



Supplement

**Main Article:** Agede OA, Wasagu IM, Fawibe AE, Salami AK. Identification of Molecular Markers Associated with COPD in Non-Smokers and Smokers: A Bioinformatics Analysis. Univ Louisville J Respir Infect. 2023 May 1;7(1):a5. doi: [10.55504/2473-2869.1261](https://doi.org/10.55504/2473-2869.1261).

**Supplemental Table 1.** Gene ontologies based on upregulated differentially expressed genes.

Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:MF	Protein binding	GO:0005515	9.04e-16	14,778
GO:MF	Binding	GO:0005488	4.59e-05	18,286
GO:MF	Ion binding	GO:0043167	0.003562	6,079
GO:MF	Cation binding	GO:0043169	0.006561	4,368
GO:MF	Catalytic activity	GO:0003824	0.011976	5,691
GO:MF	Metal ion binding	GO:0046872	0.018123	4,275
GO:MF	Identical protein binding	GO:0042802	0.021017	2,086
GO:MF	Pyrophosphatase activity	GO:0016462	0.028658	730
GO:MF	Hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	GO:0016818	0.029598	731
GO:MF	Hydrolase activity, acting on acid anhydrides	GO:0016817	0.029598	731
GO:MF	Enzyme binding	GO:0019899	0.031489	2,082
GO:BP	Cellular response to stress	GO:0033554	7.48e-12	1,941
GO:BP	Response to stress	GO:0006950	5.9e-11	3,980
GO:BP	Organonitrogen compound metabolic process	GO:1901564	9.55e-11	6,538
GO:BP	Cellular macromolecule metabolic process	GO:0044260	1.52e-10	3,263
GO:BP	Catabolic process	GO:0009056	5.69e-10	2,609
GO:BP	Cellular catabolic process	GO:0044248	6.31e-10	2,138
GO:BP	Protein metabolic process	GO:0019538	5.37e-08	5,482
GO:BP	Cellular metabolic process	GO:0044237	9.24e-07	12,122
GO:BP	Organic substance biosynthetic process	GO:1901576	1.95e-06	5,886
GO:BP	Cellular nitrogen compound biosynthetic process	GO:0044271	2.38e-06	4,890
GO:BP	Biosynthetic process	GO:0009058	3.1e-06	5,973
GO:BP	Cellular biosynthetic process	GO:0044249	3.12e-06	5,793
GO:BP	Macroautophagy	GO:0016236	8.28e-06	321
GO:BP	Autophagy	GO:0006914	2.09e-05	562
GO:BP	Process utilizing autophagic mechanism	GO:0061919	2.09e-05	562
GO:BP	Organic substance catabolic process	GO:1901575	2.5e-05	2,148
GO:BP	Macromolecule biosynthetic process	GO:0009059	0.000124	4,822
GO:BP	Metabolic process	GO:0008152	0.000189	14,417
GO:BP	Cellular response to DNA damage stimulus	GO:0006974	0.000304	881
GO:BP	Primary metabolic process	GO:0044238	0.000311	12,745
GO:BP	Cellular response to nutrient levels	GO:0031669	0.000313	230
GO:BP	Proteolysis involved in protein catabolic process	GO:0051603	0.000419	799
GO:BP	Macromolecule catabolic process	GO:0009057	0.000421	1,391
GO:BP	Response to nutrient levels	GO:0031667	0.000424	478
GO:BP	Negative regulation of cellular metabolic process	GO:0031324	0.000463	2,244

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Organic substance transport	GO:0071702	0.000508	2,680
GO:BP	Nitrogen compound transport	GO:0071705	0.000553	2,252
GO:BP	Intracellular transport	GO:0046907	0.000556	1,806
GO:BP	Response to extracellular stimulus	GO:0009991	0.000688	508
GO:BP	Modification-dependent protein catabolic process	GO:0019941	0.000709	701
GO:BP	Cellular response to extracellular stimulus	GO:0031668	0.00083	260
GO:BP	Macromolecule localization	GO:0033036	0.000846	3,177
GO:BP	Protein localization	GO:0008104	0.000894	2,708
GO:BP	Protein catabolic process	GO:0030163	0.000986	1,031
GO:BP	Organonitrogen compound biosynthetic process	GO:1901566	0.001024	1,805
GO:BP	Cellular macromolecule localization	GO:0070727	0.001091	2,718
GO:BP	Cellular localization	GO:0051641	0.001103	3,588
GO:BP	Modification-dependent macromolecule catabolic process	GO:0043632	0.00115	713
GO:BP	Nitrogen compound metabolic process	GO:0006807	0.001307	12,235
GO:BP	Negative regulation of nitrogen compound metabolic process	GO:0051172	0.001349	2,401
GO:BP	Autophagosome assembly	GO:0000045	0.002413	110
GO:BP	Regulation of binding	GO:0051098	0.002615	372
GO:BP	Regulation of cellular metabolic process	GO:0031323	0.002651	5,653
GO:BP	Ubiquitin-dependent protein catabolic process	GO:0006511	0.002797	691
GO:BP	Cell death	GO:0008219	0.002819	2,113
GO:BP	Proteasome-mediated ubiquitin-dependent protein catabolic process	GO:0043161	0.002941	455
GO:BP	Protein modification by small protein conjugation	GO:0032446	0.003371	903
GO:BP	Cellular macromolecule catabolic process	GO:0044265	0.004328	1,030
GO:BP	Programmed cell death	GO:0012501	0.004495	1,948
GO:BP	Establishment of protein localization	GO:0045184	0.004804	1,898
GO:BP	Autophagosome organization	GO:1905037	0.00533	117
GO:BP	Heterocycle biosynthetic process	GO:0018130	0.005494	4,150
GO:BP	Organonitrogen compound catabolic process	GO:1901565	0.005626	1,386
GO:BP	Negative regulation of nucleobase-containing compound metabolic process	GO:0045934	0.005627	1,565
GO:BP	Mitochondrial gene expression	GO:0140053	0.005894	165
GO:BP	Cellular response to external stimulus	GO:0071496	0.006025	328
GO:BP	Cellular response to chemical stress	GO:0062197	0.007564	332
GO:BP	Protein transport	GO:0015031	0.007842	1,788
GO:BP	Apoptotic process	GO:0006915	0.00786	1,894
GO:BP	Protein modification by small protein conjugation or removal	GO:0070647	0.008359	1,052
GO:BP	Aromatic compound biosynthetic process	GO:0019438	0.010066	4,161
GO:BP	Proteasomal protein catabolic process	GO:0010498	0.010866	526
GO:BP	Negative regulation of RNA metabolic process	GO:0051253	0.010953	1,438
GO:BP	Organic cyclic compound biosynthetic process	GO:1901362	0.015121	4,307
GO:BP	Nucleobase-containing compound biosynthetic process	GO:0034654	0.015332	4,072
GO:BP	Negative regulation of cellular biosynthetic process	GO:0031327	0.021266	1,596
GO:BP	Peptide biosynthetic process	GO:0043043	0.022328	772
GO:BP	Regulation of catabolic process	GO:0009894	0.024977	992
GO:BP	Cellular response to oxidative stress	GO:0034599	0.025031	275
GO:BP	Establishment of localization in cell	GO:0051649	0.029275	2,340
GO:BP	Negative regulation of macromolecule biosynthetic process	GO:0010558	0.033016	1,537
GO:BP	Amide biosynthetic process	GO:0043604	0.033975	905
GO:BP	Regulation of DNA binding	GO:0051101	0.037929	121
GO:BP	Regulation of molecular function	GO:0065009	0.038238	3,059

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Regulation of RNA metabolic process	GO:0051252	0.038347	3,783
GO:BP	Cellular macromolecule biosynthetic process	GO:0034645	0.038584	1,208
GO:BP	Macromolecule modification	GO:0043412	0.039457	3,873
GO:BP	Response to organic substance	GO:0010033	0.039596	2,664
GO:BP	Intracellular signal transduction	GO:0035556	0.041648	2,667
GO:BP	Establishment of protein localization to mitochondrion	GO:0072655	0.041673	122
GO:BP	Negative regulation of biosynthetic process	GO:0009890	0.041983	1,627
GO:BP	Mitochondrion organization	GO:0007005	0.044888	539
GO:BP	Cellular response to starvation	GO:0009267	0.047885	174
GO:BP	Regulation of nitrogen compound metabolic process	GO:0051171	0.048347	5,724
GO:CC	Cytoplasm	GO:0005737	1.18e−29	12,321
GO:CC	Nucleoplasm	GO:0005654	1.79e−25	4,203
GO:CC	Organelle lumen	GO:0043233	1.67e−22	6,627
GO:CC	Intracellular organelle lumen	GO:0070013	1.67e−22	6,627
GO:CC	Membrane-enclosed lumen	GO:0031974	1.67e−22	6,627
GO:CC	Cytosol	GO:0005829	8.82e−19	5,440
GO:CC	Membrane-bounded organelle	GO:0043227	2.68e−17	15,667
GO:CC	Intracellular membrane-bounded organelle	GO:0043231	4.24e−17	14,610
GO:CC	Nuclear lumen	GO:0031981	7.72e−16	5,495
GO:CC	Organelle	GO:0043226	1.33e−13	16,765
GO:CC	Intracellular anatomical structure	GO:0005622	1.36e−13	17,853
GO:CC	Intracellular organelle	GO:0043229	1.73e−12	15,991
GO:CC	Mitochondrion	GO:0005739	6.31e−12	1,693
GO:CC	Intracellular protein-containing complex	GO:0140535	2.1e−10	942
GO:CC	Catalytic complex	GO:1902494	3.71e−10	1,778
GO:CC	Spliceosomal complex	GO:0005681	3.66e−09	196
GO:CC	Nuclear body	GO:0016604	4.57e−06	882
GO:CC	Precatalytic spliceosome	GO:0071011	1.36e−05	52
GO:CC	Transferase complex	GO:1990234	2.47e−05	880
GO:CC	Organelle membrane	GO:0031090	2.48e−05	3,681
GO:CC	Autophagosome	GO:0005776	2.56e−05	115
GO:CC	U2-type spliceosomal complex	GO:0005684	4e−05	92
GO:CC	Vacuole	GO:0005773	0.000106	851
GO:CC	Mitochondrial matrix	GO:0005759	0.000141	489
GO:CC	Organelle envelope	GO:0031967	0.000354	1,268
GO:CC	Envelope	GO:0031975	0.000354	1,268
GO:CC	Mitochondrial envelope	GO:0005740	0.000704	812
GO:CC	U2-type precatalytic spliceosome	GO:0071005	0.000769	50
GO:CC	Nuclear speck	GO:0016607	0.00086	423
GO:CC	Catalytic step 2 spliceosome	GO:0071013	0.000887	88
GO:CC	Nucleus	GO:0005634	0.00263	10,111
GO:CC	Mitochondrial membrane	GO:0031966	0.002944	761
GO:CC	Lysosome	GO:0005764	0.005419	756
GO:CC	Lytic vacuole	GO:0000323	0.005419	756
GO:CC	Vesicle	GO:0031982	0.010611	3,973
GO:CC	Vacuolar membrane	GO:0005774	0.013109	462
GO:CC	RNA polymerase II transcription regulator complex	GO:0090575	0.013481	255
GO:CC	Cullin-RING ubiquitin ligase complex	GO:0031461	0.020128	186
GO:CC	Organelle inner membrane	GO:0019866	0.045059	563

**Abbreviations:** BP, biological process; CC, cellular process; GO, gene ontology; MF, molecular function.

**Supplemental Table 2.** Gene ontologies based on downregulated differentially expressed genes.

Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:MF	Protein binding	GO:0005515	3.92e-24	14,778
GO:MF	Channel activity	GO:0015267	4.43e-16	498
GO:MF	Passive transmembrane transporter activity	GO:0022803	5.67e-16	499
GO:MF	Transporter activity	GO:0005215	1.91e-15	1,230
GO:MF	Transmembrane transporter activity	GO:0022857	8.77e-15	1,124
GO:MF	Inorganic molecular entity transmembrane transporter activity	GO:0015318	1.25e-13	679
GO:MF	Monoatomic ion transmembrane transporter activity	GO:0015075	1.32e-13	725
GO:MF	Monoatomic ion channel activity	GO:0005216	3.24e-13	443
GO:MF	Gated channel activity	GO:0022836	7.3e-13	330
GO:MF	Monoatomic ion gated channel activity	GO:0022839	1.09e-12	328
GO:MF	Metal ion transmembrane transporter activity	GO:0046873	3.18e-12	442
GO:MF	Inorganic cation transmembrane transporter activity	GO:0022890	5.71e-10	561
GO:MF	Calcium ion binding	GO:0005509	1e-09	724
GO:MF	Monoatomic cation transmembrane transporter activity	GO:0008324	8.28e-09	596
GO:MF	Neurotransmitter receptor activity	GO:0030594	9.08e-09	107
GO:MF	Signaling receptor regulator activity	GO:0030545	1.04e-08	543
GO:MF	Cation binding	GO:0043169	1.2e-08	4,368
GO:MF	Signaling receptor binding	GO:0005102	1.66e-08	1,556
GO:MF	DNA-binding transcription factor activity, RNA polymerase II-specific	GO:0000981	2.63e-08	1,360
GO:MF	Molecular transducer activity	GO:0060089	2.92e-08	1,489
GO:MF	Signaling receptor activity	GO:0038023	2.92e-08	1,489
GO:MF	DNA-binding transcription factor activity	GO:0003700	5.92e-08	1,415
GO:MF	Ligand-gated monoatomic ion channel activity	GO:0015276	6.47e-08	146
GO:MF	Ligand-gated channel activity	GO:0022834	6.47e-08	146
GO:MF	Metal ion binding	GO:0046872	1.03e-07	4,275
GO:MF	Postsynaptic neurotransmitter receptor activity	GO:0098960	1.56e-07	75
GO:MF	Ion binding	GO:0043167	2.25e-07	6,079
GO:MF	Transmitter-gated monoatomic ion channel activity	GO:0022824	3e-07	65
GO:MF	Transmitter-gated channel activity	GO:0022835	3e-07	65
GO:MF	RNA polymerase II transcription regulatory region sequence-specific DNA binding	GO:0000977	3.23e-07	1,407
GO:MF	Monoatomic cation channel activity	GO:0005261	3.73e-07	331
GO:MF	Chloride transmembrane transporter activity	GO:0015108	4.62e-07	107
GO:MF	Receptor ligand activity	GO:0048018	8.77e-07	500
GO:MF	Signaling receptor activator activity	GO:0030546	8.99e-07	508
GO:MF	Cytoskeletal motor activity	GO:0003774	9.19e-07	115
GO:MF	Potassium channel activity	GO:0005267	1.08e-06	125
GO:MF	Transmembrane signaling receptor activity	GO:0004888	2.72e-06	1,271
GO:MF	Sequence-specific double-stranded DNA binding	GO:1990837	2.99e-06	1,562
GO:MF	Transmitter-gated monoatomic ion channel activity involved in regulation of postsynaptic membrane potential	GO:1904315	3.09e-06	58
GO:MF	Potassium ion transmembrane transporter activity	GO:0015079	3.8e-06	162
GO:MF	RNA polymerase II cis-regulatory region sequence-specific DNA binding	GO:0000978	4.65e-06	1,191
GO:MF	Monoatomic anion transmembrane transporter activity	GO:0008509	5.44e-06	133
GO:MF	Transcription cis-regulatory region binding	GO:0000976	5.54e-06	1,504
GO:MF	Cis-regulatory region sequence-specific DNA binding	GO:0000987	6.09e-06	1,211
GO:MF	Transcription regulatory region nucleic acid binding	GO:0001067	6.55e-06	1,506
GO:MF	Extracellular ligand-gated monoatomic ion channel activity	GO:0005230	7.33e-06	74

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:MF	Inorganic anion transmembrane transporter activity	GO:0015103	1.01e-05	145
GO:MF	Voltage-gated potassium channel activity	GO:0005249	1.35e-05	100
GO:MF	Neurotransmitter receptor activity involved in regulation of postsynaptic membrane potential	GO:0099529	1.58e-05	61
GO:MF	Metalloendopeptidase activity	GO:0004222	2.21e-05	111
GO:MF	Metallopeptidase activity	GO:0008237	2.28e-05	186
GO:MF	Cytoskeletal protein binding	GO:0008092	2.56e-05	1,004
GO:MF	Voltage-gated monoatomic cation channel activity	GO:0022843	3.65e-05	146
GO:MF	Ligand-gated monoatomic anion channel activity	GO:0099095	3.98e-05	19
GO:MF	Transmembrane receptor protein tyrosine kinase activity	GO:0004714	4.31e-05	63
GO:MF	Voltage-gated channel activity	GO:0022832	5.55e-05	204
GO:MF	Transmembrane receptor protein kinase activity	GO:0019199	6.28e-05	82
GO:MF	Double-stranded DNA binding	GO:0003690	6.59e-05	1,663
GO:MF	Voltage-gated monoatomic ion channel activity	GO:0005244	8.02e-05	202
GO:MF	Extracellular matrix structural constituent	GO:0005201	9.43e-05	174
GO:MF	G protein-coupled peptide receptor activity	GO:0008528	0.000142	144
GO:MF	Peptide receptor activity	GO:0001653	0.000275	150
GO:MF	Molecular function regulator activity	GO:0098772	0.000288	2,006
GO:MF	Potassium channel regulator activity	GO:0015459	0.00041	53
GO:MF	Secondary active transmembrane transporter activity	GO:0015291	0.000417	247
GO:MF	Sequence-specific DNA binding	GO:0043565	0.00042	1,667
GO:MF	Chloride channel activity	GO:0005254	0.000738	79
GO:MF	Actin binding	GO:0003779	0.000742	447
GO:MF	Organic anion transmembrane transporter activity	GO:0008514	0.001323	193
GO:MF	Microtubule motor activity	GO:0003777	0.001397	68
GO:MF	Sodium ion transmembrane transporter activity	GO:0015081	0.001895	158
GO:MF	Integrin binding	GO:0005178	0.001895	158
GO:MF	DNA-binding transcription activator activity	GO:0001216	0.002551	469
GO:MF	Cell-cell adhesion mediator activity	GO:0098632	0.002561	54
GO:MF	Cell adhesion molecule binding	GO:0050839	0.002857	561
GO:MF	Growth factor activity	GO:0008083	0.003951	165
GO:MF	Organic cation transmembrane transporter activity	GO:0015101	0.004024	29
GO:MF	DNA-binding transcription activator activity, RNA polymerase II-specific	GO:0001228	0.004229	465
GO:MF	Excitatory extracellular ligand-gated monoatomic ion channel activity	GO:0005231	0.005901	56
GO:MF	Monoatomic anion channel activity	GO:0005253	0.005956	92
GO:MF	Carboxylic acid transmembrane transporter activity	GO:0046943	0.006519	160
GO:MF	Glycosaminoglycan binding	GO:0005539	0.007175	244
GO:MF	Organic acid transmembrane transporter activity	GO:0005342	0.008031	161
GO:MF	Inhibitory extracellular ligand-gated monoatomic ion channel activity	GO:0005237	0.008363	15
GO:MF	Transcription regulator activity	GO:0140110	0.00925	1,929
GO:MF	GABA-gated chloride ion channel activity	GO:0022851	0.010632	13
GO:MF	Amine binding	GO:0043176	0.010632	13
GO:MF	Serotonin receptor activity	GO:0099589	0.014762	34
GO:MF	Minus-end-directed microtubule motor activity	GO:0008569	0.015214	18
GO:MF	Cytokine activity	GO:0005125	0.015338	237
GO:MF	Cell adhesion mediator activity	GO:0098631	0.015567	65
GO:MF	Alanine transmembrane transporter activity	GO:0022858	0.021803	16
GO:MF	Sodium-independent organic anion transmembrane transporter activity	GO:0015347	0.021803	16

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:MF	Monoatomic anion:sodium symporter activity	GO:0015373	0.021803	16
GO:MF	Serine-type peptidase activity	GO:0008236	0.028348	198
GO:MF	Serine hydrolase activity	GO:0017171	0.029001	202
GO:MF	Monooxygenase activity	GO:0004497	0.030002	105
GO:MF	Sodium:chloride symporter activity	GO:0015378	0.030365	14
GO:MF	Modified amino acid binding	GO:0072341	0.031002	91
GO:MF	Ligand-gated monoatomic cation channel activity	GO:0099094	0.033203	109
GO:MF	Glutamate receptor activity	GO:0008066	0.033355	27
GO:MF	GABA-A receptor activity	GO:0004890	0.033606	19
GO:MF	Ionotropic glutamate receptor activity	GO:0004970	0.033606	19
GO:MF	Calmodulin binding	GO:0005516	0.034271	203
GO:MF	Serine-type endopeptidase activity	GO:0004252	0.035089	180
GO:MF	Transition metal ion binding	GO:0046914	0.036997	1,115
GO:MF	Solute:sodium symporter activity	GO:0015370	0.03924	78
GO:MF	Heparin binding	GO:0008201	0.039405	173
GO:MF	Serotonin binding	GO:0051378	0.040448	12
GO:MF	Growth factor binding	GO:0019838	0.042518	132
GO:MF	Protein tyrosine kinase activity	GO:0004713	0.043332	147
GO:MF	GABA receptor activity	GO:0016917	0.044152	22
GO:MF	Hormone binding	GO:0042562	0.046098	89
GO:MF	Ion channel regulator activity	GO:0099106	0.047721	140
GO:BP	Multicellular organismal process	GO:0032501	1.22e-111	7,657
GO:BP	Developmental process	GO:0032502	3.37e-101	6,446
GO:BP	Anatomical structure development	GO:0048856	2.18e-98	5,861
GO:BP	System development	GO:0048731	7.16e-82	3,962
GO:BP	Multicellular organism development	GO:0007275	2.04e-79	4,627
GO:BP	Regulation of cellular process	GO:0050794	2.21e-65	11,139
GO:BP	Animal organ development	GO:0048513	1.87e-64	3,109
GO:BP	Biological regulation	GO:0065007	1.18e-59	12,926
GO:BP	Cell differentiation	GO:0030154	3.61e-59	4,287
GO:BP	Cellular developmental process	GO:0048869	1.87e-58	4,312
GO:BP	Anatomical structure morphogenesis	GO:0009653	2.11e-57	2,697
GO:BP	Response to stimulus	GO:0050896	1.56e-52	9,039
GO:BP	Cell communication	GO:0007154	2.13e-51	6,573
GO:BP	Regulation of biological process	GO:0050789	6.3e-51	12,378
GO:BP	Nervous system development	GO:0007399	2.35e-50	2,525
GO:BP	Signaling	GO:0023052	5.53e-50	6,462
GO:BP	Tissue development	GO:0009888	6.15e-45	1,995
GO:BP	Cell-cell signaling	GO:0007267	4.32e-44	1,666
GO:BP	System process	GO:0003008	6.62e-38	2,280
GO:BP	Cellular response to stimulus	GO:0051716	1.94e-37	7,491
GO:BP	Regulation of biological quality	GO:0065008	3.73e-37	2,790
GO:BP	Animal organ morphogenesis	GO:0009887	1.03e-36	1,070
GO:BP	Signal transduction	GO:0007165	1.49e-35	6,012
GO:BP	Cell development	GO:0048468	3.54e-35	2,728
GO:BP	Neurogenesis	GO:0022008	1.25e-34	1,688
GO:BP	Neuron differentiation	GO:0030182	1.05e-33	1,401
GO:BP	Generation of neurons	GO:0048699	1.65e-32	1,473
GO:BP	Cell adhesion	GO:0007155	9.09e-29	1,521
GO:BP	Epithelium development	GO:0060429	2.92e-27	1,220

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Transmembrane transport	GO:0055085	5.3e-26	1,555
GO:BP	Reproductive process	GO:0022414	6.08e-26	1,509
GO:BP	Reproduction	GO:0000003	1.32e-25	1,518
GO:BP	Plasma membrane bounded cell projection organization	GO:0120036	1.32e-25	1,518
GO:BP	Trans-synaptic signaling	GO:0099537	1.88e-25	731
GO:BP	Chemical synaptic transmission	GO:0007268	2.19e-25	724
GO:BP	Anterograde trans-synaptic signaling	GO:0098916	2.19e-25	724
GO:BP	Cell projection organization	GO:0030030	4.81e-25	1,556
GO:BP	Synaptic signaling	GO:0099536	7.59e-25	756
GO:BP	Positive regulation of biological process	GO:0048518	1.51e-24	6,348
GO:BP	Cell surface receptor signaling pathway	GO:0007166	6.23e-24	2,869
GO:BP	Cell junction organization	GO:0034330	7.55e-24	708
GO:BP	Monoatomic ion transport	GO:0006811	3.84e-22	1,270
GO:BP	Regulation of cell communication	GO:0010646	1.2e-21	3,388
GO:BP	Cell motility	GO:0048870	2e-21	1,699
GO:BP	Anatomical structure formation involved in morphogenesis	GO:0048646	5.35e-21	1,168
GO:BP	Central nervous system development	GO:0007417	5.81e-21	1,085
GO:BP	Tissue morphogenesis	GO:0048729	6.87e-21	633
GO:BP	Neuron development	GO:0048666	1.03e-20	1,130
GO:BP	Regulation of signaling	GO:0023051	2.96e-20	3,378
GO:BP	Positive regulation of cellular process	GO:0048522	3.12e-20	5,657
GO:BP	Negative regulation of cellular process	GO:0048523	4.25e-20	4,755
GO:BP	Monoatomic ion transmembrane transport	GO:0034220	5.25e-20	1,027
GO:BP	Cell junction assembly	GO:0034329	1.27e-19	435
GO:BP	Regulation of multicellular organismal process	GO:0051239	1.94e-19	3,004
GO:BP	Morphogenesis of an epithelium	GO:0002009	2.41e-19	526
GO:BP	Circulatory system development	GO:0072359	3.81e-19	1,118
GO:BP	Regulation of developmental process	GO:0050793	6.68e-19	2,474
GO:BP	Embryo development	GO:0009790	8.79e-19	1,140
GO:BP	Cell-cell adhesion	GO:0098609	9.09e-19	948
GO:BP	Sensory organ development	GO:0007423	3.32e-18	594
GO:BP	Circulatory system process	GO:0003013	5.24e-18	596
GO:BP	Inorganic ion transmembrane transport	GO:0098660	9.59e-18	920
GO:BP	Nervous system process	GO:0050877	1.48e-17	1,518
GO:BP	Behavior	GO:0007610	1.59e-17	640
GO:BP	Cell morphogenesis	GO:0000902	3.57e-17	965
GO:BP	Tube development	GO:0035295	3.84e-17	1,079
GO:BP	Cell-cell adhesion via plasma-membrane adhesion molecules	GO:0098742	5.99e-17	285
GO:BP	Cellular component morphogenesis	GO:0032989	1.18e-16	778
GO:BP	Synapse organization	GO:0050808	1.25e-16	438
GO:BP	Neuron projection development	GO:0031175	4.4e-16	976
GO:BP	Homophilic cell adhesion via plasma membrane adhesion molecules	GO:0007156	7.43e-16	170
GO:BP	Metal ion transport	GO:0030001	9.71e-16	897
GO:BP	Embryonic morphogenesis	GO:0048598	1.45e-15	618
GO:BP	Pattern specification process	GO:0007389	1.88e-15	479
GO:BP	Cytoskeleton organization	GO:0007010	1.95e-15	1,507
GO:BP	Regulation of membrane potential	GO:0042391	2.38e-15	427
GO:BP	Positive regulation of developmental process	GO:0051094	2.78e-15	1,311
GO:BP	Neuron projection morphogenesis	GO:0048812	4.06e-15	635
GO:BP	Cell projection morphogenesis	GO:0048858	4.92e-15	656

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Blood circulation	GO:0008015	6.13e-15	511
GO:BP	Cell part morphogenesis	GO:0032990	8.6e-15	675
GO:BP	Plasma membrane bounded cell projection morphogenesis	GO:0120039	8.91e-15	651
GO:BP	Cell morphogenesis involved in differentiation	GO:0000904	1.09e-14	648
GO:BP	Heart development	GO:0007507	1.6e-14	590
GO:BP	Brain development	GO:0007420	2.28e-14	795
GO:BP	Response to chemical	GO:0042221	2.89e-14	4,088
GO:BP	Regulation of signal transduction	GO:0009966	3.18e-14	2,991
GO:BP	Tube morphogenesis	GO:0035239	3.93e-14	865
GO:BP	Cell migration	GO:0016477	4.91e-14	1,502
GO:BP	Head development	GO:0060322	1.53e-13	844
GO:BP	Regionalization	GO:0003002	2.13e-13	434
GO:BP	Epithelial cell differentiation	GO:0030855	2.18e-13	713
GO:BP	Synapse assembly	GO:0007416	3.69e-13	191
GO:BP	Enzyme-linked receptor protein signaling pathway	GO:0007167	4.01e-13	982
GO:BP	Localization	GO:0051179	4.43e-13	5,578
GO:BP	Response to endogenous stimulus	GO:0009719	6.58e-13	1,692
GO:BP	Regulation of response to stimulus	GO:0048583	6.82e-13	3,998
GO:BP	Cell morphogenesis involved in neuron differentiation	GO:0048667	7.03e-13	577
GO:BP	Monoatomic cation transport	GO:0006812	1.23e-12	1,059
GO:BP	Regulation of localization	GO:0032879	1.41e-12	2,101
GO:BP	Axonogenesis	GO:0007409	1.72e-12	447
GO:BP	Axon guidance	GO:0007411	2e-12	240
GO:BP	Neuron projection guidance	GO:0097485	2.76e-12	241
GO:BP	Locomotion	GO:0040011	3.06e-12	1,353
GO:BP	Inorganic cation transmembrane transport	GO:0098662	4.87e-12	828
GO:BP	Axon development	GO:0061564	6.01e-12	496
GO:BP	Cell fate commitment	GO:0045165	8.58e-12	284
GO:BP	Cell population proliferation	GO:0008283	1.39e-11	1,985
GO:BP	Multicellular organism reproduction	GO:0032504	1.49e-11	934
GO:BP	Skeletal system development	GO:0001501	2.36e-11	547
GO:BP	Monoatomic cation transmembrane transport	GO:0098655	4.08e-11	855
GO:BP	Sensory organ morphogenesis	GO:0090596	6.53e-11	284
GO:BP	Mesenchyme development	GO:0060485	9.75e-11	304
GO:BP	Regulation of cell differentiation	GO:0045595	1.16e-10	1,567
GO:BP	Developmental process involved in reproduction	GO:0003006	1.21e-10	971
GO:BP	Regulation of nitrogen compound metabolic process	GO:0051171	1.86e-10	5,724
GO:BP	Regulation of transport	GO:0051049	2.35e-10	1,754
GO:BP	Regulation of system process	GO:0044057	2.42e-10	572
GO:BP	Ear development	GO:0043583	3.63e-10	232
GO:BP	Establishment of localization	GO:0051234	3.66e-10	4,933
GO:BP	Inner ear development	GO:0048839	4.01e-10	204
GO:BP	Cell surface receptor signaling pathway involved in cell-cell signaling	GO:1905114	4.86e-10	576
GO:BP	Modulation of chemical synaptic transmission	GO:0050804	5.69e-10	455
GO:BP	Embryo development ending in birth or egg hatching	GO:0009792	5.82e-10	694
GO:BP	Regulation of trans-synaptic signaling	GO:0099177	6.92e-10	456
GO:BP	External encapsulating structure organization	GO:0045229	8.47e-10	324
GO:BP	Chordate embryonic development	GO:0043009	9.75e-10	672
GO:BP	Extracellular matrix organization	GO:0030198	1.03e-09	321
GO:BP	Extracellular structure organization	GO:0043062	1.3e-09	322

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Cellular response to endogenous stimulus	GO:0071495	1.46e-09	1,445
GO:BP	Regulation of cellular component organization	GO:0051128	1.55e-09	2,365
GO:BP	Regulation of primary metabolic process	GO:0080090	1.76e-09	5,882
GO:BP	Multicellular organismal reproductive process	GO:0048609	2.05e-09	892
GO:BP	Regulation of multicellular organismal development	GO:2000026	2.53e-09	1,400
GO:BP	Chemical homeostasis	GO:0048878	3.06e-09	1,014
GO:BP	Positive regulation of cell population proliferation	GO:0008284	3.42e-09	953
GO:BP	Developmental growth	GO:0048589	4.27e-09	652
GO:BP	Regulation of cell population proliferation	GO:0042127	6.14e-09	1,677
GO:BP	Regulation of molecular function	GO:0065009	7.42e-09	3,059
GO:BP	Sexual reproduction	GO:0019953	1.04e-08	909
GO:BP	Forebrain development	GO:0030900	1.07e-08	402
GO:BP	Locomotory behavior	GO:0007626	1.2e-08	208
GO:BP	Homeostatic process	GO:0042592	1.24e-08	1,666
GO:BP	Regulation of hormone levels	GO:0010817	1.53e-08	526
GO:BP	Sensory system development	GO:0048880	1.58e-08	408
GO:BP	Actin filament-based process	GO:0030029	1.93e-08	813
GO:BP	Vascular process in circulatory system	GO:0003018	1.95e-08	265
GO:BP	Eye development	GO:0001654	2.34e-08	398
GO:BP	Transport	GO:0006810	2.39e-08	4,773
GO:BP	Striated muscle tissue development	GO:0014706	2.6e-08	240
GO:BP	Response to oxygen-containing compound	GO:1901700	2.64e-08	1,665
GO:BP	Cognition	GO:0050890	2.7e-08	316
GO:BP	Regulation of anatomical structure morphogenesis	GO:0022603	2.91e-08	882
GO:BP	Mesenchymal cell differentiation	GO:0048762	3.38e-08	241
GO:BP	Muscle tissue development	GO:0060537	3.42e-08	408
GO:BP	Regulation of nervous system development	GO:0051960	3.66e-08	457
GO:BP	Embryonic organ morphogenesis	GO:0048562	3.74e-08	302
GO:BP	Response to organic substance	GO:0010033	4.08e-08	2,664
GO:BP	Muscle structure development	GO:0061061	4.15e-08	663
GO:BP	Potassium ion transport	GO:0006813	4.38e-08	242
GO:BP	Epithelial tube morphogenesis	GO:0060562	4.66e-08	338
GO:BP	Response to external stimulus	GO:0009605	4.7e-08	2,861
GO:BP	Visual system development	GO:0150063	5.06e-08	402
GO:BP	Potassium ion transmembrane transport	GO:0071805	5.5e-08	217
GO:BP	Regulation of phosphorylation	GO:0042325	6.38e-08	1,244
GO:BP	Growth	GO:0040007	6.61e-08	933
GO:BP	Response to growth factor	GO:0070848	6.63e-08	705
GO:BP	Cellular process involved in reproduction in multicellular organism	GO:0022412	6.82e-08	436
GO:BP	Learning or memory	GO:0007611	6.92e-08	274
GO:BP	Positive regulation of multicellular organismal process	GO:0051240	7.12e-08	1,695
GO:BP	Gland development	GO:0048732	7.92e-08	445
GO:BP	Cilium or flagellum-dependent cell motility	GO:0001539	7.94e-08	161
GO:BP	Cilium-dependent cell motility	GO:0060285	7.94e-08	161
GO:BP	Vasculature development	GO:0001944	8.34e-08	737
GO:BP	Central nervous system neuron differentiation	GO:0021953	9.02e-08	179
GO:BP	Negative regulation of biological process	GO:0048519	9.07e-08	5,927
GO:BP	Secretion	GO:0046903	9.51e-08	945
GO:BP	Regulation of neuron differentiation	GO:0045664	1.03e-07	201
GO:BP	Regulation of transcription by RNA polymerase II	GO:0006357	1.16e-07	2,572

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Cellular response to chemical stimulus	GO:0070887	1.46e-07	2,697
GO:BP	Regulation of phosphate metabolic process	GO:0019220	1.5e-07	1,400
GO:BP	Regulation of phosphorus metabolic process	GO:0051174	1.65e-07	1,401
GO:BP	Regulation of monoatomic ion transport	GO:0043269	1.87e-07	588
GO:BP	Action potential	GO:0001508	1.98e-07	143
GO:BP	Positive regulation of phosphorus metabolic process	GO:0010562	2.05e-07	907
GO:BP	Positive regulation of phosphate metabolic process	GO:0045937	2.05e-07	907
GO:BP	Regulation of blood circulation	GO:1903522	2.08e-07	252
GO:BP	Taxis	GO:0042330	2.13e-07	623
GO:BP	Plasma membrane bounded cell projection assembly	GO:0120031	2.16e-07	572
GO:BP	Regulation of protein phosphorylation	GO:0001932	2.19e-07	1,101
GO:BP	Retina development in camera-type eye	GO:0060041	2.44e-07	161
GO:BP	Regulation of neurotransmitter levels	GO:0001505	2.71e-07	223
GO:BP	Chemotaxis	GO:0006935	2.95e-07	621
GO:BP	Protein phosphorylation	GO:0006468	3.06e-07	1,571
GO:BP	Positive regulation of phosphorylation	GO:0042327	3.2e-07	822
GO:BP	Cardiac muscle tissue development	GO:0048738	3.5e-07	224
GO:BP	Positive regulation of cell communication	GO:0010647	3.83e-07	1,729
GO:BP	Cellular response to growth factor stimulus	GO:0071363	4.04e-07	675
GO:BP	Camera-type eye development	GO:0043010	4.34e-07	345
GO:BP	Stem cell differentiation	GO:0048863	4.92e-07	248
GO:BP	Neural crest cell differentiation	GO:0014033	5.78e-07	96
GO:BP	Cell projection assembly	GO:0030031	5.86e-07	583
GO:BP	Positive regulation of cell differentiation	GO:0045597	6.44e-07	850
GO:BP	Positive regulation of molecular function	GO:0044093	6.65e-07	1,580
GO:BP	Adenylate cyclase-modulating G protein-coupled receptor signaling pathway	GO:0007188	7.56e-07	246
GO:BP	Blood vessel development	GO:0001568	7.73e-07	706
GO:BP	Regulation of heart contraction	GO:0008016	8.27e-07	205
GO:BP	Supramolecular fiber organization	GO:0097435	1.03e-06	814
GO:BP	Regulation of cell projection organization	GO:0031344	1.04e-06	656
GO:BP	Regulation of transmembrane transport	GO:0034762	1.04e-06	587
GO:BP	G protein-coupled receptor signaling pathway	GO:0007186	1.06e-06	1,245
GO:BP	Embryonic organ development	GO:0048568	1.2e-06	461
GO:BP	Regulation of plasma membrane bounded cell projection organization	GO:0120035	1.24e-06	640
GO:BP	Heart process	GO:0003015	1.25e-06	252
GO:BP	Intracellular signal transduction	GO:0035556	1.36e-06	2,667
GO:BP	Heart contraction	GO:0060047	1.4e-06	241
GO:BP	Regulation of locomotion	GO:0040012	1.48e-06	1,033
GO:BP	Positive regulation of signaling	GO:0023056	1.52e-06	1,727
GO:BP	Developmental growth involved in morphogenesis	GO:0060560	1.7e-06	238
GO:BP	Monoatomic anion transport	GO:0006820	1.88e-06	157
GO:BP	Transmembrane receptor protein tyrosine kinase signaling pathway	GO:0007169	1.95e-06	626
GO:BP	Regulation of synapse structure or activity	GO:0050803	2.15e-06	220
GO:BP	Response to organic cyclic compound	GO:0014070	2.31e-06	933
GO:BP	Import into cell	GO:0098657	2.31e-06	247
GO:BP	Heart morphogenesis	GO:0003007	2.47e-06	255
GO:BP	Renal system development	GO:0072001	3.04e-06	323
GO:BP	Cardiac muscle cell differentiation	GO:0055007	3.08e-06	110
GO:BP	Regulation of synapse organization	GO:0050807	3.15e-06	214

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Striated muscle cell differentiation	GO:0051146	3.48e-06	280
GO:BP	Regulation of synapse assembly	GO:0051963	3.49e-06	107
GO:BP	Negative regulation of developmental process	GO:0051093	3.58e-06	919
GO:BP	Regulation of postsynaptic membrane potential	GO:0060078	3.69e-06	145
GO:BP	Cardiac muscle cell development	GO:0055013	3.76e-06	75
GO:BP	Neuron fate commitment	GO:0048663	3.99e-06	69
GO:BP	Transcription by RNA polymerase II	GO:0006366	3.99e-06	2,674
GO:BP	Negative regulation of cell communication	GO:0010648	4.22e-06	1,353
GO:BP	Microtubule-based movement	GO:0007018	4.38e-06	419
GO:BP	Microtubule-based process	GO:0007017	4.39e-06	939
GO:BP	Muscle cell development	GO:0055001	5.12e-06	186
GO:BP	Regulation of MAPK cascade	GO:0043408	5.34e-06	673
GO:BP	Muscle cell differentiation	GO:0042692	5.37e-06	383
GO:BP	Chloride transport	GO:0006821	5.55e-06	115
GO:BP	Anterior/posterior pattern specification	GO:0009952	5.61e-06	224
GO:BP	Regulation of cellular metabolic process	GO:0031323	5.64e-06	5,653
GO:BP	Cardiocyte differentiation	GO:0035051	5.94e-06	143
GO:BP	Cilium movement	GO:0003341	6.32e-06	198
GO:BP	Organic hydroxy compound transport	GO:0015850	6.32e-06	275
GO:BP	Negative regulation of signaling	GO:0023057	6.34e-06	1,353
GO:BP	Regulation of developmental growth	GO:0048638	6.54e-06	323
GO:BP	Mesenchymal cell migration	GO:0090497	6.68e-06	61
GO:BP	Blood vessel morphogenesis	GO:0048514	6.75e-06	618
GO:BP	Regulation of cell junction assembly	GO:1901888	7.11e-06	206
GO:BP	Regulation of animal organ morphogenesis	GO:2000027	8.35e-06	130
GO:BP	Meiotic cell cycle	GO:0051321	9.67e-06	285
GO:BP	Synaptic vesicle cycle	GO:0099504	9.8e-06	196
GO:BP	Regulation of monoatomic ion transmembrane transport	GO:0034765	1.01e-05	462
GO:BP	Positive regulation of protein phosphorylation	GO:0001934	1.07e-05	745
GO:BP	Chloride transmembrane transport	GO:1902476	1.08e-05	100
GO:BP	Inorganic ion homeostasis	GO:0098771	1.1e-05	548
GO:BP	Response to xenobiotic stimulus	GO:0009410	1.15e-05	425
GO:BP	Kidney development	GO:0001822	1.17e-05	314
GO:BP	Carboxylic acid transport	GO:0046942	1.18e-05	290
GO:BP	Monoatomic ion homeostasis	GO:0050801	1.25e-05	614
GO:BP	Positive regulation of nitrogen compound metabolic process	GO:0051173	1.32e-05	3,154
GO:BP	Actin filament-based movement	GO:0030048	1.35e-05	128
GO:BP	Cardiac cell development	GO:0055006	1.37e-05	81
GO:BP	Monoatomic anion transmembrane transport	GO:0098656	1.58e-05	132
GO:BP	Vesicle-mediated transport in synapse	GO:0099003	1.59e-05	217
GO:BP	Organic anion transport	GO:0015711	1.62e-05	373
GO:BP	Signal release	GO:0023061	1.71e-05	474
GO:BP	Telencephalon development	GO:0021537	1.72e-05	272
GO:BP	Detection of external stimulus	GO:0009581	1.74e-05	143
GO:BP	Actin cytoskeleton organization	GO:0030036	1.75e-05	727
GO:BP	Negative regulation of cell differentiation	GO:0045596	1.79e-05	674
GO:BP	Response to lipid	GO:0033993	2.06e-05	913
GO:BP	Regulation of neurogenesis	GO:0050767	2.27e-05	375
GO:BP	Gamete generation	GO:0007276	2.29e-05	774
GO:BP	Eye morphogenesis	GO:0048592	2.43e-05	166

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Regulation of DNA-templated transcription	GO:0006355	2.45e-05	3,465
GO:BP	Camera-type eye morphogenesis	GO:0048593	2.54e-05	130
GO:BP	Actin-mediated cell contraction	GO:0070252	2.6e-05	99
GO:BP	Cilium movement involved in cell motility	GO:0060294	2.62e-05	148
GO:BP	Adult behavior	GO:0030534	2.62e-05	148
GO:BP	Epithelial cell proliferation	GO:0050673	2.64e-05	443
GO:BP	Cell-cell junction organization	GO:0045216	2.72e-05	204
GO:BP	Regulation of nucleic acid-templated transcription	GO:1903506	2.72e-05	3,467
GO:BP	Hormone metabolic process	GO:0042445	2.91e-05	243
GO:BP	Export from cell	GO:0140352	2.93e-05	871
GO:BP	Negative regulation of multicellular organismal process	GO:0051241	2.97e-05	1,105
GO:BP	Positive regulation of metabolic process	GO:0009893	3.12e-05	3,857
GO:BP	Positive regulation of nervous system development	GO:0051962	3.13e-05	283
GO:BP	Positive regulation of macromolecule metabolic process	GO:0010604	3.15e-05	3,540
GO:BP	Neural crest cell development	GO:0014032	3.18e-05	83
GO:BP	Metal ion homeostasis	GO:0055065	3.38e-05	526
GO:BP	Sensory perception of mechanical stimulus	GO:0050954	3.43e-05	186
GO:BP	Kidney epithelium development	GO:0072073	3.48e-05	149
GO:BP	Neural retina development	GO:0003407	3.51e-05	80
GO:BP	Meiotic nuclear division	GO:0140013	3.81e-05	194
GO:BP	Regulation of cell motility	GO:2000145	3.91e-05	988
GO:BP	Regulation of RNA biosynthetic process	GO:2001141	4.14e-05	3,490
GO:BP	Cell fate specification	GO:0001708	4.14e-05	114
GO:BP	Detection of abiotic stimulus	GO:0009582	4.16e-05	146
GO:BP	Muscle system process	GO:0003012	4.25e-05	425
GO:BP	Calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	GO:0016339	4.29e-05	44
GO:BP	Positive regulation of signal transduction	GO:0009967	4.49e-05	1,528
GO:BP	Regulation of secretion	GO:0051046	4.6e-05	620
GO:BP	Regulation of heart rate	GO:0002027	4.63e-05	104
GO:BP	Regulation of neuron projection development	GO:0010975	4.79e-05	447
GO:BP	Epidermis development	GO:0008544	5.13e-05	380
GO:BP	Neural crest cell migration	GO:0001755	5.36e-05	59
GO:BP	Ear morphogenesis	GO:0042471	5.55e-05	129
GO:BP	Inorganic anion transmembrane transport	GO:0098661	5.71e-05	122
GO:BP	Developmental cell growth	GO:0048588	7.55e-05	224
GO:BP	Skeletal system morphogenesis	GO:0048705	7.82e-05	232
GO:BP	Sodium ion transport	GO:0006814	8.17e-05	248
GO:BP	Limb development	GO:0060173	8.18e-05	182
GO:BP	Appendage development	GO:0048736	8.18e-05	182
GO:BP	Transmembrane receptor protein serine/threonine kinase signaling pathway	GO:0007178	8.77e-05	375
GO:BP	MAPK cascade	GO:0000165	8.94e-05	773
GO:BP	Monoatomic cation homeostasis	GO:0055080	9.62e-05	604
GO:BP	Respiratory system development	GO:0060541	0.000109	214
GO:BP	Neurotransmitter transport	GO:0006836	0.000109	214
GO:BP	Phosphorylation	GO:0016310	0.000113	1,872
GO:BP	Metanephros development	GO:0001656	0.000116	93
GO:BP	Regulation of cell migration	GO:0030334	0.000118	926
GO:BP	Organic acid transport	GO:0015849	0.000122	323

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Regulation of epithelial cell proliferation	GO:0050678	0.000124	373
GO:BP	Phosphate-containing compound metabolic process	GO:0006796	0.000138	2,843
GO:BP	Cilium organization	GO:0044782	0.000139	399
GO:BP	Response to abiotic stimulus	GO:0009628	0.000139	1,141
GO:BP	Phosphorus metabolic process	GO:0006793	0.000139	2,868
GO:BP	Columnar/cuboidal epithelial cell differentiation	GO:0002065	0.000148	118
GO:BP	Microtubule cytoskeleton organization	GO:0000226	0.000148	652
GO:BP	Synaptic transmission, GABAergic	GO:0051932	0.000148	58
GO:BP	Negative regulation of response to stimulus	GO:0048585	0.000149	1,611
GO:BP	Meiotic cell cycle process	GO:1903046	0.000164	212
GO:BP	Response to BMP	GO:0071772	0.000175	170
GO:BP	Cellular response to BMP stimulus	GO:0071773	0.000175	170
GO:BP	Inner ear morphogenesis	GO:0042472	0.000177	108
GO:BP	Cardiac muscle cell contraction	GO:0086003	0.00018	71
GO:BP	Cell-substrate adhesion	GO:0031589	0.00018	367
GO:BP	Microtubule bundle formation	GO:0001578	0.000191	126
GO:BP	Visual perception	GO:0007601	0.00021	221
GO:BP	DNA-templated transcription	GO:0006351	0.000225	3,584
GO:BP	Digestive system development	GO:0055123	0.000236	145
GO:BP	Nucleic acid-templated transcription	GO:0097659	0.000237	3,585
GO:BP	Cell-cell signaling by wnt	GO:0198738	0.000248	450
GO:BP	Positive regulation of transcription by RNA polymerase II	GO:0045944	0.00025	1,242
GO:BP	Inorganic anion transport	GO:0015698	0.000255	183
GO:BP	Cell-cell junction assembly	GO:0007043	0.000255	149
GO:BP	Cardiac chamber development	GO:0003205	0.000271	168
GO:BP	Cellular chemical homeostasis	GO:0055082	0.00028	689
GO:BP	Cilium assembly	GO:0060271	0.000286	370
GO:BP	Lipid transport	GO:0006869	0.000287	421
GO:BP	Secretion by cell	GO:0032940	0.000301	812
GO:BP	Limb morphogenesis	GO:0035108	0.000307	146
GO:BP	Appendage morphogenesis	GO:0035107	0.000307	146
GO:BP	Stem cell development	GO:0048864	0.000315	89
GO:BP	Regulation of protein modification process	GO:0031399	0.000316	1,540
GO:BP	Renal system process	GO:0003014	0.00034	128
GO:BP	Wnt signaling pathway	GO:0016055	0.000341	448
GO:BP	Embryonic appendage morphogenesis	GO:0035113	0.000364	121
GO:BP	Embryonic limb morphogenesis	GO:0030326	0.000364	121
GO:BP	Fertilization	GO:0009566	0.000365	204
GO:BP	Cranial nerve development	GO:0021545	0.000382	60
GO:BP	Cellular response to organic substance	GO:0071310	0.000385	1,993
GO:BP	Dorsal/ventral pattern formation	GO:0009953	0.000386	93
GO:BP	Positive regulation of cellular metabolic process	GO:0031325	0.000386	3,097
GO:BP	Sensory perception of light stimulus	GO:0050953	0.000387	224
GO:BP	Positive regulation of cell junction assembly	GO:1901890	0.000394	107
GO:BP	Kidney morphogenesis	GO:0060993	0.000396	100
GO:BP	Sensory perception	GO:0007600	0.000409	981
GO:BP	Sperm motility	GO:0097722	0.000411	136
GO:BP	Flagellated sperm motility	GO:0030317	0.000411	136
GO:BP	Nephron morphogenesis	GO:0072028	0.000415	83
GO:BP	Presynapse assembly	GO:0099054	0.000431	51

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Import across plasma membrane	GO:0098739	0.000434	197
GO:BP	Morphogenesis of a polarized epithelium	GO:0001738	0.000464	97
GO:BP	Neuron migration	GO:0001764	0.000471	178
GO:BP	RNA biosynthetic process	GO:0032774	0.000529	3,622
GO:BP	Developmental maturation	GO:0021700	0.000534	307
GO:BP	Positive regulation of synapse assembly	GO:0051965	0.000552	64
GO:BP	Adenylate cyclase-activating G protein-coupled receptor signaling pathway	GO:0007189	0.00058	156
GO:BP	Nephron epithelium development	GO:0072009	0.00058	119
GO:BP	Chemical synaptic transmission, postsynaptic	GO:0099565	0.000592	130
GO:BP	Cardiac muscle cell action potential	GO:0086001	0.000608	74
GO:BP	Segmentation	GO:0035282	0.000614	112
GO:BP	Glial cell differentiation	GO:0010001	0.000701	231
GO:BP	Positive regulation of MAPK cascade	GO:0043410	0.000713	484
GO:BP	Nerve development	GO:0021675	0.000734	88
GO:BP	Regulation of RNA metabolic process	GO:0051252	0.000803	3,783
GO:BP	Cellular homeostasis	GO:0019725	0.000803	790
GO:BP	Sensory perception of sound	GO:0007605	0.00081	165
GO:BP	Regulation of growth	GO:0040008	0.000821	627
GO:BP	Negative regulation of signal transduction	GO:0009968	0.000842	1,248
GO:BP	Motile cilium assembly	GO:0044458	0.000843	65
GO:BP	Excitatory postsynaptic potential	GO:0060079	0.000853	124
GO:BP	Negative regulation of transcription by RNA polymerase II	GO:0000122	0.000895	962
GO:BP	Nephron development	GO:0072006	0.000896	154
GO:BP	Spermatid differentiation	GO:0048515	0.001009	201
GO:BP	Nuclear division	GO:0000280	0.001034	452
GO:BP	Male gamete generation	GO:0048232	0.001075	616
GO:BP	Peptidyl-tyrosine phosphorylation	GO:0018108	0.001083	379
GO:BP	Odontogenesis	GO:0042476	0.001092	136
GO:BP	Regulation of kinase activity	GO:0043549	0.001108	775
GO:BP	Cardiac muscle cell action potential involved in contraction	GO:0086002	0.001197	50
GO:BP	Spermatid development	GO:0007286	0.001211	194
GO:BP	Morphogenesis of a branching structure	GO:0001763	0.001237	202
GO:BP	Negative regulation of DNA-templated transcription	GO:0045892	0.001312	1,311
GO:BP	Smoothed signaling pathway	GO:0007224	0.001313	148
GO:BP	Learning	GO:0007612	0.00138	152
GO:BP	Phospholipase C-activating G protein-coupled receptor signaling pathway	GO:0007200	0.001391	104
GO:BP	Peptidyl-tyrosine modification	GO:0018212	0.001439	381
GO:BP	Regulation of potassium ion transmembrane transport	GO:1901379	0.00144	90
GO:BP	Hindbrain development	GO:0030902	0.001503	160
GO:BP	Negative regulation of nucleic acid-templated transcription	GO:1903507	0.001519	1,313
GO:BP	Germ cell development	GO:0007281	0.001544	322
GO:BP	Spermatogenesis	GO:0007283	0.001566	597
GO:BP	Nephron epithelium morphogenesis	GO:0072088	0.001616	80
GO:BP	Presynapse organization	GO:0099172	0.00182	54
GO:BP	Negative regulation of cell development	GO:0010721	0.001834	273
GO:BP	Regulation of potassium ion transport	GO:0043266	0.001875	105
GO:BP	Positive regulation of cell cycle	GO:0045787	0.001892	353
GO:BP	Cochlea development	GO:0090102	0.001933	51

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Regulation of transporter activity	GO:0032409	0.001958	290
GO:BP	Muscle organ development	GO:0007517	0.001964	349
GO:BP	Neuron recognition	GO:0008038	0.00202	48
GO:BP	Cell growth	GO:0016049	0.002061	497
GO:BP	Retina morphogenesis in camera-type eye	GO:0060042	0.002122	64
GO:BP	Renal tubule development	GO:0061326	0.002232	102
GO:BP	Regulation of anatomical structure size	GO:0090066	0.002247	511
GO:BP	Cardiac chamber morphogenesis	GO:0003206	0.002307	124
GO:BP	Axoneme assembly	GO:0035082	0.002319	95
GO:BP	Gamma-aminobutyric acid signaling pathway	GO:0007214	0.00233	28
GO:BP	Nephron tubule development	GO:0072080	0.002655	99
GO:BP	Nephron tubule morphogenesis	GO:0072078	0.002657	78
GO:BP	Positive regulation of neuron differentiation	GO:0045666	0.002741	92
GO:BP	Regulation of nucleobase-containing compound metabolic process	GO:0019219	0.002831	4,097
GO:BP	Negative regulation of synaptic transmission	GO:0050805	0.002842	55
GO:BP	Positive regulation of developmental growth	GO:0048639	0.002963	163
GO:BP	Negative regulation of RNA metabolic process	GO:0051253	0.003045	1,438
GO:BP	Negative regulation of neuron differentiation	GO:0045665	0.003072	75
GO:BP	Regulation of metal ion transport	GO:0010959	0.003147	404
GO:BP	Regulation of secretion by cell	GO:1903530	0.003148	563
GO:BP	Cardiac conduction	GO:0061337	0.003154	96
GO:BP	Embryonic skeletal system development	GO:0048706	0.003208	129
GO:BP	Renal tubule morphogenesis	GO:0061333	0.003216	82
GO:BP	Muscle contraction	GO:0006936	0.003401	340
GO:BP	Digestive tract development	GO:0048565	0.00341	133
GO:BP	Positive regulation of cell projection organization	GO:0031346	0.003488	353
GO:BP	Nephric duct development	GO:0072176	0.003494	16
GO:BP	Cellular response to oxygen-containing compound	GO:1901701	0.003526	1,191
GO:BP	Connective tissue development	GO:0061448	0.003545	277
GO:BP	Spinal cord development	GO:0021510	0.003576	100
GO:BP	Regulation of cellular component biogenesis	GO:0044087	0.003593	955
GO:BP	Renal system process involved in regulation of systemic arterial blood pressure	GO:0003071	0.00379	26
GO:BP	Central nervous system neuron development	GO:0021954	0.00381	86
GO:BP	Negative regulation of RNA biosynthetic process	GO:1902679	0.004117	1,327
GO:BP	Cardiac muscle contraction	GO:0060048	0.004361	134
GO:BP	Morphogenesis of embryonic epithelium	GO:0016331	0.004372	157
GO:BP	Response to nitrogen compound	GO:1901698	0.004512	1,123
GO:BP	Cellular process	GO:0009987	0.004524	19,271
GO:BP	Skin development	GO:0043588	0.004554	308
GO:BP	Meiosis I cell cycle process	GO:0061982	0.004584	138
GO:BP	Axis elongation	GO:0003401	0.004652	29
GO:BP	Lipid localization	GO:0010876	0.004961	469
GO:BP	Pancreatic A cell differentiation	GO:0003310	0.005282	10
GO:BP	Neuron fate specification	GO:0048665	0.005299	32
GO:BP	Actin filament bundle assembly	GO:0051017	0.005451	158
GO:BP	Membrane repolarization	GO:0086009	0.005506	47
GO:BP	Organ growth	GO:0035265	0.005573	162
GO:BP	Angiogenesis	GO:0001525	0.005662	528
GO:BP	Positive regulation of potassium ion transmembrane transport	GO:1901381	0.005767	44

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Negative regulation of developmental growth	GO:0048640	0.00583	109
GO:BP	Positive regulation of cellular component organization	GO:0051130	0.006168	1,056
GO:BP	Positive regulation of epithelial cell proliferation	GO:0050679	0.007016	211
GO:BP	Sodium ion transmembrane transport	GO:0035725	0.007162	175
GO:BP	Striated muscle contraction	GO:0006941	0.007162	175
GO:BP	Actomyosin structure organization	GO:0031032	0.007194	199
GO:BP	Morphogenesis of a branching epithelium	GO:0061138	0.007252	187
GO:BP	Regulation of cytosolic calcium ion concentration	GO:0051480	0.007332	54
GO:BP	Forebrain generation of neurons	GO:0021872	0.007332	54
GO:BP	Response to hormone	GO:0009725	0.007574	861
GO:BP	Branching morphogenesis of an epithelial tube	GO:0048754	0.008234	156
GO:BP	Calcium ion transport	GO:0006816	0.008338	438
GO:BP	ERK1 and ERK2 cascade	GO:0070371	0.008453	325
GO:BP	Cranial nerve morphogenesis	GO:0021602	0.00887	30
GO:BP	Regulation of monoatomic ion transmembrane transporter activity	GO:0032412	0.0091	262
GO:BP	Actin filament organization	GO:0007015	0.009105	452
GO:BP	Calcium ion transmembrane transport	GO:0070588	0.009475	343
GO:BP	Positive regulation of protein modification process	GO:0031401	0.009622	1,005
GO:BP	Ventricular cardiac muscle cell action potential	GO:0086005	0.009628	33
GO:BP	Cellular response to retinoic acid	GO:0071300	0.009636	68
GO:BP	Regulation of catalytic activity	GO:0050790	0.009657	2,356
GO:BP	Olfactory lobe development	GO:0021988	0.009988	36
GO:BP	Actin filament bundle organization	GO:0061572	0.010362	161
GO:BP	Regulation of blood pressure	GO:0008217	0.010613	193
GO:BP	Organelle fission	GO:0048285	0.010777	498
GO:BP	Regulation of microtubule–based process	GO:0032886	0.010985	259
GO:BP	Regulation of transferase activity	GO:0051338	0.011282	908
GO:BP	Adult locomotory behavior	GO:0008344	0.011529	86
GO:BP	Amino acid transport	GO:0006865	0.011894	146
GO:BP	Regulation of protein metabolic process	GO:0051246	0.011895	2,560
GO:BP	Regulation of receptor signaling pathway via STAT	GO:1904892	0.012001	108
GO:BP	Cartilage development	GO:0051216	0.012383	206
GO:BP	Calcium ion homeostasis	GO:0055074	0.012647	315
GO:BP	Cell maturation	GO:0048469	0.012891	190
GO:BP	Mesonephric epithelium development	GO:0072163	0.01332	101
GO:BP	Mesonephric tubule development	GO:0072164	0.01332	101
GO:BP	Positive regulation of catalytic activity	GO:0043085	0.013479	1,181
GO:BP	Regulation of transmembrane transporter activity	GO:0022898	0.01365	273
GO:BP	Regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	GO:0090092	0.01365	273
GO:BP	Pancreas development	GO:0031016	0.013692	83
GO:BP	Monoamine transport	GO:0015844	0.013692	83
GO:BP	Lipid metabolic process	GO:0006629	0.014092	1,413
GO:BP	Epithelial cell development	GO:0002064	0.014322	215
GO:BP	Response to organonitrogen compound	GO:0010243	0.014378	1,034
GO:BP	Regulation of tube diameter	GO:0035296	0.014459	143
GO:BP	Blood vessel diameter maintenance	GO:0097746	0.014459	143
GO:BP	Mesonephros development	GO:0001823	0.014474	105
GO:BP	Canonical Wnt signaling pathway	GO:0060070	0.014795	299
GO:BP	Epidermal cell differentiation	GO:0009913	0.014826	240

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Negative regulation of nervous system development	GO:0051961	0.015087	151
GO:BP	Regulation of biosynthetic process	GO:0009889	0.015234	4,190
GO:BP	BMP signaling pathway	GO:0030509	0.015515	159
GO:BP	Anatomical structure maturation	GO:0071695	0.015999	253
GO:BP	Regulation of amine transport	GO:0051952	0.016019	98
GO:BP	Water homeostasis	GO:0030104	0.016516	40
GO:BP	Meiosis I	GO:0007127	0.01655	132
GO:BP	Regulation of axon extension involved in axon guidance	GO:0048841	0.0169	34
GO:BP	Sperm flagellum assembly	GO:0120316	0.016951	37
GO:BP	Synaptic transmission, glutamatergic	GO:0035249	0.017449	102
GO:BP	Regulation of tube size	GO:0035150	0.017995	144
GO:BP	Positive regulation of RNA biosynthetic process	GO:1902680	0.018299	1,710
GO:BP	Amine transport	GO:0015837	0.018819	106
GO:BP	Regulation of axonogenesis	GO:0050770	0.019043	160
GO:BP	Inositol lipid-mediated signaling	GO:0048017	0.019136	180
GO:BP	Phosphatidylinositol-mediated signaling	GO:0048015	0.01921	176
GO:BP	Postsynapse organization	GO:0099173	0.019226	168
GO:BP	Cellular metal ion homeostasis	GO:0006875	0.019427	423
GO:BP	Positive regulation of potassium ion transport	GO:0043268	0.020666	50
GO:BP	Positive regulation of locomotion	GO:0040017	0.020824	572
GO:BP	Cell-matrix adhesion	GO:0007160	0.021069	238
GO:BP	Positive regulation of response to stimulus	GO:0048584	0.021196	2,267
GO:BP	Negative regulation of neurogenesis	GO:0050768	0.022317	145
GO:BP	Signal release from synapse	GO:0099643	0.022954	153
GO:BP	Neurotransmitter secretion	GO:0007269	0.022954	153
GO:BP	Regulation of macromolecule biosynthetic process	GO:0010556	0.023236	3,965
GO:BP	Cellular monoatomic ion homeostasis	GO:0006873	0.024236	510
GO:BP	Cellular monoatomic cation homeostasis	GO:0030003	0.024294	501
GO:BP	Atrial cardiac muscle cell to AV node cell communication	GO:0086066	0.024523	18
GO:BP	Atrial cardiac muscle cell action potential	GO:0086014	0.024523	18
GO:BP	Atrial cardiac muscle cell to AV node cell signaling	GO:0086026	0.024523	18
GO:BP	Retina layer formation	GO:0010842	0.024797	26
GO:BP	Cell fate determination	GO:0001709	0.024823	44
GO:BP	Hormone transport	GO:0009914	0.025019	307
GO:BP	Embryonic epithelial tube formation	GO:0001838	0.025256	130
GO:BP	Response to wounding	GO:0009611	0.025384	574
GO:BP	Multicellular organismal homeostasis	GO:0048871	0.025487	754
GO:BP	Regulation of synaptic vesicle cycle	GO:0098693	0.025644	9
GO:BP	Gliogenesis	GO:0042063	0.026362	316
GO:BP	Regulation of monoatomic cation transmembrane transport	GO:1904062	0.02644	329
GO:BP	Neurotransmitter metabolic process	GO:0042133	0.027372	29
GO:BP	Cellular response to monoamine stimulus	GO:0071868	0.02744	100
GO:BP	Ureteric bud development	GO:0001657	0.02744	100
GO:BP	Cellular response to catecholamine stimulus	GO:0071870	0.02744	100
GO:BP	Positive regulation of transferase activity	GO:0051347	0.027628	584
GO:BP	Axon extension involved in axon guidance	GO:0048846	0.027993	38
GO:BP	Neuron projection extension involved in neuron projection guidance	GO:1902284	0.027993	38
GO:BP	Positive regulation of nucleic acid-templated transcription	GO:1903508	0.028374	1,703
GO:BP	Positive regulation of DNA-templated transcription	GO:0045893	0.028374	1,703
GO:BP	Serotonin receptor signaling pathway	GO:0007210	0.028743	35

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:BP	Cell-cell signaling involved in cardiac conduction	GO:0086019	0.028743	35
GO:BP	Positive regulation of kinase activity	GO:0033674	0.030082	494
GO:BP	Dopamine transport	GO:0015872	0.031035	51
GO:BP	Glandular epithelial cell differentiation	GO:0002067	0.03114	75
GO:BP	Meiotic chromosome segregation	GO:0045132	0.031311	108
GO:BP	Organic cyclic compound biosynthetic process	GO:1901362	0.031593	4,307
GO:BP	Negative regulation of nitrogen compound metabolic process	GO:0051172	0.032916	2,401
GO:BP	Axis specification	GO:0009798	0.033119	97
GO:BP	Epithelial tube formation	GO:0072175	0.033559	143
GO:BP	Olefinic compound metabolic process	GO:0120254	0.034578	159
GO:BP	Autonomic nervous system development	GO:0048483	0.034709	48
GO:BP	Embryonic pattern specification	GO:0009880	0.035545	79
GO:BP	Negative regulation of apoptotic process	GO:0043066	0.038008	881
GO:BP	Forebrain neuron differentiation	GO:0021879	0.038403	45
GO:BP	Regulation of cell growth	GO:0001558	0.038739	429
GO:BP	Ameboidal-type cell migration	GO:0001667	0.038739	429
GO:BP	Regulation of body fluid levels	GO:0050878	0.039027	367
GO:BP	Embryonic skeletal system morphogenesis	GO:0048704	0.039958	94
GO:BP	Second-messenger-mediated signaling	GO:0019932	0.041203	315
GO:BP	Regulation of cellular biosynthetic process	GO:0031326	0.041424	4,124
GO:BP	Negative regulation of cell death	GO:0060548	0.041807	1,001
GO:BP	Synaptic vesicle exocytosis	GO:0016079	0.042038	113
GO:BP	Tube formation	GO:0035148	0.04206	156
GO:BP	Transmission of nerve impulse	GO:0019226	0.042349	76
GO:BP	Animal organ formation	GO:0048645	0.043584	69
GO:BP	Regulation of systemic arterial blood pressure by hormone	GO:0001990	0.04508	39
GO:BP	Signaling receptor ligand precursor processing	GO:0140448	0.04508	39
GO:BP	Regulation of receptor signaling pathway via JAK-STAT	GO:0046425	0.045937	102
GO:BP	Bone morphogenesis	GO:0060349	0.045937	102
GO:BP	Membrane repolarization during action potential	GO:0086011	0.04618	27
GO:BP	Cellular calcium ion homeostasis	GO:0006874	0.046687	290
GO:BP	Cardiac muscle cell membrane repolarization	GO:0099622	0.047498	36
GO:BP	Peptide hormone processing	GO:0016486	0.047498	36
GO:BP	Negative regulation of monoatomic ion transport	GO:0043271	0.04792	129
GO:BP	Mesodermal cell differentiation	GO:0048333	0.048798	33
GO:CC	Cell periphery	GO:0071944	2.57e-85	6,168
GO:CC	Plasma membrane	GO:0005886	3.43e-69	5,682
GO:CC	Cell projection	GO:0042995	1.03e-53	2,389
GO:CC	Plasma membrane bounded cell projection	GO:0120025	2.86e-51	2,276
GO:CC	Cell junction	GO:0030054	1.97e-47	2,122
GO:CC	Plasma membrane region	GO:0098590	4.16e-38	1,207
GO:CC	Synapse	GO:0045202	4.6e-37	1,337
GO:CC	Neuron projection	GO:0043005	3.43e-36	1,391
GO:CC	Membrane	GO:0016020	1.69e-34	9,840
GO:CC	Extracellular region	GO:0005576	6e-28	4,234
GO:CC	Somatodendritic compartment	GO:0036477	9.22e-25	859
GO:CC	Dendritic tree	GO:0097447	2.56e-19	631
GO:CC	Dendrite	GO:0030425	3.89e-19	629
GO:CC	Ion channel complex	GO:0034702	1.25e-18	309
GO:CC	Extracellular matrix	GO:0031012	7.85e-18	565

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:CC	External encapsulating structure	GO:0030312	9.86e-18	566
GO:CC	Cellular anatomical entity	GO:0110165	4.34e-17	21,569
GO:CC	Apical plasma membrane	GO:0016324	8.22e-17	372
GO:CC	Neuronal cell body	GO:0043025	1.44e-15	507
GO:CC	Anchoring junction	GO:0070161	1.54e-15	983
GO:CC	Cell body	GO:0044297	2.57e-15	576
GO:CC	Apical part of cell	GO:0045177	4.26e-15	439
GO:CC	Axon	GO:0030424	4.87e-14	651
GO:CC	Postsynapse	GO:0098794	5.26e-14	591
GO:CC	Cytoskeleton	GO:0005856	1.42e-13	2,399
GO:CC	Synaptic membrane	GO:0097060	1.83e-13	305
GO:CC	Supramolecular polymer	GO:0099081	2.84e-13	1,053
GO:CC	Cell-cell junction	GO:0005911	4.23e-13	510
GO:CC	Supramolecular fiber	GO:0099512	8.82e-13	1,044
GO:CC	Transmembrane transporter complex	GO:1902495	9.25e-13	397
GO:CC	Transporter complex	GO:1990351	9.55e-13	424
GO:CC	Cation channel complex	GO:0034703	2.43e-12	204
GO:CC	Postsynaptic membrane	GO:0045211	3.45e-11	212
GO:CC	Extracellular space	GO:0005615	7.16e-11	3,379
GO:CC	Presynapse	GO:0098793	8.37e-11	473
GO:CC	Cilium	GO:0005929	5.55e-10	733
GO:CC	Plasma membrane protein complex	GO:0098797	2.3e-09	713
GO:CC	Collagen-containing extracellular matrix	GO:0062023	3.89e-09	429
GO:CC	Cell surface	GO:0009986	5.53e-09	955
GO:CC	Glutamatergic synapse	GO:0098978	6.17e-09	340
GO:CC	Cell projection membrane	GO:0031253	7.86e-09	349
GO:CC	Potassium channel complex	GO:0034705	1.48e-08	98
GO:CC	Cytoplasm	GO:0005737	1.61e-08	12,321
GO:CC	Supramolecular complex	GO:0099080	2.37e-08	1,408
GO:CC	Voltage-gated potassium channel complex	GO:0008076	4.6e-08	88
GO:CC	Polymeric cytoskeletal fiber	GO:0099513	9.44e-08	802
GO:CC	Basal part of cell	GO:0045178	2.25e-07	275
GO:CC	GABA-ergic synapse	GO:0098982	1e-06	76
GO:CC	Contractile fiber	GO:0043292	1.01e-06	247
GO:CC	I band	GO:0031674	1.19e-06	147
GO:CC	Myofibril	GO:0030016	1.8e-06	238
GO:CC	Cytoplasmic region	GO:0099568	1.81e-06	289
GO:CC	Basal plasma membrane	GO:0009925	3.02e-06	256
GO:CC	Neuron to neuron synapse	GO:0098984	3.04e-06	336
GO:CC	Actin cytoskeleton	GO:0015629	3.35e-06	508
GO:CC	Axoneme	GO:0005930	3.54e-06	158
GO:CC	Z disc	GO:0030018	3.7e-06	133
GO:CC	Adherens junction	GO:0005912	4.44e-06	181
GO:CC	Ciliary plasm	GO:0097014	4.66e-06	159
GO:CC	Sarcomere	GO:0030017	6.83e-06	217
GO:CC	Motile cilium	GO:0031514	9.84e-06	246
GO:CC	Sarcolemma	GO:0042383	1.62e-05	138
GO:CC	Dendritic spine	GO:0043197	1.64e-05	175
GO:CC	Basolateral plasma membrane	GO:0016323	1.7e-05	229
GO:CC	Neuron spine	GO:0044309	1.73e-05	179

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:CC	Tight junction	GO:0070160	1.93e-05	135
GO:CC	Apical junction complex	GO:0043296	3.02e-05	155
GO:CC	Cluster of actin-based cell projections	GO:0098862	3.46e-05	163
GO:CC	Plasma membrane bounded cell projection cytoplasm	GO:0032838	4.74e-05	250
GO:CC	Cortical cytoskeleton	GO:0030863	5.6e-05	110
GO:CC	Neurotransmitter receptor complex	GO:0098878	6.77e-05	45
GO:CC	Chromatin	GO:0000785	7.28e-05	1,363
GO:CC	Receptor complex	GO:0043235	0.000158	529
GO:CC	Asymmetric synapse	GO:0032279	0.00019	307
GO:CC	Leading edge membrane	GO:0031256	0.000193	178
GO:CC	Bicellular tight junction	GO:0005923	0.000205	129
GO:CC	Postsynaptic density	GO:0014069	0.000276	301
GO:CC	Cortical actin cytoskeleton	GO:0030864	0.000374	81
GO:CC	Perikaryon	GO:0043204	0.00039	158
GO:CC	Postsynaptic specialization	GO:0099572	0.000516	305
GO:CC	Microtubule	GO:0005874	0.000589	474
GO:CC	Distal axon	GO:0150034	0.000612	281
GO:CC	Endomembrane system	GO:0012505	0.000645	4,730
GO:CC	9+2 motile cilium	GO:0097729	0.000777	165
GO:CC	Catenin complex	GO:0016342	0.000831	32
GO:CC	Cytoplasmic microtubule	GO:0005881	0.000875	105
GO:CC	Dendrite membrane	GO:0032590	0.000935	41
GO:CC	Neuron projection membrane	GO:0032589	0.000948	60
GO:CC	Axon terminus	GO:0043679	0.00113	117
GO:CC	Cell cortex	GO:0005938	0.001567	321
GO:CC	Actin-based cell projection	GO:0098858	0.00168	221
GO:CC	Neuronal cell body membrane	GO:0032809	0.002312	28
GO:CC	Cell body membrane	GO:0044298	0.002535	31
GO:CC	Neuron projection terminus	GO:0044306	0.002744	132
GO:CC	Membrane protein complex	GO:0098796	0.00353	1,357
GO:CC	Serotonin receptor complex	GO:0098665	0.003896	9
GO:CC	Chloride channel complex	GO:0034707	0.004364	54
GO:CC	Cell leading edge	GO:0031252	0.004991	426
GO:CC	GABA receptor complex	GO:1902710	0.005252	21
GO:CC	Vesicle	GO:0031982	0.005479	3,973
GO:CC	Actin filament bundle	GO:0032432	0.005719	79
GO:CC	Brush border	GO:0005903	0.007913	106
GO:CC	GABA-A receptor complex	GO:1902711	0.008496	19
GO:CC	Cell-cell contact zone	GO:0044291	0.010909	74
GO:CC	Ionotropic glutamate receptor complex	GO:0008328	0.011103	40
GO:CC	Axonemal microtubule	GO:0005879	0.011936	37
GO:CC	Extrinsic component of plasma membrane	GO:0019897	0.011966	175
GO:CC	Contractile actin filament bundle	GO:0097517	0.012979	71
GO:CC	Stress fiber	GO:0001725	0.012979	71
GO:CC	Excitatory synapse	GO:0060076	0.015161	54
GO:CC	Chromosome	GO:0005694	0.015666	1,927
GO:CC	Presynaptic membrane	GO:0042734	0.019172	87
GO:CC	Sperm flagellum	GO:0036126	0.022199	150
GO:CC	Membrane raft	GO:0045121	0.028595	326
GO:CC	Membrane microdomain	GO:0098857	0.032182	327

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Source	Description	Term ID	Adjusted <i>P</i>	<i>n</i>
GO:CC	Microvillus	GO:0005902	0.033481	93
GO:CC	T-tubule	GO:0030315	0.035231	53
GO:CC	Non-motile cilium	GO:0097730	0.042141	170
GO:CC	Schaffer collateral - CA1 synapse	GO:0098685	0.043777	79
GO:CC	Plasma membrane raft	GO:0044853	0.047937	114

**Abbreviations:** BP, biological process; CC, cellular process; GO, gene ontology; MF, molecular function.