

id	source	term_id	term_name	term_size	intersection_size	p_value
1	GO:BP	GO:0048731	system development	1540	78	8.3e−08
2	GO:BP	GO:0048468	cell development	1458	75	1.1e−07
3	GO:BP	GO:0048856	anatomical structure development	2846	117	2.1e−07
4	GO:BP	GO:0007275	multicellular organism development	2416	103	6.9e−07
5	GO:BP	GO:0032502	developmental process	3018	120	9.2e−07
6	GO:BP	GO:0071840	cellular component organization or biogenesis	3354	129	1.2e−06
7	GO:BP	GO:0030154	cell differentiation	1784	83	1.2e−06
8	GO:BP	GO:0016043	cellular component organization	3173	123	2.5e−06
9	GO:BP	GO:0048869	cellular developmental process	1817	83	2.9e−06
10	GO:BP	GO:0009987	cellular process	8358	243	1.8e−05
11	GO:BP	GO:0007399	nervous system development	1195	60	3.3e−05
12	GO:BP	GO:0048523	negative regulation of cellular process	1334	64	5.8e−05
13	GO:BP	GO:0048477	oogenesis	588	37	1.0e−04
14	GO:BP	GO:0007281	germ cell development	724	42	1.3e−04
15	GO:BP	GO:0022412	cellular process involved in reproduction in multicellular organism	894	48	1.5e−04
16	GO:BP	GO:0032501	multicellular organismal process	3840	135	1.6e−04
17	GO:BP	GO:0048513	animal organ development	1256	60	2.0e−04
18	GO:BP	GO:0007292	female gamete generation	636	38	2.6e−04
19	GO:BP	GO:0009653	anatomical structure morphogenesis	1585	70	3.1e−04
20	GO:BP	GO:0000902	cell morphogenesis	574	35	5.0e−04
21	GO:BP	GO:0040007	growth	451	30	5.9e−04
22	GO:BP	GO:0022414	reproductive process	1272	59	7.0e−04
23	GO:BP	GO:0000904	cell morphogenesis involved in differentiation	488	31	1.0e−03
24	GO:BP	GO:0007276	gamete generation	928	47	1.1e−03
25	GO:BP	GO:0051128	regulation of cellular component organization	762	41	1.3e−03
26	GO:BP	GO:0016477	cell migration	326	24	1.5e−03
27	GO:BP	GO:0003006	developmental process involved in reproduction	943	47	1.7e−03
28	GO:BP	GO:0009888	tissue development	687	38	1.7e−03
29	GO:BP	GO:0048609	multicellular organismal reproductive process	956	47	2.5e−03
30	GO:BP	GO:0048666	neuron development	645	36	2.8e−03
31	GO:BP	GO:0048519	negative regulation of biological process	1682	70	2.9e−03
32	GO:BP	GO:0048699	generation of neurons	904	45	3.1e−03
33	GO:BP	GO:0050794	regulation of cellular process	3993	134	3.5e−03
34	GO:BP	GO:0022008	neurogenesis	972	47	4.0e−03
35	GO:BP	GO:0030182	neuron differentiation	830	42	4.6e−03
36	GO:BP	GO:0007154	cell communication	2114	82	5.0e−03
37	GO:BP	GO:0060429	epithelium development	581	33	5.2e−03
38	GO:BP	GO:0035239	tube morphogenesis	174	16	5.7e−03
39	GO:BP	GO:0048589	developmental growth	377	25	5.8e−03
40	GO:BP	GO:0010256	endomembrane system organization	220	18	7.6e−03
41	GO:BP	GO:0023051	regulation of signaling	966	46	7.7e−03
42	GO:BP	GO:0050896	response to stimulus	3256	113	8.3e−03
43	GO:BP	GO:0010646	regulation of cell communication	970	46	8.6e−03
44	GO:BP	GO:0000003	reproduction	1507	63	9.2e−03
45	GO:BP	GO:0072499	photoreceptor cell axon guidance	32	7	1.0e−02
46	GO:BP	GO:0009966	regulation of signal transduction	834	41	1.2e−02
47	GO:BP	GO:0065007	biological regulation	4751	151	1.2e−02
48	GO:BP	GO:0050789	regulation of biological process	4473	144	1.2e−02
49	GO:BP	GO:0044085	cellular component biogenesis	1658	67	1.4e−02
50	GO:BP	GO:0048870	cell motility	397	25	1.4e−02
51	GO:BP	GO:0006897	endocytosis	256	19	1.7e−02
52	GO:BP	GO:0022607	cellular component assembly	1441	60	1.8e−02
53	GO:BP	GO:0065008	regulation of biological quality	1030	47	1.9e−02
54	GO:BP	GO:0023057	negative regulation of signaling	404	25	1.9e−02
55	GO:BP	GO:0001654	eye development	405	25	2.0e−02
56	GO:BP	GO:0048880	sensory system development	405	25	2.0e−02
57	GO:BP	GO:0150063	visual system development	405	25	2.0e−02
58	GO:BP	GO:0010648	negative regulation of cell communication	406	25	2.1e−02
59	GO:BP	GO:0009968	negative regulation of signal transduction	383	24	2.3e−02
60	GO:BP	GO:0048522	positive regulation of cellular process	1688	67	2.5e−02
61	GO:BP	GO:0050808	synapse organization	312	21	2.7e−02
62	GO:BP	GO:0007423	sensory organ development	493	28	2.9e−02
63	GO:BP	GO:0032504	multicellular organism reproduction	1334	56	2.9e−02
64	GO:BP	GO:0048518	positive regulation of biological process	1936	74	3.0e−02
65	GO:BP	GO:0002064	epithelial cell development	290	20	3.0e−02
66	GO:BP	GO:0035295	tube development	247	18	3.7e−02
67	GO:BP	GO:0050793	regulation of developmental process	697	35	3.7e−02
68	GO:BP	GO:0040011	locomotion	474	27	3.8e−02
69	GO:BP	GO:0022604	regulation of cell morphogenesis	84	10	3.8e−02
70	GO:BP	GO:0019953	sexual reproduction	1219	52	4.0e−02
71	GO:BP	GO:0097435	supramolecular fiber organization	296	20	4.0e−02
72	GO:BP	GO:0048667	cell morphogenesis involved in neuron differentiation	449	26	4.1e−02
73	GO:BP	GO:0051641	cellular localization	1287	54	4.3e−02
74	GO:BP	GO:0023052	signaling	2063	77	4.5e−02
75	GO:BP	GO:0007010	cytoskeleton organization	703	35	4.5e−02
76	GO:BP	GO:0048812	neuron projection morphogenesis	454	26	4.9e−02
77	GO:CC	GO:0005737	cytoplasm	5092	168	3.9e−06
78	GO:CC	GO:0005622	intracellular anatomical structure	7264	217	7.3e−06
79	GO:CC	GO:0045177	apical part of cell	195	19	4.1e−05
80	GO:CC	GO:0043228	non−membrane−bounded organelle	1944	79	1.2e−04
81	GO:CC	GO:0043232	intracellular non−membrane−bounded organelle	1944	79	1.2e−04
82	GO:CC	GO:0030054	cell junction	609	34	6.6e−04
83	GO:CC	GO:0110165	cellular anatomical entity	10613	276	7.9e−04
84	GO:CC	GO:0005829	cytosol	1123	48	9.3e−03
85	GO:CC	GO:0043226	organelle	6327	184	9.9e−03
86	GO:CC	GO:0043229	intracellular organelle	6225	181	1.3e−02
87	GO:CC	GO:0098793	presynapse	244	17	1.5e−02
88	GO:CC	GO:0045172	germline ring canal	23	5	3.5e−02
89	GO:CC	GO:0045202	synapse	448	24	3.7e−02
90	GO:CC	GO:0101031	protein folding chaperone complex	13	4	3.8e−02
91	GO:CC	GO:0035324	female germline ring canal	13	4	3.8e−02
92	GO:CC	GO:0005700	polytene chromosome	239	16	3.9e−02
93	GO:CC	GO:0031594	neuromuscular junction	107	10	4.6e−02
94	GO:CC	GO:0045169	fusome	38	6	5.0e−02
95	GO:MF	GO:0005488	binding	6906	223	2.8e−10
96	GO:MF	GO:0005515	protein binding	3672	137	3.2e−07
97	GO:MF	GO:0043167	ion binding	2891	105	5.5e−04
98	GO:MF	GO:1901363	heterocyclic compound binding	3135	107	8.1e−03
99	GO:MF	GO:0097159	organic cyclic compound binding	3160	107	1.2e−02
100	GO:MF	GO:0097367	carbohydrate derivative binding	1241	51	3.2e−02
101	GO:MF	GO:0005509	calcium ion binding	205	15	4.6e−02
102	GO:MF	GO:0035639	purine ribonucleoside triphosphate binding	1002	43	4.8e−02
103	MIRNA	MIRNA:dme−miR−318−3p	dme−miR−318−3p	1	1	5.0e−02
104	TF	TF:M12357	Factor: BEAF32; motif: NTATCGATAKTTNN	1085	44	3.7e−02
105	TF	TF:M07142	Factor: BEAF−32A; motif: NNNNMAMTATCGATA	1025	42	4.2e−02