

GeDiPNet Cluster 619 -- 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 23:18:51

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
sphingolipid metabolic process	GO:0006665	2	B4GALNT1, GBA2	59	8	79.18	2.711e-4	6.302e-3
GMP catabolic process to guanine	GO:0006202	1	NT5C2	1	8	2335.88	4.281e-4	8.531e-3
purine ribonucleoside diphosphate catabolic process	GO:0009181	1	ENTPD1	2	8	1167.94	8.560e-4	1.331e-2
cholesterol metabolic process	GO:0008203	2	GBA2, ERLIN2	107	8	43.66	8.892e-4	1.368e-2
glucosylceramide catabolic process	GO:0006680	1	GBA2	3	8	778.63	1.284e-3	1.669e-2
dGMP metabolic process	GO:0046054	1	NT5C2	3	8	778.63	1.284e-3	1.669e-2
ADP catabolic process	GO:0046032	1	ENTPD1	3	8	778.63	1.284e-3	1.669e-2
steroid metabolic process	GO:0008202	2	GBA2, ERLIN2	135	8	34.61	1.410e-3	1.770e-2
IMP metabolic process	GO:0046040	1	NT5C2	4	8	583.97	1.711e-3	1.958e-2
negative regulation of defense response to virus by host	GO:0050689	1	NT5C2	4	8	583.97	1.711e-3	1.958e-2
nucleoside diphosphate catabolic process	GO:0009134	1	ENTPD1	4	8	583.97	1.711e-3	1.958e-2
IMP catabolic process	GO:0006204	1	NT5C2	5	8	467.18	2.139e-3	2.189e-2
GMP catabolic process	GO:0046038	1	NT5C2	5	8	467.18	2.139e-3	2.189e-2
carbohydrate metabolic process	GO:0005975	2	B4GALNT1, GBA2	175	8	26.70	2.353e-3	2.301e-2
central nervous system myelin formation	GO:0032289	1	MAG	6	8	389.31	2.566e-3	2.402e-2