

GeDiPNet Cluster 590 -- 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 23:19:17

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
protein transmembrane transport	GO:0071806	2	AP4M1, EXOC7	19	13	151.31	7.589e-5	2.521e-3
regulation of synaptic transmission, glutamatergic	GO:0051966	2	GRM7, LRRK2	33	13	87.12	2.330e-4	5.648e-3
cellular response to curcumin	GO:1904644	1	LRRK2	1	13	1437.46	6.957e-4	1.178e-2
Wnt signalosome assembly	GO:1904887	1	LRRK2	1	13	1437.46	6.957e-4	1.178e-2
regulation of isoprenoid metabolic process	GO:0019747	1	NPC2	1	13	1437.46	6.957e-4	1.178e-2
positive regulation of homophilic cell adhesion	GO:1903387	1	PTPN23	1	13	1437.46	6.957e-4	1.178e-2
regulation of kidney size	GO:0035564	1	LRRK2	2	13	718.73	1.391e-3	1.753e-2
negative regulation of late endosome to lysosome transport	GO:1902823	1	LRRK2	2	13	718.73	1.391e-3	1.753e-2
negative regulation of protein processing involved in protein targeting to mitochondrion	GO:1903217	1	LRRK2	2	13	718.73	1.391e-3	1.753e-2
positive regulation of adherens junction organization	GO:1903393	1	PTPN23	2	13	718.73	1.391e-3	1.753e-2
regulation of modification of synapse structure, modulating synaptic transmission	GO:0098987	1	KIF5B	2	13	718.73	1.391e-3	1.753e-2
dUDP biosynthetic process	GO:0006227	1	DTYMK	2	13	718.73	1.391e-3	1.753e-2
dTDP biosynthetic process	GO:0006233	1	DTYMK	2	13	718.73	1.391e-3	1.753e-2
regulation of membrane potential	GO:0042391	2	KIF5B, LRRK2	85	13	33.82	1.544e-3	1.864e-2
protein localization to basolateral plasma membrane	GO:1903361	1	AP4M1	3	13	479.15	2.086e-3	2.170e-2