

GeDiPNet Cluster 591 -- 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
gastrulation	GO:0007369	2	ACVR1, TP53	38	4	245.88	2.410e-5	1.062e-3
T cell differentiation in thymus	GO:0033077	2	BRAF, TP53	41	4	227.89	2.810e-5	1.190e-3
cellular response to xenobiotic stimulus	GO:0071466	2	BRAF, TP53	65	4	143.75	7.116e-5	2.399e-3
transforming growth factor beta receptor signaling pathway	GO:0007179	2	ACVR1, TP53	112	4	83.42	2.119e-4	5.298e-3
negative regulation of helicase activity	GO:0051097	1	TP53	1	4	4671.75	2.141e-4	5.314e-3
regulation of intrinsic apoptotic signaling pathway by p53 class mediator	GO:1902253	1	TP53	1	4	4671.75	2.141e-4	5.314e-3
negative regulation of G1 to G0 transition	GO:1903451	1	TP53	1	4	4671.75	2.141e-4	5.314e-3
endocardial cushion cell fate commitment	GO:0061445	1	ACVR1	1	4	4671.75	2.141e-4	5.314e-3
regulation of thymocyte apoptotic process	GO:0070243	1	TP53	2	4	2335.88	4.281e-4	8.531e-3
oligodendrocyte apoptotic process	GO:0097252	1	TP53	2	4	2335.88	4.281e-4	8.531e-3
negative regulation of glucose catabolic process to lactate via pyruvate	GO:1904024	1	TP53	2	4	2335.88	4.281e-4	8.531e-3
negative regulation of pentose-phosphate shunt	GO:1905856	1	TP53	2	4	2335.88	4.281e-4	8.531e-3
positive regulation of determination of dorsal identity	GO:2000017	1	ACVR1	2	4	2335.88	4.281e-4	8.531e-3
intrinsic apoptotic signaling pathway in response to hypoxia	GO:1990144	1	TP53	3	4	1557.25	6.421e-4	1.113e-2
positive T cell selection	GO:0043368	1	BRAF	3	4	1557.25	6.421e-4	1.113e-2