

GeDiPNet Cluster 605 -- 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 23:19:02

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
meiotic sister chromatid cohesion	GO:0051177	2	PPP2R5D, PPP2R5C	7	4	1334.79	7.214e-7	6.577e-5
RNA polymerase II transcription initiation surveillance	GO:0160240	2	PPP2R1A, PPP2CA	20	4	467.18	6.521e-6	3.910e-4
regulation of growth	GO:0040008	2	PPP2R1A, PPP2CA	23	4	406.24	8.682e-6	4.873e-4
negative regulation of hippo signaling	GO:0035331	2	PPP2R1A, PPP2CA	25	4	373.74	1.029e-5	5.556e-4
T cell homeostasis	GO:0043029	2	PPP2R1A, PPP2CA	39	4	239.58	2.540e-5	1.104e-3
transcription elongation by RNA polymerase II	GO:0006368	2	PPP2R1A, PPP2CA	46	4	203.12	3.546e-5	1.424e-3
regulation of cell differentiation	GO:0045595	2	PPP2R1A, PPP2CA	54	4	173.03	4.900e-5	1.817e-3
negative regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051898	2	PPP2R1A, PPP2CA	78	4	119.79	1.026e-4	3.156e-3
meiotic spindle elongation	GO:0051232	1	PPP2R1A	1	4	4671.75	2.141e-4	5.314e-3
regulation of meiotic cell cycle process involved in oocyte maturation	GO:1903538	1	PPP2R1A	2	4	2335.88	4.281e-4	8.531e-3
negative regulation of glycolytic process through fructose-6-phosphate	GO:1904539	1	PPP2CA	4	4	1167.94	8.560e-4	1.331e-2
meiotic sister chromatid cohesion, centromeric	GO:0051754	1	PPP2R1A	5	4	934.35	1.070e-3	1.514e-2
mitotic sister chromatid separation	GO:0051306	1	PPP2R1A	5	4	934.35	1.070e-3	1.514e-2
vascular endothelial cell response to oscillatory fluid shear stress	GO:0097706	1	PPP2CA	5	4	934.35	1.070e-3	1.514e-2
transcription by RNA polymerase II	GO:0006366	2	PPP2R1A, PPP2CA	261	4	35.80	1.145e-3	1.571e-2