

GeDiPNet Cluster 267 -- 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 07:21:44

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cerebral cortex radially oriented cell migration	GO:0021799	2	CCDC141, MDGA1	13	45	63.89	4.349e-4	8.872e-3
prepulse inhibition	GO:0060134	2	GRIN3A, MDGA1	14	45	59.32	5.066e-4	9.833e-3
nervous system development	GO:0007399	7	UGT8, CAMK1D, MDGA1, NAV2, NRXN3, SOX4, SMARCA2	631	45	4.61	7.194e-4	1.251e-2
cochlea morphogenesis	GO:0090103	2	MYO3B, TIFAB	28	45	29.66	2.060e-3	2.355e-2
regulation of granulocyte chemotaxis	GO:0071622	1	CAMK1D	1	45	415.27	2.408e-3	2.570e-2
regulation of systemic arterial blood pressure by baroreceptor feedback	GO:0003025	1	NAV2	1	45	415.27	2.408e-3	2.570e-2
glossopharyngeal nerve development	GO:0021563	1	NAV2	1	45	415.27	2.408e-3	2.570e-2
vagus nerve development	GO:0021564	1	NAV2	1	45	415.27	2.408e-3	2.570e-2
microtubule-based transport	GO:0099111	1	GJA1	1	45	415.27	2.408e-3	2.570e-2
protein alpha-1,2-demannosylation	GO:0036508	1	MAN1B1	1	45	415.27	2.408e-3	2.570e-2
negative regulation of growth rate	GO:0045967	1	TMPRSS4	1	45	415.27	2.408e-3	2.570e-2
guanosine metabolic process	GO:0008617	1	DGUOK	1	45	415.27	2.408e-3	2.570e-2
dGTP metabolic process	GO:0046070	1	DGUOK	1	45	415.27	2.408e-3	2.570e-2
purine deoxyribonucleoside metabolic process	GO:0046122	1	DGUOK	1	45	415.27	2.408e-3	2.570e-2
brain development	GO:0007420	4	CCDC141, MACROD2, MDGA1, SOX4	244	45	6.81	2.777e-3	2.776e-2