

GeDiPNet Cluster 298 -- 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 11:05:22

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
neural tube closure	GO:0001843	4	TRIM71, PTCH1, FZD3, IFT122	85	37	23.77	2.348e-5	1.015e-3
cilium movement	GO:0003341	3	CCDC88C, DNAH9, HYDIN	48	37	31.57	1.162e-4	3.389e-3
animal organ morphogenesis	GO:0009887	4	PTCH1, SMARCC1, SYCP2, FGFR2	130	37	15.54	1.236e-4	3.547e-3
mucociliary clearance	GO:0120197	2	CCDC88C, DNAH9	12	37	84.18	2.486e-4	5.900e-3
commissural neuron axon guidance	GO:0071679	2	PTCH1, FZD3	14	37	72.15	3.420e-4	7.344e-3
prostate gland development	GO:0030850	2	PTCH1, SMARCC1	16	37	63.13	4.498e-4	8.903e-3
protein O-linked glycosylation via mannose	GO:0035269	2	CRPPA, POMGNT1	18	37	56.12	5.721e-4	1.049e-2
female gamete generation	GO:0007292	2	DMC1, M1AP	21	37	48.10	7.823e-4	1.287e-2
negative regulation of keratinocyte proliferation	GO:0010839	2	PTCH1, FGFR2	24	37	42.09	1.024e-3	1.529e-2
basement membrane organization	GO:0071711	2	NID1, POMGNT1	29	37	34.83	1.497e-3	1.912e-2
regulation of smoothened signaling pathway	GO:0008589	2	PTCH1, FGFR2	29	37	34.83	1.497e-3	1.912e-2
non-canonical Wnt signaling pathway	GO:0035567	2	CCDC88C, FZD3	33	37	30.61	1.938e-3	2.213e-2
response to methylglyoxal	GO:0051595	1	SIN3A	1	37	505.05	1.980e-3	2.242e-2
cellular response to tert-butyl hydroperoxide	GO:0072736	1	SIN3A	1	37	505.05	1.980e-3	2.242e-2
phosphatidylserine exposure on blood platelet	GO:0097045	1	ANO6	1	37	505.05	1.980e-3	2.242e-2