

GeDiPNet Cluster 581 -- 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 03:23:14. · Rows: 15 · Generated: 2026-10-19 23:18:23

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
skin development	GO:0043588	2	IRF6, RIPK4	55	3	226.51	2.547e-5	1.106e-3
positive regulation of NF-kappaB transcription factor activity	GO:0051092	2	RIPK4, CHUK	80	3	155.73	5.415e-5	1.958e-3
response to acetate	GO:0010034	1	CHUK	1	3	6229.00	1.605e-4	4.340e-3
response to cholecystokinin	GO:0061847	1	CHUK	2	3	3114.50	3.211e-4	7.044e-3
response to hydroperoxide	GO:0033194	1	CHUK	9	3	692.11	1.444e-3	1.794e-2
mammary gland epithelial cell differentiation	GO:0060644	1	IRF6	14	3	444.93	2.246e-3	2.244e-2
cranial skeletal system development	GO:1904888	1	IRF6	18	3	346.06	2.887e-3	2.555e-2
striated muscle cell differentiation	GO:0051146	1	CHUK	20	3	311.45	3.208e-3	2.689e-2
negative regulation of stem cell proliferation	GO:2000647	1	IRF6	20	3	311.45	3.208e-3	2.689e-2
pattern recognition receptor signaling pathway	GO:0002221	1	CHUK	21	3	296.62	3.368e-3	2.763e-2
response to amino acid	GO:0043200	1	CHUK	22	3	283.14	3.528e-3	2.816e-2
negative regulation of keratinocyte proliferation	GO:0010839	1	IRF6	24	3	259.54	3.848e-3	2.937e-2
positive regulation of interferon-alpha production	GO:0032727	1	CHUK	26	3	239.58	4.168e-3	3.062e-2
keratinocyte proliferation	GO:0043616	1	IRF6	29	3	214.79	4.649e-3	3.237e-2
skeletal muscle contraction	GO:0003009	1	CHUK	32	3	194.66	5.129e-3	3.369e-2