

GeDiPNet Cluster 530 -- 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 03:23:13. · Rows: 15 · Generated: 2026-10-19 23:19:35

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
response to cocaine	GO:0042220	2	CACNG4, HTR2A	35	22	48.54	7.689e-4	1.254e-2
presynaptic modulation of chemical synaptic transmission	GO:0099171	2	APBA2, HTR2A	37	22	45.91	8.594e-4	1.334e-2
monocyte activation involved in immune response	GO:0002280	1	DYSF	1	22	849.41	1.177e-3	1.592e-2
asymmetric protein localization involved in cell fate determination	GO:0045167	1	WNT7A	1	22	849.41	1.177e-3	1.592e-2
ER-dependent peroxisome organization	GO:0032581	1	PEX16	1	22	849.41	1.177e-3	1.592e-2
ER-dependent peroxisome localization	GO:0106101	1	PEX16	1	22	849.41	1.177e-3	1.592e-2
sphinganine metabolic process	GO:0006667	1	DEGS2	1	22	849.41	1.177e-3	1.592e-2
protein localization to cytoskeleton	GO:0044380	1	HTR2A	2	22	424.70	2.353e-3	2.301e-2
postsynapse assembly	GO:0099068	1	WNT7A	2	22	424.70	2.353e-3	2.301e-2
positive regulation of protein localization to presynapse	GO:1905386	1	WNT7A	2	22	424.70	2.353e-3	2.301e-2
protein deamination	GO:0018277	1	LOXL1	2	22	424.70	2.353e-3	2.301e-2
oviduct development	GO:0060066	1	WNT7A	3	22	283.14	3.528e-3	2.816e-2
skeletal muscle satellite cell activation	GO:0014719	1	WNT7A	3	22	283.14	3.528e-3	2.816e-2
cGMP metabolic process	GO:0046068	1	PDE9A	3	22	283.14	3.528e-3	2.816e-2
sensitization	GO:0046960	1	HTR2A	3	22	283.14	3.528e-3	2.816e-2