

GeDiPNet Cluster 66 -- 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 19:39:15

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
signal transduction	GO:0007165	81	AVP, CSF2, GNAI1, GNAI3, GRP, HRH3, NGF, POMC, TRH, ADORA1, CHRM2, CRH	2125	226	3.15	2.885e-22	6.348e-19
chemical synaptic transmission	GO:0007268	30	APP, HRH3, PDYN, TAC1, CHRM2, CRH, HTR1A, UTS2, CHRM4, CARTPT, GRIN1, GRIN2B	236	226	10.51	4.186e-22	9.040e-19
G protein-coupled receptor signaling pathway	GO:0007186	53	APOE, APP, GNAI1, GNAI3, HRH3, IL2, ADORA1, AGT, CHRM2, DRD2, EDN1, GCG	1031	226	4.25	1.057e-19	1.635e-16
adenylate cyclase-activating G protein-coupled receptor signaling pathway	GO:0007189	24	APP, AVP, GNAI1, GCG, GNAI2, HTR1A, CALCA, CNR1, CNR2, DRD1, PTHLH, VIP	161	226	12.33	1.595e-19	2.395e-16
response to xenobiotic stimulus	GO:0009410	28	AVP, CRH, CYP1A1, DRD2, EDN1, DRD1, FYN, AHR, CASP3, CAT, TNF, DRD3	248	226	9.34	2.801e-19	4.083e-16
vasodilation	GO:0042311	16	APOE, ADORA1, KNG1, CALCA, DRD1, INS, TNF, BDKRB2, GPER1, NOS1, ADORA2A, ACE	50	226	26.46	4.197e-19	5.992e-16
G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	GO:0007187	16	HRH3, CHRM2, HTR1A, CNR1, CNR2, DRD1, CHRM4, CCL2, HTR2A, MC1R, OPRM1, HTR2C	54	226	24.50	1.723e-18	2.228e-15
response to ethanol	GO:0045471	20	AVP, IL2, CRH, DRD2, GNRH1, TACR1, FYN, TH, CASP8, CAT, TNF, DRD3	110	226	15.03	3.229e-18	4.006e-15
response to hypoxia	GO:0001666	23	ADORA1, CYP1A1, DRD2, EDN1, TH, CASP3, CASP9, CAT, TNF, AGER, COMT, ITGA2	176	226	10.81	1.929e-17	2.136e-14
positive regulation of MAPK cascade	GO:0043410	25	APP, IL6, ADORA1, EDN1, EDN3, DRD1, IL11, INS, MAP2K6, TNF, CARTPT, GPER1	224	226	9.23	3.398e-17	3.570e-14
sensory perception of pain	GO:0019233	14	NGF, TAC1, AQP1, CCL2, HOXD1, MAPK3, MC1R, MECP2, OPRM1, PNOC, PROK2, SCN11A	44	226	26.31	7.968e-17	7.807e-14
regulation of blood pressure	GO:0008217	17	POMC, TAC1, AGT, EDN1, TACR1, UTS2, CALCA, PTGS2, COMT, PTGS1, NPY, ACE	83	226	16.94	1.391e-16	1.277e-13
negative regulation of blood pressure	GO:0045776	12	ADORA1, DRD2, CALCA, OXT, DRD3, BDKRB1, NOS1, NOS2, NPY, APLN, NPPA, UCN	28	226	35.44	1.873e-16	1.667e-13
blood vessel diameter maintenance	GO:0097746	13	AVP, AGT, EDN1, EDN2, EDN3, KNG1, NTS, UTS2, NPPC, ACE, NPPA, NPPB	37	226	29.05	2.308e-16	2.039e-13
neuropeptide signaling pathway	GO:0007218	18	GNAI1, GRP, PDYN, POMC, TAC1, NTS, CARTPT, CCKBR, GAL, OPRM1, PNOC, PROK2	111	226	13.41	1.366e-15	1.034e-12