

GeDiPNet Cluster 606 -- 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: 14 · Generated: 2026-10-19 23:18:29

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
spindle assembly	GO:0051225	2	MAPRE2, TUBB	40	2	467.18	4.468e-6	2.895e-4
positive regulation of ARF protein signal transduction	GO:0032014	1	MAPRE2	2	2	4671.75	2.140e-4	5.314e-3
cell division	GO:0051301	2	MAPRE2, TUBB	406	2	46.03	4.709e-4	9.150e-3
odontoblast differentiation	GO:0071895	1	TUBB	8	2	1167.94	8.560e-4	1.331e-2
positive regulation of focal adhesion disassembly	GO:0120183	1	MAPRE2	8	2	1167.94	8.560e-4	1.331e-2
protein localization to microtubule	GO:0035372	1	MAPRE2	10	2	934.35	1.070e-3	1.514e-2
positive regulation of keratinocyte migration	GO:0051549	1	MAPRE2	12	2	778.63	1.284e-3	1.669e-2
cytoskeleton-dependent intracellular transport	GO:0030705	1	TUBB	14	2	667.39	1.498e-3	1.821e-2
regulation of microtubule polymerization or depolymerization	GO:0031110	1	MAPRE2	15	2	622.90	1.605e-3	1.885e-2
regulation of synapse organization	GO:0050807	1	TUBB	30	2	311.45	3.208e-3	2.689e-2
natural killer cell mediated cytotoxicity	GO:0042267	1	TUBB	41	2	227.89	4.383e-3	3.145e-2
microtubule-based process	GO:0007017	1	TUBB	46	2	203.12	4.917e-3	3.307e-2
mitotic cell cycle	GO:0000278	1	TUBB	142	2	65.80	1.514e-2	5.684e-2
microtubule cytoskeleton organization	GO:0000226	1	TUBB	149	2	62.71	1.588e-2	5.833e-2