

GeDiPNet Cluster 592 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:01:14

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
prepulse inhibition	GO:0060134	2	GRIN3A, MDGA1	14	33	80.90	2.716e-4	6.311e-3
cochlea morphogenesis	GO:0090103	2	MYO3B, TIFAB	28	33	40.45	1.111e-3	1.550e-2
regulation of granulocyte chemotaxis	GO:0071622	1	CAMK1D	1	33	566.27	1.766e-3	1.990e-2
regulation of systemic arterial blood pressure by baroreceptor feedback	GO:0003025	1	NAV2	1	33	566.27	1.766e-3	1.990e-2
glossopharyngeal nerve development	GO:0021563	1	NAV2	1	33	566.27	1.766e-3	1.990e-2
vagus nerve development	GO:0021564	1	NAV2	1	33	566.27	1.766e-3	1.990e-2
microtubule-based transport	GO:0099111	1	GJA1	1	33	566.27	1.766e-3	1.990e-2
protein alpha-1,2-demannosylation	GO:0036508	1	MAN1B1	1	33	566.27	1.766e-3	1.990e-2
Golgi calcium ion homeostasis	GO:0032468	1	TMEM165	2	33	283.14	3.529e-3	2.816e-2
Golgi calcium ion transport	GO:0032472	1	TMEM165	2	33	283.14	3.529e-3	2.816e-2
negative regulation of endothelial cell-matrix adhesion via fibronectin	GO:1904905	1	MMP12	2	33	283.14	3.529e-3	2.816e-2
negative regulation of gonadotropin secretion	GO:0032277	1	GJA1	2	33	283.14	3.529e-3	2.816e-2
positive regulation of morphogenesis of an epithelium	GO:1905332	1	GJA1	2	33	283.14	3.529e-3	2.816e-2
cellular response to Thyroid stimulating hormone	GO:1904401	1	TIFAB	2	33	283.14	3.529e-3	2.816e-2
regulation of intrinsic apoptotic signaling pathway in response to osmotic stress by p53 class mediator	GO:1902238	1	TIFAB	2	33	283.14	3.529e-3	2.816e-2