

GeDiPNet Cluster 524 -- 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 03:23:13. · Rows: 15 · Generated: 2026-10-19 23:18:56

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
morphogenesis of an epithelium	GO:0002009	2	KRT10, KRT14	51	5	146.56	7.264e-5	2.437e-3
keratinocyte differentiation	GO:0030216	2	KRT10, KRT14	69	5	108.33	1.334e-4	3.795e-3
intermediate filament organization	GO:0045109	2	KRT10, KRT14	70	5	106.78	1.373e-4	3.876e-3
urokinase plasminogen activator signaling pathway	GO:0038195	1	SLURP1	3	5	1245.80	8.025e-4	1.283e-2
chromosome separation	GO:0051304	1	SMARCAD1	4	5	934.35	1.070e-3	1.514e-2
regulation of DNA recombination	GO:0000018	1	SMARCAD1	5	5	747.48	1.337e-3	1.709e-2
positive regulation of epidermis development	GO:0045684	1	KRT10	5	5	747.48	1.337e-3	1.709e-2
intermediate filament bundle assembly	GO:0045110	1	KRT14	7	5	533.91	1.872e-3	2.050e-2
positive regulation of proteolysis involved in protein catabolic process	GO:1903052	1	CTSC	7	5	533.91	1.872e-3	2.050e-2
positive regulation of microglial cell activation	GO:1903980	1	CTSC	9	5	415.27	2.406e-3	2.324e-2
negative regulation of myelination	GO:0031642	1	CTSC	9	5	415.27	2.406e-3	2.324e-2
cell activation	GO:0001775	1	SLURP1	11	5	339.76	2.940e-3	2.584e-2
neuromuscular process controlling posture	GO:0050884	1	SLURP1	15	5	249.16	4.007e-3	3.008e-2
DNA double-strand break processing	GO:0000729	1	SMARCAD1	15	5	249.16	4.007e-3	3.008e-2
protein heterotetramerization	GO:0051290	1	KRT10	16	5	233.59	4.274e-3	3.094e-2