

GeDiPNet Cluster 306 -- 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 15:47:55

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
ammonium homeostasis	GO:0097272	3	RHD, RHAG, RHCE	6	5	1868.70	1.839e-10	4.959e-8
ammonium transmembrane transport	GO:0072488	3	RHD, RHAG, RHCE	11	5	1019.29	1.516e-9	3.258e-7
methylammonium transmembrane transport	GO:0072489	1	RHAG	2	5	1868.70	5.351e-4	9.981e-3
intracellular monoatomic ion homeostasis	GO:0006873	1	RHAG	4	5	934.35	1.070e-3	1.569e-2
carbon dioxide transmembrane transport	GO:0035378	1	RHAG	5	5	747.48	1.337e-3	1.795e-2
carbon dioxide transport	GO:0015670	1	RHAG	13	5	287.49	3.474e-3	3.064e-2
maintenance of gastrointestinal epithelium	GO:0030277	1	SERPINA3	16	5	233.59	4.274e-3	3.381e-2
inorganic cation transmembrane transport	GO:0098662	1	RHAG	23	5	162.50	6.140e-3	4.074e-2
multicellular organismal-level iron ion homeostasis	GO:0060586	1	RHAG	28	5	133.48	7.470e-3	4.462e-2
spliceosomal complex assembly	GO:0000245	1	RSRP1	28	5	133.48	7.470e-3	4.462e-2
erythrocyte development	GO:0048821	1	RHAG	32	5	116.79	8.534e-3	4.724e-2
bicarbonate transport	GO:0015701	1	RHAG	33	5	113.25	8.799e-3	4.794e-2
acute-phase response	GO:0006953	1	SERPINA3	37	5	101.01	9.862e-3	5.090e-2
regulation of lipid metabolic process	GO:0019216	1	SERPINA3	41	5	91.16	1.092e-2	5.367e-2
response to cytokine	GO:0034097	1	SERPINA3	56	5	66.74	1.490e-2	6.199e-2