

GeDiPNet Cluster 357 -- 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 20:37:38

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
negative regulation of mitochondrial fission	GO:0090258	2	MAPT, PRKN	5	48	155.73	6.429e-5	2.171e-3
positive regulation of tissue remodeling	GO:0034105	2	IL2, IL21	6	48	129.77	9.628e-5	2.938e-3
positive regulation of amyloid-beta formation	GO:1902004	2	SLC2A13, SP1	21	48	37.08	1.315e-3	1.780e-2
chondrocyte development	GO:0002063	2	EIF2AK3, RUNX2	21	48	37.08	1.315e-3	1.780e-2
regulation of JNK cascade	GO:0046328	2	TNXB, EPHB1	23	48	33.85	1.579e-3	1.983e-2
positive regulation of interleukin-17 production	GO:0032740	2	IL2, IL21	27	48	28.84	2.177e-3	2.372e-2
positive regulation of cell population proliferation	GO:0008284	6	IL2, IL21, RUNX2, TBC1D8, TNXB, SMARCA2	532	48	4.39	2.303e-3	2.451e-2
cell-cell adhesion	GO:0098609	4	TNXB, CDH18, COL13A1, PDLIM5	218	48	7.14	2.346e-3	2.480e-2
amyloid fibril formation	GO:1990000	2	MAPT, PRKN	29	48	26.85	2.510e-3	2.568e-2
plus-end-directed organelle transport along microtubule	GO:0072386	1	MAPT	1	48	389.31	2.569e-3	2.584e-2
positive regulation of neurotransmitter uptake	GO:0051582	1	PRKN	1	48	389.31	2.569e-3	2.584e-2
negative regulation of spontaneous neurotransmitter secretion	GO:1904049	1	PRKN	1	48	389.31	2.569e-3	2.584e-2
ligamentous ossification	GO:0036076	1	RUNX2	1	48	389.31	2.569e-3	2.584e-2
positive regulation of cell fate determination	GO:1905935	1	TNXB	1	48	389.31	2.569e-3	2.584e-2
mitochondrial tryptophanyl-tRNA aminoacylation	GO:0070183	1	WARS2	1	48	389.31	2.569e-3	2.584e-2