

GeDiPNet Cluster 329 -- 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: 2026-10-07 22:58:53

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
peptide cross-linking	GO:0018149	2	LORICRIN, KRT2	19	6	327.84	1.466e-5	7.146e-4
keratinization	GO:0031424	2	LORICRIN, KRT2	73	6	85.33	2.235e-4	5.558e-3
cell communication	GO:0007154	2	GJB2, GJB3	80	6	77.86	2.685e-4	6.332e-3
omega-hydroxyceramide biosynthetic process	GO:0106342	1	PNPLA1	1	6	3114.50	3.211e-4	7.182e-3
mitochondrial ncRNA surveillance	GO:0035945	1	SUPV3L1	1	6	3114.50	3.211e-4	7.182e-3
mitochondrial mRNA surveillance	GO:0035946	1	SUPV3L1	1	6	3114.50	3.211e-4	7.182e-3
mitochondrial RNA surveillance	GO:2000827	1	SUPV3L1	1	6	3114.50	3.211e-4	7.182e-3
keratinocyte activation	GO:0032980	1	KRT2	2	6	1557.25	6.421e-4	1.151e-2
mitochondrial mRNA catabolic process	GO:0000958	1	SUPV3L1	3	6	1038.17	9.630e-4	1.501e-2
positive regulation of mitochondrial RNA catabolic process	GO:0000962	1	SUPV3L1	3	6	1038.17	9.630e-4	1.501e-2
mitochondrial RNA 3'-end processing	GO:0000965	1	SUPV3L1	3	6	1038.17	9.630e-4	1.501e-2
positive regulation of epidermis development	GO:0045684	1	KRT2	5	6	622.90	1.605e-3	2.035e-2
mitochondrial RNA catabolic process	GO:0000957	1	SUPV3L1	6	6	519.08	1.925e-3	2.259e-2
gap junction-mediated intercellular transport	GO:1990349	1	GJB2	6	6	519.08	1.925e-3	2.259e-2
keratinocyte migration	GO:0051546	1	KRT2	6	6	519.08	1.925e-3	2.259e-2