

GeDiPNet Cluster 146 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 07:41:37

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
leukemia inhibitory factor signaling pathway	GO:0048861	2	LIFR, IL6ST	4	20	467.18	6.521e-6	3.701e-4
oncostatin-M-mediated signaling pathway	GO:0038165	2	LIFR, IL6ST	4	20	467.18	6.521e-6	3.701e-4
ciliary neurotrophic factor-mediated signaling pathway	GO:0070120	2	LIFR, IL6ST	5	20	373.74	1.086e-5	5.555e-4
positive regulation of platelet aggregation	GO:1901731	2	PDPN, IL6ST	13	20	143.75	8.429e-5	2.664e-3
neural fold bending	GO:0021503	1	LUZP1	1	20	934.35	1.070e-3	1.569e-2
contractile ring contraction	GO:0036213	1	LUZP1	1	20	934.35	1.070e-3	1.569e-2
regulation of myofibroblast contraction	GO:1904328	1	PDPN	1	20	934.35	1.070e-3	1.569e-2
granzyme-mediated apoptotic signaling pathway	GO:0008626	1	UBE4B	1	20	934.35	1.070e-3	1.569e-2
regulation of melanocyte differentiation	GO:0045634	1	GNA11	1	20	934.35	1.070e-3	1.569e-2
response to cytokine	GO:0034097	2	LIFR, IL6ST	56	20	33.37	1.619e-3	1.996e-2
cerebellar Purkinje cell layer maturation	GO:0021691	1	RERE	2	20	467.18	2.139e-3	2.343e-2
ciliary basal body-plasma membrane docking	GO:0097711	1	CEP290	2	20	467.18	2.139e-3	2.343e-2
camera-type eye development	GO:0043010	2	SKI, CEP290	74	20	25.25	2.807e-3	2.725e-2
radial glia guided migration of Purkinje cell	GO:0021942	1	RERE	3	20	311.45	3.208e-3	2.913e-2
nose morphogenesis	GO:0043585	1	SKI	3	20	311.45	3.208e-3	2.913e-2