

GeDiPNet Cluster 207 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 21:17:19

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
inorganic diphosphate transport	GO:0030505	2	ABCC6, ENPP1	4	8	1167.94	9.618e-7	8.049e-5
carboxylic acid transport	GO:0046942	2	ABCC2, ABCC6	5	8	934.35	1.603e-6	1.207e-4
xenobiotic transport across blood-brain barrier	GO:1990962	2	ABCC2, ABCG2	6	8	778.63	2.404e-6	1.667e-4
leukotriene transport	GO:0071716	2	ABCC2, ABCC6	7	8	667.39	3.364e-6	2.190e-4
intracellular phosphate ion homeostasis	GO:0030643	2	ABCC6, ENPP1	10	8	467.18	7.204e-6	4.018e-4
glycosaminoglycan metabolic process	GO:0030203	2	XYLT1, XYLT2	12	8	389.31	1.056e-5	5.431e-4
transepithelial transport	GO:0070633	2	ABCC2, ABCG2	13	8	359.37	1.248e-5	6.208e-4
phosphate ion homeostasis	GO:0055062	2	ABCC6, ENPP1	15	8	311.45	1.679e-5	7.830e-4
glycosaminoglycan biosynthetic process	GO:0006024	2	XYLT1, XYLT2	20	8	233.59	3.035e-5	1.230e-3
proteoglycan biosynthetic process	GO:0030166	2	XYLT1, XYLT2	21	8	222.46	3.354e-5	1.332e-3
glycoprotein biosynthetic process	GO:0009101	2	XYLT1, XYLT2	21	8	222.46	3.354e-5	1.332e-3
chondroitin sulfate proteoglycan biosynthetic process	GO:0050650	2	XYLT1, XYLT2	26	8	179.68	5.185e-5	1.853e-3
heparan sulfate proteoglycan biosynthetic process	GO:0015012	2	XYLT1, XYLT2	30	8	155.73	6.935e-5	2.300e-3
ATP metabolic process	GO:0046034	2	ABCC6, ENPP1	36	8	129.77	1.003e-4	3.030e-3
monoatomic anion transmembrane transport	GO:0098656	2	ABCC2, ABCC6	40	8	116.79	1.241e-4	3.557e-3