

GeDiPNet Cluster 2 -- 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 00:25:02

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	450	ACTL6B, AGRN, APBA1, APOB, ARHGEF2, ARID1A, ARID1B, ATOH7, ATXN10, BARHL2, BORCS5, BPNT1	631	9677	1.38	2.166e-24	6.211e-21
positive regulation of transcription by RNA polymerase II	GO:0045944	781	ACTN4, AGRN, APP, ARHGEF2, ATF7, ATOH7, AUTS2, BARHL2, BAZ1B, BCAS3, BCL11A, BCL3	1208	9677	1.25	7.036e-21	1.289e-17
modulation of chemical synaptic transmission	GO:0050804	106	ADCY8, BSN, BTBD9, CACNA1A, CAMKV, DLGAP2, EIF4EBP2, GRIA1, GRIK1, GRIK2, GRIK3, GRIN3B	121	9677	1.69	4.656e-17	4.804e-14
chemical synaptic transmission	GO:0007268	182	APBA1, APP, BSN, CACNA1A, CACNA1E, CACNA1G, CACNB2, CHRM3, CHRNA6, CHRNE, DLG2, DOC2A	236	9677	1.49	6.124e-16	5.005e-13
response to hypoxia	GO:0001666	141	ABAT, ADAM17, BMP2, BNIP3, CD24, DPP4, ERCC2, HSPG2, PAK1, PLOD1, PRKAA1, TGFB2	176	9677	1.55	4.295e-15	3.010e-12
axon guidance	GO:0007411	149	ALCAM, B3GNT2, CDH4, DAG1, DCC, DLX5, DRAXIN, DSCAM, EFNA5, EMB, EPHA4, EPHA5	192	9677	1.50	1.055e-13	5.774e-11
positive regulation of DNA-templated transcription	GO:0045893	501	DYRK1B, ABT1, ACTB, ACTL6B, AGT, APOE, ARID1A, ARID1B, ATF7IP, BCL3, BMP2, CAMK4	778	9677	1.24	2.769e-13	1.428e-10
response to xenobiotic stimulus	GO:0009410	184	ABAT, ABCA1, ABCG8, ADAM17, ADCYAP1R1, ADRA1A, BCAR3, BLOC1S3, COL18A1, CPS1, DUSP6, GABRG3	248	9677	1.43	2.843e-13	1.458e-10
cell population proliferation	GO:0008283	191	ALDH1A2, CCDC85C, CD2AP, CEBPA, CNTNAP2, CRK, DAPL1, DLX5, EGFR, ELAVL1, ERCC1, ESRRB	263	9677	1.40	2.911e-12	1.209e-9
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	162	AGT, APP, CASS4, CCR7, EFNA5, EGFR, ERBB3, ERBB4, F2R, F2RL1, FERMT2, FGFR3	217	9677	1.44	3.132e-12	1.287e-9
xenobiotic metabolic process	GO:0006805	98	CYP1A2, CYP2F1, RORA, SLC28A3, SMOX, BCHE, CYP2D6, CYP46A1, GSTO2, GSTP1, CYP2J2, HNF4A	120	9677	1.58	7.557e-12	2.851e-9
social behavior	GO:0035176	54	CNTNAP2, DSCAM, EIF4EBP2, MKKS, NEGR1, NLGN4X, NRXN1, NRXN2, NRXN3, RPTOR, SEPTIN5, SHANK2	58	9677	1.80	8.618e-12	3.214e-9
positive regulation of MAPK cascade	GO:0043410	165	ADRA1A, ADRA1B, ADRA1D, APP, AVPI1, BANK1, BCAR3, BMP2, CDON, EGFR, ERBB3, ERBB4	224	9677	1.42	1.302e-11	4.672e-9
neuron migration	GO:0001764	105	ABI3, AUTS2, BARHL2, CELSR1, CRK, DAB1, DCC, DISC1, GFRA3, MARK2, MEF2C, NEO1	132	9677	1.54	3.077e-11	9.956e-9
regulation of postsynaptic membrane potential	GO:0060078	54	CHRNA2, CHRNA6, CHRNE, GABBR1, GABRA2, GABRA4, GABRG3, GRIA1, GRIK1, GRIK3, GRIN3B, HCN1	59	9677	1.77	5.019e-11	1.551e-8