

GeDiPNet Cluster 524 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See scripts/build_cluster_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 13 · Generated: 2026-10-20 00:03:20

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Staphylococcus aureus infection	KEGG	2	KRT10, KRT14	99	5	48.53	6.619e-4	8.277e-3
Formation of the cornified envelope	Reactome	2	KRT10, KRT14	130	5	36.95	1.138e-3	1.250e-2
Estrogen signaling pathway	KEGG	2	KRT10, KRT14	139	5	34.56	1.300e-3	1.384e-2
Keratinization	Reactome	2	KRT10, KRT14	152	5	31.61	1.552e-3	1.580e-2
Type I hemidesmosome assembly	Reactome	1	KRT14	11	5	218.36	4.572e-3	3.438e-2
Cargo concentration in the ER	Reactome	1	CTSC	33	5	72.79	1.367e-2	6.870e-2
COPII-mediated vesicle transport	Reactome	1	CTSC	68	5	35.32	2.800e-2	1.039e-1
MHC class II antigen presentation	Reactome	1	CTSC	123	5	19.53	5.018e-2	1.451e-1
Lysosome	KEGG	1	CTSC	133	5	18.06	5.417e-2	1.513e-1
Apoptosis	KEGG	1	CTSC	137	5	17.53	5.576e-2	1.542e-1
Signaling pathways regulating pluripotency of stem cells	KEGG	1	SMARCAD1	144	5	16.68	5.854e-2	1.581e-1
Neuroactive ligand-receptor interaction	KEGG	1	SLURP1	370	5	6.49	1.449e-1	2.702e-1
Neutrophil degranulation	Reactome	1	CTSC	480	5	5.00	1.845e-1	3.145e-1