

GeDiPNet Cluster 209 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 16:30:24

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
chemical synaptic transmission	GO:0007268	12	GRIN2A, GRM1, GRM2, GRM3, GRM4, GRM5, KCNC4, NPY, PDYN, SLC12A5, SLC1A1, CDK5	236	39	24.36	3.600e-14	2.138e-11
adenylate cyclase-inhibiting G protein-coupled glutamate receptor signaling pathway	GO:0007196	5	GRM1, GRM2, GRM3, GRM4, GRM5	9	39	266.20	3.799e-12	1.522e-9
regulation of synaptic transmission, glutamatergic	GO:0051966	6	GRM1, GRM2, GRM3, GRM4, GRM5, CDK5	33	39	87.12	5.870e-11	1.779e-8
G protein-coupled glutamate receptor signaling pathway	GO:0007216	5	GRM1, GRM2, GRM3, GRM4, GRM5	14	39	171.13	5.991e-11	1.810e-8
sensory perception of pain	GO:0019233	6	GRIN2A, GRM1, P2RX4, P2RX7, TRPV1, CDK5	44	39	65.34	3.679e-10	9.140e-8
excitatory postsynaptic potential	GO:0060079	5	GRIN2A, P2RX4, P2RX7, TRPV1, CDK5	69	39	34.72	3.094e-7	3.126e-5
positive regulation of MAPK cascade	GO:0043410	7	GRM1, GRM4, GRM5, KDR, P2RX7, TEK, VEGFA	224	39	14.97	3.594e-7	3.538e-5
learning or memory	GO:0007611	5	GRIN2A, GRM5, KCNAB1, MAPT, SLC1A1	72	39	33.27	3.834e-7	3.741e-5
synaptic signaling via neuropeptide	GO:0099538	3	GRM1, NPY, NPY2R	9	39	159.72	6.999e-7	6.217e-5
monoatomic ion transport	GO:0006811	10	GRIN2A, KCNAB1, KCNC4, NALCN, P2RX4, P2RX7, SLC12A2, SLC12A5, SLC1A1, TRPV1	667	39	7.18	7.813e-7	6.786e-5
locomotory behavior	GO:0007626	5	RELN, GRM1, GRM5, NPY2R, SLC1A1	99	39	24.20	1.881e-6	1.370e-4
positive regulation of endothelial cell chemotaxis	GO:2001028	3	KDR, P2RX4, VEGFA	13	39	110.57	2.369e-6	1.648e-4
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	6	RELN, GRM2, KDR, P2RX4, TEK, VEGFA	217	39	13.25	5.421e-6	3.203e-4
regulation of postsynaptic membrane potential	GO:0060078	4	GRIN2A, GRM1, GRM5, CDK5	59	39	32.49	6.787e-6	3.826e-4
cellular response to ATP	GO:0071318	3	P2RX4, P2RX7, TRPV1	19	39	75.66	7.958e-6	4.356e-4