	46	9	9.9e-04
33	GO:BP	GO:1901606	alpha-amino acid catabolic process	59	10	1.2e-03
34	GO:BP	GO:0006559	L-phenylalanine catabolic process	12	5	1.2e-03
35	GO:BP	GO:0072330	monocarboxylic acid biosynthetic process	142	16	1.2e-03
36	GO:BP	GO:0006596	polyamine biosynthetic process	19	6	1.2e-03
37	GO:BP	GO:1902222	erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process	12	5	1.2e-03
38	GO:BP	GO:0016053	organic acid biosynthetic process	337	27	1.2e-03
39	GO:BP	GO:0046394	carboxylic acid biosynthetic process	337	27	1.2e-03
40	GO:MF	GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	56	10	1.3e-03
41	GO:BP	GO:0008610	lipid biosynthetic process	436	32	1.3e-03
42	GO:MF	GO:0043169	cation binding	2414	119	1.3e-03
43	GO:BP	GO:0009803	cinnamic acid metabolic process	3	3	1.4e-03
44	GO:BP	GO:0009800	cinnamic acid biosynthetic process	3	3	1.4e-03
45	KEGG	KEGG:00941	Flavonoid biosynthesis	34	8	1.4e-03
46	GO:BP	GO:0010112	regulation of systemic acquired resistance	7	4	1.4e-03
47	GO:MF	GO:0046872	metal ion binding	2376	117	1.5e-03
48	GO:BP	GO:0016036	cellular response to phosphate starvation	13	5	1.5e-03
49	GO:BP	GO:1901362	organic cyclic compound biosynthetic process	2291	110	1.8e-03
50	GO:MF	GO:0004867	serine-type endopeptidase inhibitor activity	38	8	1.9e-03
51	GO:BP	GO:0009813	flavonoid biosynthetic process	14	5	2.1e-03
52	GO:BP	GO:0006595	polyamine metabolic process	23	6	2.8e-03
53	GO:BP	GO:0006355	regulation of DNA-templated transcription	1589	81	2.8e-03
54	GO:BP	GO:0009812	flavonoid metabolic process	15	5	2.8e-03
55	GO:BP	GO:2001141	regulation of RNA biosynthetic process	1589	81	2.8e-03
56	GO:BP	GO:0044282	small molecule catabolic process	130	14	3.6e-03
57	GO:MF	GO:0003993	acid phosphatase activity	32	7	3.8e-03
58	GO:MF	GO:0003700	DNA-binding transcription factor activity	1013	58	3.8e-03
59	GO:BP	GO:0009309	amine biosynthetic process	36	7	4.4e-03
60	GO:BP	GO:0019438	aromatic compound biosynthetic process	2201	104	4.4e-03
61	GO:BP	GO:0051252	regulation of RNA metabolic process	1639	82	4.4e-03
62	GO:BP	GO:0042401	biogenic amine biosynthetic process	36	7	4.4e-03
63	GO:BP	GO:0006576	biogenic amine metabolic process	48	8	4.6e-03
64	GO:MF	GO:0045548	phenylalanine ammonia-lyase activity	4	3	6.3e-03
65	GO:BP	GO:0009074	aromatic amino acid family catabolic process	19	5	8.3e-03
66	GO:BP	GO:0009308	amine metabolic process	80	10	8.4e-03
67	GO:BP	GO:0031667	response to nutrient levels	54	8	1.0e-02
68	GO:BP	GO:0019219	regulation of nucleobase-containing compound metabolic process	1692	82	1.0e-02
69	GO:BP	GO:0019748	secondary metabolic process	100	11	1.3e-02
70	GO:BP	GO:0009065	glutamine family amino acid catabolic process	13	4	1.5e-02
71	GO:BP	GO:0009698	phenylpropanoid metabolic process	72	9	1.5e-02
72	GO:BP	GO:0009627	systemic acquired resistance	22	5	1.5e-02
73	GO:BP	GO:0006714	sesquiterpenoid metabolic process	13	4	1.5e-02
74	GO:BP	GO:0032774	RNA biosynthetic process	1817	86	1.5e-02
75	GO:BP	GO:0006869	lipid transport	103	11	1.5e-02
76	GO:BP	GO:0031347	regulation of defense response	59	8	1.5e-02
77	GO:BP	GO:0009991	response to extracellular stimulus	59	8	1.5e-02
78	GO:BP	GO:0006950	response to stress	1546	75	1.5e-02
79	GO:BP	GO:0009267	cellular response to starvation	34	6	1.6e-02
80	GO:BP	GO:0044283	small molecule biosynthetic process	437	28	1.7e-02
81	GO:BP	GO:0006351	DNA-templated transcription	1810	85	1.7e-02
82	GO:BP	GO:0044281	small molecule metabolic process	1254	63	1.7e-02
83	GO:BP	GO:0009889	regulation of biosynthetic process	1942	90	1.8e-02
84	GO:BP	GO:0018130	heterocycle biosynthetic process	2181	99	1.9e-02
85	GO:MF	GO:0031072	heat shock protein binding	31	6	2.1e-02
86	GO:BP	GO:0030258	lipid modification	78	9	2.1e-02
87	GO:BP	GO:0010468	regulation of gene expression	1907	88	2.2e-02
88	GO:BP	GO:0031326	regulation of cellular biosynthetic process	1937	89	2.3e-02
89	GO:BP	GO:0042594	response to starvation	37	6	2.3e-02
90	GO:BP	GO:0010556	regulation of macromolecule biosynthetic process	1917	88	2.5e-02
91	GO:BP	GO:0034440	lipid oxidation	51	7	2.5e-02
92	GO:BP	GO:0031669	cellular response to nutrient levels	38	6	2.5e-02
93	GO:BP	GO:1902074	response to salt	98	10	2.7e-02
94	GO:BP	GO:0002831	regulation of response to biotic stimulus	39	6	2.8e-02
95	GO:MF	GO:0003824	catalytic activity	8848	342	2.8e-02
96	GO:MF	GO:0016841	ammonia-lyase activity	14	4	2.9e-02
97	GO:MF	GO:0102128	chalcone synthase activity	2	2	2.9e-02
98	GO:MF	GO:0140110	transcription regulator activity	1139	59	2.9e-02
99	GO:MF	GO:0016210	naringenin-chalcone synthase activity	2	2	2.9e-02
100	GO:MF	GO:0046510	UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity	2	2	2.9e-02
101	GO:MF	GO:0008970	phospholipase A1 activity	14	4	2.9e-02
102	GO:MF	GO:0008792	arginine decarboxylase activity	2	2	2.9e-02
103	GO:BP	GO:0010876	lipid localization	117	11	3.1e-02
104	GO:BP	GO:0051171	regulation of nitrogen compound metabolic process	1937	88	3.1e-02
105	GO:BP	GO:0009605	response to external stimulus	506	30	3.1e-02
106	GO:BP	GO:0070542	response to fatty acid	54	7	3.2e-02
107	KEGG	KEGG:00592	alpha-Linolenic acid metabolism	22	5	3.4e-02
108	GO:BP	GO:0034605	cellular response to heat	41	6	3.4e-02
109	GO:MF	GO:0005506	iron ion binding	402	26	3.7e-02
110	GO:BP	GO:0043288	apocarotenoid metabolic process	9	3	3.7e-02
111	GO:BP	GO:0015996	chlorophyll catabolic process	9	3	3.7e-02
112	GO:BP	GO:0080090	regulation of primary metabolic process	1955	88	3.7e-02
113	GO:BP	GO:0009687	abscisic acid metabolic process	9	3	3.7e-02
114	GO:BP	GO:0046149	pigment catabolic process	9	3	3.7e-02
115	GO:BP	GO:1902644	tertiary alcohol metabolic process	9	3	3.7e-02
116	GO:BP	GO:0065007	biological regulation	3308	138	3.9e-02
117	GO:BP	GO:0032101	regulation of response to external stimulus	43	6	3.9e-02
118	GO:BP	GO:0031668	cellular response to extracellular stimulus	43	6	3.9e-02
119	GO:BP	GO:0071496	cellular response to external stimulus	43	6	3.9e-02
120	GO:BP	GO:0009620	response to fungus	106	10	4.0e-02
121	GO:BP	GO:0030639	polyketide biosynthetic process	3	2	4.0e-02
122	GO:BP	GO:0030638	polyketide metabolic process	3	2	4.0e-02
123	GO:BP	GO:0009064	glutamine family amino acid metabolic process	58	7	4.0e-02
124	GO:BP	GO:0034214	protein hexamerization	3	2	4.0e-02
125	GO:BP	GO:0009408	response to heat	90	9	4.0e-02
126	GO:BP	GO:0120252	hydrocarbon metabolic process	31	5	4.2e-02
127	GO:MF	GO:0004857	enzyme inhibitor activity	205	16	4.3e-02
128	GO:MF	GO:0140678	molecular function inhibitor activity	206	16	4.3e-02
129	GO:MF	GO:0000981	DNA-binding transcription factor activity, RNA polymerase II-specific	150	13	4.3e-02
130	GO:BP	GO:0016106	sesquiterpenoid biosynthetic process	10	3	4.5e-02
131	GO:BP	GO:0006631	fatty acid metabolic process	224	16	4.7e-02
132	GO:BP	GO:0009414	response to water deprivation	76	8	4.7e-02
133	KEGG	KEGG:00330	Arginine and proline metabolism	37	6	5.0e-02
134	KEGG	KEGG:00906	Carotenoid biosynthesis	17	4	5.0e-02
135	KEGG	KEGG:00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	27	5	5.0e-02