

GeDiPNet Cluster 75 -- 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 06:16:13

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	31	BSN, CACNB2, DLG2, EXOC4, GRIN2A, GRM3, SYN2, APP, CACNA1A, SNCA, NPY, UTS2	236	816	3.01	4.459e-8	6.151e-6
modulation of chemical synaptic transmission	GO:0050804	21	BSN, DRD2, GRID1, GRIK3, GRIN2A, GRM3, NTNG1, PPP3CA, CACNA1A, CHMP2B, TNF, NRG3	121	816	3.97	5.849e-8	7.732e-6
axonogenesis	GO:0007409	21	BCL11B, CELSR3, CNTN4, DCC, DRD2, NTNG1, APP, ATP8A2, ANK3, BAIAP2, LLGL1, SLITRK1	125	816	3.85	1.045e-7	1.254e-5
postsynaptic modulation of chemical synaptic transmission	GO:0099170	9	BRAF, DCC, DRD2, GRM3, INA, NRGN, PPP3CA, SORCS3, RASGRF2	25	816	8.24	6.004e-7	5.456e-5
negative regulation of synaptic transmission, glutamatergic	GO:0051967	6	DRD2, GRIK3, HCN1, DRD3, GRIK2, HTR2A	10	816	13.74	1.230e-6	9.784e-5
response to xenobiotic stimulus	GO:0009410	27	ACSL1, CHUK, DRD2, GRIN2A, RPTOR, TFAP2B, GCLM, MTHFR, SNCA, TNF, SLC6A4, DRD3	248	816	2.49	1.234e-5	6.145e-4
endocytosis	GO:0006897	25	LRP2, MYO19, MYO1D, MYO1E, NCKIPSD, RAB5B, SGIP1, APP, TSC2, RUFY1, CLTA, CSNK1G3	223	816	2.57	1.554e-5	7.396e-4
synaptic membrane adhesion	GO:0099560	8	LRFN5, NTNG1, PCDH17, PTPRF, SLITRK1, SLITRK5, TENM4, CDH6	29	816	6.32	2.419e-5	1.038e-3
cardiac muscle hypertrophy in response to stress	GO:0014898	6	ATP2A2, PPP3CA, NPPA, SMAD4, HDAC4, KDM4A	15	816	9.16	2.427e-5	1.040e-3
synaptic transmission, dopaminergic	GO:0001963	6	DRD2, SNCA, DRD3, DRD4, COMT, CRH	15	816	9.16	2.427e-5	1.040e-3
neuron projection development	GO:0031175	20	CNTN4, FGFR1, GDNF, NEGR1, PTPRG, APP, LAMB1, NPY, MAPT, WNT7B, CNTNAP2, EDN2	161	816	2.84	2.480e-5	1.057e-3
calcium-mediated signaling	GO:0019722	16	CAMKK2, GRIK3, GRIN2A, MCTP1, PPP3CA, APP, TNF, CCL20, RYR2, GRIK2, P2RX7, PPP1R9A	114	816	3.21	3.546e-5	1.391e-3
nervous system development	GO:0007399	50	AMBRA1, BRINP1, CAMK1D, CHRNA3, CNTN4, DLG2, ERBB4, FBXL17, GDNF, IGSF9B, INA, LRP2	631	816	1.81	3.606e-5	1.409e-3
regulation of synaptic plasticity	GO:0048167	12	CNTN4, GRID1, GRIN2A, SORCS3, VPS13A, MAPT, BAIAP2, CPEB3, LYPD6, GRID2, IGSF11, MECP2	69	816	3.98	3.943e-5	1.504e-3
positive regulation of MAPK cascade	GO:0043410	24	BANK1, ERBB3, ERBB4, FGFR1, GSDME, KIT, VEGFA, APP, IGF1R, TNF, DRD4, ADRB1	224	816	2.45	4.790e-5	1.738e-3