

GeDiPNet Cluster 351 -- 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: 2026-10-07 22:58:06

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 cell proliferation involved in kidney development	GO:1901723	1	FLCN	1	5	3737.40	2.676e-4	6.316e-3
spermine biosynthetic process	GO:0006597	1	SMS	2	5	1868.70	5.351e-4	1.019e-2
spermine metabolic process	GO:0008215	1	SMS	2	5	1868.70	5.351e-4	1.019e-2
cell proliferation involved in kidney development	GO:0072111	1	FLCN	3	5	1245.80	8.025e-4	1.336e-2
negative regulation of post-translational protein modification	GO:1901874	1	FLCN	4	5	934.35	1.070e-3	1.602e-2
negative regulation of lysosome organization	GO:1905672	1	FLCN	4	5	934.35	1.070e-3	1.602e-2
regulation of pro-B cell differentiation	GO:2000973	1	FLCN	4	5	934.35	1.070e-3	1.602e-2
negative regulation of brown fat cell differentiation	GO:1903444	1	FLCN	5	5	747.48	1.337e-3	1.833e-2
polyamine metabolic process	GO:0006595	1	SMS	5	5	747.48	1.337e-3	1.833e-2
methionine metabolic process	GO:0006555	1	SMS	6	5	622.90	1.605e-3	2.035e-2
positive regulation of long-term synaptic depression	GO:1900454	1	IQSEC2	7	5	533.91	1.872e-3	2.238e-2
regulation of Ras protein signal transduction	GO:0046578	1	FLCN	8	5	467.18	2.139e-3	2.400e-2
polyamine biosynthetic process	GO:0006596	1	SMS	12	5	311.45	3.207e-3	2.987e-2
negative regulation of multicellular organism growth	GO:0040015	1	RAI1	13	5	287.49	3.474e-3	3.132e-2
negative regulation of glycolytic process	GO:0045820	1	FLCN	16	5	233.59	4.274e-3	3.437e-2