

GeDiPNet Cluster 355 -- 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 18:18:13

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
intrinsic apoptotic signaling pathway by p53 class mediator	GO:0072332	2	FHIT, WWOX	29	18	71.60	3.503e-4	7.650e-3
diadenosine triphosphate catabolic process	GO:0015964	1	FHIT	1	18	1038.17	9.632e-4	1.501e-2
negative regulation of cornification	GO:1905716	1	CDSN	1	18	1038.17	9.632e-4	1.501e-2
corneocyte desquamation	GO:0003336	1	CDSN	2	18	519.08	1.926e-3	2.259e-2
keratinocyte differentiation	GO:0030216	2	CSTA, CDSN	69	18	30.09	1.979e-3	2.299e-2
regulation of lipid kinase activity	GO:0043550	1	RBL2	3	18	346.06	2.887e-3	2.824e-2
cell adhesion	GO:0007155	4	CSTA, CDSN, FLG2, SDK2	665	18	6.24	3.265e-3	3.023e-2
carboxylic acid catabolic process	GO:0046395	1	ACADSB	4	18	259.54	3.848e-3	3.281e-2
regulation of homophilic cell adhesion	GO:1903385	1	PTPRG	4	18	259.54	3.848e-3	3.281e-2
L-isoleucine catabolic process	GO:0006550	1	ACADSB	5	18	207.63	4.807e-3	3.655e-2
camera-type eye photoreceptor cell differentiation	GO:0060219	1	SDK2	5	18	207.63	4.807e-3	3.655e-2
epidermis development	GO:0008544	2	TGM5, CDSN	114	18	18.21	5.295e-3	3.855e-2
epidermis morphogenesis	GO:0048730	1	FLG2	7	18	148.31	6.724e-3	4.339e-2
purine nucleotide metabolic process	GO:0006163	1	FHIT	8	18	129.77	7.681e-3	4.600e-2
protein localization to perinuclear region of cytoplasm	GO:1905719	1	AKTIP	8	18	129.77	7.681e-3	4.600e-2