

A

| GOTERM_BP_5 | Count | % | P-Value | FDR |
|--|-------|-----|---------|------|
| synaptic vesicle transport | 15 | 1.1 | 0.000 | 0.1 |
| exocytosis | 23 | 1.6 | 0.000 | 0.2 |
| synaptic transmission | 58 | 4.1 | 0.000 | 0.4 |
| intracellular transport | 81 | 5.7 | 0.000 | 0.4 |
| secretory pathway | 41 | 2.9 | 0.000 | 0.5 |
| regulation of neurotransmitter levels | 27 | 1.9 | 0.000 | 0.5 |
| secretion by cell | 46 | 3.2 | 0.000 | 0.6 |
| neuron development | 36 | 2.5 | 0.000 | 0.6 |
| catecholamine metabolic process | 11 | 0.8 | 0.001 | 1.5 |
| microtubule-based process | 30 | 2.1 | 0.001 | 1.9 |
| cellular morphogenesis during differentiation | 30 | 2.1 | 0.002 | 2.6 |
| neuron differentiation | 42 | 3 | 0.002 | 2.8 |
| neurite morphogenesis | 28 | 2 | 0.002 | 3.3 |
| cell part morphogenesis | 36 | 2.5 | 0.002 | 4.2 |
| cell projection organization and biogenesis | 36 | 2.5 | 0.002 | 4.2 |
| cell projection morphogenesis | 36 | 2.5 | 0.002 | 4.2 |
| monosaccharide catabolic process | 15 | 1.1 | 0.003 | 4.9 |
| cell redox homeostasis | 11 | 0.8 | 0.003 | 5.1 |
| protein transport | 67 | 4.7 | 0.003 | 5.3 |
| cytoskeleton-dependent intracellular transport | 18 | 1.3 | 0.004 | 6.3 |
| microtubule-based movement | 16 | 1.1 | 0.004 | 6.7 |
| neurogenesis | 49 | 3.4 | 0.004 | 7.5 |
| dopamine metabolic process | 8 | 0.6 | 0.006 | 10.2 |
| modification-dependent macromolecule catabolic process | 21 | 1.5 | 0.007 | 10.8 |
| cellular carbohydrate catabolic process | 17 | 1.2 | 0.009 | 14.3 |
| forebrain development | 11 | 0.8 | 0.011 | 17.6 |
| vesicle coating | 4 | 0.3 | 0.011 | 18 |
| cellular protein catabolic process | 21 | 1.5 | 0.012 | 18.8 |
| regulation of neuronal synaptic plasticity | 9 | 0.6 | 0.014 | 21.8 |
| regulated secretory pathway | 17 | 1.2 | 0.018 | 27.8 |
| endocytosis | 23 | 1.6 | 0.019 | 28.5 |
| regulation of exocytosis | 8 | 0.6 | 0.020 | 29.4 |
| mRNA metabolic process | 25 | 1.8 | 0.020 | 30 |
| protein folding | 24 | 1.7 | 0.022 | 31.8 |
| synaptic vesicle exocytosis | 7 | 0.5 | 0.023 | 33.9 |
| biogenic amine metabolic process | 14 | 1 | 0.025 | 35.6 |
| neurotransmitter secretion | 15 | 1.1 | 0.026 | 37 |
| regulation of synapse structure and activity | 12 | 0.8 | 0.026 | 37.2 |
| dendrite development | 8 | 0.6 | 0.027 | 38 |
| tricarboxylic acid cycle | 6 | 0.4 | 0.027 | 38.3 |
| membrane budding | 4 | 0.3 | 0.028 | 38.8 |
| dopamine biosynthetic process | 4 | 0.3 | 0.028 | 38.8 |
| central nervous system development | 30 | 2.1 | 0.028 | 38.8 |
| cell morphogenesis | 53 | 3.7 | 0.028 | 39.5 |
| actin filament-based process | 25 | 1.8 | 0.029 | 40.2 |
| protein catabolic process | 24 | 1.7 | 0.033 | 44.5 |
| amine biosynthetic process | 14 | 1 | 0.035 | 46.8 |
| ER to Golgi vesicle-mediated transport | 10 | 0.7 | 0.037 | 48.4 |
| protein polymerization | 10 | 0.7 | 0.037 | 48.4 |
| synaptogenesis | 7 | 0.5 | 0.038 | 49.8 |
| regulation of RNA metabolic process | 6 | 0.4 | 0.040 | 50.9 |
| positive regulation of protein catabolic process | 3 | 0.2 | 0.042 | 52.6 |
| acetyl-CoA metabolic process | 8 | 0.6 | 0.046 | 56.6 |
| translational elongation | 6 | 0.4 | 0.047 | 57.2 |
| hexose metabolic process | 22 | 1.5 | 0.048 | 58 |

B

| GOTERM_BP_5 | Count | % | P-Value | FDR |
|---|-------|-----|---------|------|
| modification-dependent macromolecule catabolic process | 52 | 2 | 0.000 | 0 |
| cellular protein catabolic process | 52 | 2 | 0.000 | 0 |
| intracellular transport | 156 | 6 | 0.000 | 0 |
| protein catabolic process | 58 | 2.2 | 0.000 | 0 |
| protein transport | 124 | 4.8 | 0.000 | 0 |
| synaptic vesicle transport | 19 | 0.7 | 0.000 | 0.5 |
| cellular carbohydrate catabolic process | 30 | 1.2 | 0.000 | 0.5 |
| acetyl-CoA metabolic process | 16 | 0.6 | 0.000 | 0.8 |
| cell redox homeostasis | 17 | 0.7 | 0.000 | 0.8 |
| cell part morphogenesis | 60 | 2.3 | 0.000 | 0.8 |
| cell projection morphogenesis | 60 | 2.3 | 0.000 | 0.8 |
| cell projection organization and biogenesis | 60 | 2.3 | 0.000 | 0.8 |
| intracellular protein transport | 87 | 3.4 | 0.000 | 0.9 |
| secretory pathway | 62 | 2.4 | 0.001 | 1.4 |
| exocytosis | 31 | 1.2 | 0.001 | 1.7 |
| monosaccharide catabolic process | 23 | 0.9 | 0.001 | 1.8 |
| Golgi vesicle transport | 28 | 1.1 | 0.001 | 2.4 |
| phosphorylation | 128 | 4.9 | 0.002 | 3.6 |
| ER to Golgi vesicle-mediated transport | 18 | 0.7 | 0.002 | 4 |
| cytoskeleton-dependent intracellular transport | 27 | 1 | 0.004 | 5.9 |
| G1/S transition of mitotic cell cycle | 15 | 0.6 | 0.004 | 6 |
| protein depolymerization | 13 | 0.5 | 0.004 | 6.4 |
| interphase of mitotic cell cycle | 23 | 0.9 | 0.004 | 6.7 |
| protein modification process | 223 | 8.6 | 0.005 | 7.6 |
| interphase | 23 | 0.9 | 0.005 | 7.9 |
| synaptic transmission | 85 | 3.3 | 0.006 | 9.5 |
| regulation of cytoskeleton organization and biogenesis | 14 | 0.5 | 0.006 | 10.2 |
| regulation of organelle organization and biogenesis | 14 | 0.5 | 0.006 | 10.2 |
| neuron differentiation | 64 | 2.5 | 0.006 | 10.5 |
| microtubule-based movement | 23 | 0.9 | 0.007 | 10.8 |
| microtubule-based process | 43 | 1.7 | 0.007 | 11.2 |
| secretion by cell | 66 | 2.5 | 0.007 | 11.4 |
| neuron development | 50 | 1.9 | 0.007 | 11.7 |
| cell morphogenesis | 93 | 3.6 | 0.008 | 13.1 |
| nerve-nerve synaptic transmission | 16 | 0.6 | 0.008 | 13.3 |
| catecholamine metabolic process | 13 | 0.5 | 0.008 | 13.6 |
| protein folding | 40 | 1.5 | 0.009 | 14.2 |
| tricarboxylic acid cycle | 9 | 0.3 | 0.009 | 14.7 |
| coenzyme catabolic process | 10 | 0.4 | 0.009 | 15 |
| cellular morphogenesis during differentiation | 43 | 1.7 | 0.010 | 16.2 |
| regulation of neurotransmitter levels | 35 | 1.3 | 0.010 | 16.8 |
| central nervous system development | 51 | 2 | 0.011 | 17.2 |
| neurite morphogenesis | 40 | 1.5 | 0.012 | 18.7 |
| mitochondrial transport | 14 | 0.5 | 0.012 | 19.1 |
| protein polymerization | 16 | 0.6 | 0.014 | 22.5 |
| dopamine metabolic process | 10 | 0.4 | 0.016 | 25.1 |
| regulation of RNA metabolic process | 9 | 0.3 | 0.017 | 26 |
| mRNA metabolic process | 40 | 1.5 | 0.019 | 28.1 |
| small GTPase mediated signal transduction | 69 | 2.7 | 0.019 | 28.7 |
| regulation of actin polymerization and/or depolymerization | 11 | 0.4 | 0.020 | 29.3 |
| negative regulation of cellular component organization and biogenesis | 11 | 0.4 | 0.020 | 29.3 |
| aerobic respiration | 10 | 0.4 | 0.021 | 31.3 |
| translational elongation | 9 | 0.3 | 0.022 | 32.9 |
| forebrain development | 15 | 0.6 | 0.023 | 33.5 |
| vesicle docking | 9 | 0.3 | 0.029 | 40.4 |
| Wnt receptor signaling pathway | 22 | 0.8 | 0.029 | 40.6 |
| biogenic amine metabolic process | 21 | 0.8 | 0.029 | 40.8 |
| RNA transport | 11 | 0.4 | 0.030 | 41.6 |
| nucleic acid transport | 11 | 0.4 | 0.030 | 41.6 |
| protein targeting to mitochondrion | 8 | 0.3 | 0.031 | 42.5 |
| actin filament depolymerization | 7 | 0.3 | 0.032 | 43.7 |
| foregut morphogenesis | 4 | 0.2 | 0.032 | 43.7 |
| synaptic vesicle exocytosis | 9 | 0.3 | 0.046 | 56.3 |
| actin filament-based process | 39 | 1.5 | 0.047 | 56.8 |