

GeDiPNet Cluster 107 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-07 22:19:27

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cobalamin transport	GO:0015889	6	AMN, CUBN, TCN1, TCN2, CD320, ABCD4	9	37	336.70	3.290e-15	2.279e-12
cobalamin metabolic process	GO:0009235	4	AMN, CUBN, MMAA, ABCD4	9	37	224.47	1.627e-9	3.371e-7
oligosaccharide biosynthetic process	GO:0009312	4	FUT1, FUT2, FUT3, FUT6	26	37	77.70	1.884e-7	2.094e-5
vitamin transport	GO:0051180	3	SLC19A2, SLC19A1, GC	10	37	151.52	8.493e-7	7.336e-5
L-fucose catabolic process	GO:0042355	3	FUT1, FUT2, FUT6	10	37	151.52	8.493e-7	7.336e-5
fucosylation	GO:0036065	3	FUT1, FUT2, FUT3	12	37	126.26	1.553e-6	1.195e-4
glycosphingolipid biosynthetic process	GO:0006688	3	FUT1, FUT2, FUT6	25	37	60.61	1.595e-5	7.625e-4
folic acid transport	GO:0015884	2	SLC19A2, SLC19A1	8	37	126.26	1.060e-4	3.226e-3
cobalt ion transport	GO:0006824	2	TCN1, TCN2	8	37	126.26	1.060e-4	3.226e-3
regulation of endothelial cell proliferation	GO:0001936	2	FUT1, FUT2	9	37	112.23	1.361e-4	3.882e-3
homocysteine metabolic process	GO:0050667	2	MMUT, MTHFR	10	37	101.01	1.700e-4	4.586e-3
tetrahydrofolate metabolic process	GO:0046653	2	DHFR, MTHFR	11	37	91.83	2.075e-4	5.299e-3
vitamin D metabolic process	GO:0042359	2	CYP2R1, GC	12	37	84.18	2.486e-4	5.988e-3
folic acid metabolic process	GO:0046655	2	DHFR, SLC19A1	15	37	67.34	3.941e-4	8.318e-3
protein glycosylation	GO:0006486	4	FUT1, FUT2, FUT3, FUT6	181	37	11.16	4.380e-4	8.912e-3