

GeDiPNet Cluster 5 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 06:19:42

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
nervous system development	GO:0007399	177	BRSK2, CAMK2B, DEAF1, DPYSL2, ERBB4, KCNQ2, MBD5, SEMA6B, TCF4, DCDC2, TNIK, SIAH1	631	1741	3.01	3.611e-43	5.042e-39
chromatin organization	GO:0006325	124	HNRNPU, ASH1L, JARID2, KDM5B, SETD1B, ZMYND11, METTL23, ATXN7L3, CHD1, CHD2, CHD8, HDAC2	449	1741	2.96	1.248e-29	5.890e-26
chromatin remodeling	GO:0006338	96	ASH1L, JARID2, KDM5B, SETD1B, BAZ2B, CHD1, CHD2, CHD8, DYRK1A, HDAC2, JMJD1C, KDM4B	320	1741	3.22	4.157e-26	1.451e-22
brain development	GO:0007420	73	CIC, GRIN1, GRIN2B, SMG9, CNTNAP2, CHD8, CNTN4, DMBX1, DSCAML1, GRIN2A, GRIN2D, KDM4B	244	1741	3.21	4.605e-20	7.375e-17
positive regulation of DNA-templated transcription	GO:0045893	147	DEAF1, ERBB4, TCF4, KARS1, ATXN7L3, CAMK4, CHD8, CNOT9, DYRK1A, FEZF2, HDAC2, HNRNPD	778	1741	2.03	2.844e-17	2.861e-14
monoatomic ion transmembrane transport	GO:0034220	94	CACNA1I, CACNG2, GRIA1, GRIN1, GRIN2B, KCNQ2, KCNQ5, SCN8A, TRPM3, SLC26A5, TMC1, GRIK2	404	1741	2.50	3.355e-17	3.308e-14
synapse organization	GO:0050808	33	CTNND2, SLC6A1, CHRNA7, CNTN2, CNTN4, CNTN6, GPHN, PPFIA3, SEMA3E, SHANK1, SHANK2, CTNNB1	72	1741	4.92	6.743e-16	5.232e-13
chemical synaptic transmission	GO:0007268	64	GRIA1, GRIN1, GRIN2B, KCNQ2, SLC6A1, GRIK2, GRM7, CHRNA7, DLG4, GABBR2, GABRB2, GABRD	236	1741	2.91	1.933e-15	1.391e-12
monoatomic ion transport	GO:0006811	126	CACNA1I, CACNG2, GRIA1, GRIN1, GRIN2B, KCNQ2, KCNQ5, SCN8A, TRPM3, LHFPL5, TMC1, GRIK2	667	1741	2.03	6.186e-15	4.090e-12
axon guidance	GO:0007411	55	SEMA6B, SIAH1, ARHGAP35, CNTN2, CNTN4, CNTN6, CYFIP2, DSCAML1, EPHA4, LHX2, NRXN1, RELN	192	1741	3.07	1.486e-14	9.198e-12
cerebral cortex development	GO:0021987	34	GRIA1, TRAPPC9, CNTNAP2, LHX2, RELN, TBR1, YWHAE, ASPM, FOXG1, MCPH1, PAX6, PSEN1	88	1741	4.15	1.204e-13	6.437e-11
neuron migration	GO:0001764	42	KIRREL3, DCDC2, CNTN2, MEF2C, NR4A2, RELN, YWHAE, MYH10, ASPM, CDKL5, CTNNB1, DCX	132	1741	3.42	3.974e-13	1.927e-10
cognition	GO:0050890	27	LINS1, METTL23, TUSC3, WASHC4, CHRNA7, SHANK1, SHANK2, SHROOM4, SLC1A4, HOXA1, CUX2, CHRNA4	64	1741	4.53	3.387e-12	1.382e-9
tRNA aminoacylation for protein translation	GO:0006418	20	KARS1, SARS1, RARS2, AARS1, PARS2, DALRD3, NARS1, EARS2, EPRS1, FARS2, IARS1, LARS1	36	1741	5.96	3.699e-12	1.497e-9
positive regulation of transcription by RNA polymerase II	GO:0045944	182	HNRNPU, ASH1L, DLL1, GRIN1, MED12L, PPP3CA, TCF4, ZNF292, MET, EEF1D, MED25, METTL23	1208	1741	1.62	2.224e-11	7.460e-9