

GeDiPNet Cluster 48 -- 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 06:31:11

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
TORC1 signaling	GO:0038202	4	TSC2, MTOR, RHEB, TSC1	67	22	50.71	1.051e-6	8.632e-5
negative regulation of TORC1 signaling	GO:1904262	4	TSC2, SZT2, MTOR, TSC1	71	22	47.85	1.329e-6	1.039e-4
positive regulation of TORC1 signaling	GO:1904263	4	TSC2, MTOR, RHEB, TSC1	71	22	47.85	1.329e-6	1.039e-4
cell projection organization	GO:0030030	5	CEP290, CC2D2A, CPLANE1, MTOR, TSC1	214	22	19.85	4.223e-6	2.622e-4
positive regulation of translational initiation	GO:0045948	3	TSC2, MTOR, RHEB	42	22	60.67	1.578e-5	7.483e-4
negative regulation of translational initiation	GO:0045947	3	TSC2, MTOR, RHEB	44	22	57.91	1.818e-5	8.317e-4
kidney development	GO:0001822	4	PKD1, CEP290, CC2D2A, TSC1	146	22	23.27	2.344e-5	1.014e-3
response to fluid shear stress	GO:0034405	2	PKD1, NOS3	8	22	212.35	3.689e-5	1.432e-3
regulation of macroautophagy	GO:0016241	3	TSC2, MTOR, RHEB	57	22	44.71	3.977e-5	1.514e-3
negative regulation of cell size	GO:0045792	2	MTOR, TSC1	9	22	188.76	4.739e-5	1.725e-3
anoikis	GO:0043276	2	TSC2, MTOR	12	22	141.57	8.670e-5	2.720e-3
response to nutrient levels	GO:0031667	3	SZT2, MTOR, SRD5A2	79	22	32.26	1.057e-4	3.152e-3
negative regulation of macroautophagy	GO:0016242	2	MTOR, TSC1	14	22	121.34	1.194e-4	3.457e-3
cellular response to nutrient levels	GO:0031669	3	TSC2, MTOR, RHEB	83	22	30.70	1.224e-4	3.516e-3
neural tube closure	GO:0001843	3	TSC2, CC2D2A, TSC1	85	22	29.98	1.314e-4	3.713e-3