

GeDiPNet Cluster 311 -- 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: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-08 22:39:48

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
glycolytic process	GO:0006096	6	PKLR, GPI, HK1, PGK1, TPI1, BPGM	49	63	36.32	1.437e-8	2.326e-6
erythrocyte development	GO:0048821	5	GATA1, HBB, RHAG, SLC4A1, BPGM	32	63	46.35	6.954e-8	8.795e-6
ammonium homeostasis	GO:0097272	3	RHAG, RHCE, RHD	6	63	148.31	7.251e-7	6.355e-5
canonical glycolysis	GO:0061621	4	GPI, HK1, PGK1, TPI1	22	63	53.93	8.197e-7	7.035e-5
response to nutrient	GO:0007584	5	PKLR, GCLC, EPO, ABCG5, ABCG8	63	63	23.54	2.240e-6	1.590e-4
glucose 6-phosphate metabolic process	GO:0051156	3	G6PD, GPI, HK1	11	63	80.90	5.910e-6	3.460e-4
ammonium transmembrane transport	GO:0072488	3	RHAG, RHCE, RHD	11	63	80.90	5.910e-6	3.460e-4
response to hydrogen peroxide	GO:0042542	4	HBB, HMOX1, HP, GPX1	39	63	30.42	8.829e-6	4.786e-4
negative regulation of intestinal phytosterol absorption	GO:0010949	2	ABCG5, ABCG8	2	63	296.62	1.119e-5	5.727e-4
negative regulation of intestinal cholesterol absorption	GO:0045796	2	ABCG5, ABCG8	2	63	296.62	1.119e-5	5.727e-4
glutathione metabolic process	GO:0006749	4	G6PD, GSR, GCLC, GPX1	49	63	24.21	2.218e-5	9.770e-4
response to cadmium ion	GO:0046686	3	GPI, GSS, GCLC	21	63	42.37	4.651e-5	1.713e-3
intracellular monoatomic ion homeostasis	GO:0006873	2	RHAG, SLC4A1	4	63	148.31	6.682e-5	2.245e-3
cellular oxidant detoxification	GO:0098869	4	GSR, HBB, HP, GPX1	66	63	17.98	7.227e-5	2.379e-3
multicellular organismal-level iron ion homeostasis	GO:0060586	3	EIF2AK1, HMOX1, RHAG	28	63	31.78	1.126e-4	3.313e-3