

GeDiPNet Cluster 186 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 19:43:59

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Melanogenesis	KEGG	4	EDNRB, KITLG, MITF, TYR	101	24	19.82	4.399e-5	1.150e-3
Peptide ligand-binding receptors	Reactome	3	KISS1R, EDN3, EDNRB	106	24	14.16	1.182e-3	1.535e-2
RNA Polymerase III Transcription Initiation From Type 2 Promoter	Reactome	2	BDP1, POLR2F	27	24	37.07	1.303e-3	1.654e-2
RNA Polymerase III Transcription Initiation From Type 3 Promoter	Reactome	2	BDP1, POLR2F	28	24	35.74	1.402e-3	1.751e-2
RNA Polymerase III Transcription Initiation From Type 1 Promoter	Reactome	2	BDP1, POLR2F	28	24	35.74	1.402e-3	1.751e-2
Pathways in cancer	KEGG	5	ESR1, IL23R, EDNRB, KITLG, MITF	533	24	4.69	3.560e-3	3.472e-2
G alpha (q) signalling events	Reactome	3	KISS1R, EDN3, EDNRB	172	24	8.73	4.683e-3	4.195e-2
Constitutive Signaling by Aberrant PI3K in Cancer	Reactome	2	ESR1, KITLG	75	24	13.34	9.717e-3	6.741e-2
Melanin biosynthesis	Reactome	1	TYR	5	24	100.08	9.953e-3	6.820e-2
RUNX1 regulates estrogen receptor mediated transcription	Reactome	1	ESR1	6	24	83.40	1.193e-2	7.605e-2
RUNX1 regulates transcription of genes involved in WNT signaling	Reactome	1	ESR1	6	24	83.40	1.193e-2	7.605e-2
PIP3 activates AKT signaling	Reactome	2	ESR1, KITLG	93	24	10.76	1.466e-2	8.590e-2
Netrin-1 signaling	Reactome	1	PRKCQ	8	24	62.55	1.588e-2	9.016e-2
PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	Reactome	2	ESR1, KITLG	103	24	9.72	1.778e-2	9.657e-2
Interleukin-23 signaling	Reactome	1	IL23R	9	24	55.60	1.785e-2	9.668e-2