

GeDiPNet Cluster 353 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 15:26:44

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of protein-containing complex assembly	GO:0031334	4	BAK1, BAX, BIK, IFNG	50	12	124.58	2.209e-8	3.370e-6
B cell negative selection	GO:0002352	2	BAK1, BAX	2	12	1557.25	3.780e-7	3.732e-5
positive regulation of release of cytochrome c from mitochondria	GO:0090200	3	BAK1, BAX, BIK	25	12	186.87	4.616e-7	4.420e-5
extrinsic apoptotic signaling pathway in absence of ligand	GO:0097192	3	BAK1, BAX, IL2	36	12	129.77	1.427e-6	1.118e-4
post-embryonic camera-type eye morphogenesis	GO:0048597	2	BAK1, BAX	4	12	778.63	2.267e-6	1.621e-4
apoptotic process involved in blood vessel morphogenesis	GO:1902262	2	BAK1, BAX	5	12	622.90	3.776e-6	2.445e-4
intrinsic apoptotic signaling pathway in response to DNA damage	GO:0008630	3	ATM, BAK1, BAX	54	12	86.51	4.927e-6	3.021e-4
cellular response to UV	GO:0034644	3	BAK1, BAX, PCNA	55	12	84.94	5.209e-6	3.161e-4
negative regulation of endoplasmic reticulum calcium ion concentration	GO:0032471	2	BAK1, BAX	6	12	519.08	5.662e-6	3.378e-4
positive regulation of IRE1-mediated unfolded protein response	GO:1903896	2	BAK1, BAX	8	12	389.31	1.056e-5	5.527e-4
regulation of apoptotic signaling pathway	GO:2001233	2	BAK1, BAX	9	12	346.06	1.357e-5	6.728e-4
leukocyte homeostasis	GO:0001776	2	BAK1, BAX	9	12	346.06	1.357e-5	6.728e-4
regulation of apoptotic process	GO:0042981	4	ATM, BAK1, BAX, BIK	254	12	24.52	1.515e-5	7.336e-4
vagina development	GO:0060068	2	BAK1, BAX	10	12	311.45	1.696e-5	7.999e-4
establishment or maintenance of transmembrane electrochemical gradient	GO:0010248	2	BAK1, BAX	11	12	283.14	2.072e-5	9.382e-4