

GeDiPNet Cluster 371 -- 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 01:45:24

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
glucose 6-phosphate metabolic process	GO:0051156	3	G6PC2, GCK, HK1	11	10	509.65	1.817e-8	2.869e-6
canonical glycolysis	GO:0061621	3	GCK, HK1, TPI1	22	10	254.82	1.690e-7	1.879e-5
glyceraldehyde-3-phosphate metabolic process	GO:0019682	2	TALDO1, TPI1	3	10	1245.80	7.730e-7	6.731e-5
carbohydrate metabolic process	GO:0005975	4	GCK, HK1, MPI, TALDO1	175	10	42.71	1.494e-6	1.142e-4
glycolytic process	GO:0006096	3	GCK, HK1, TPI1	49	10	114.41	2.007e-6	1.446e-4
hexose metabolic process	GO:0019318	2	GCK, HK1	6	10	622.90	3.862e-6	2.440e-4
GDP-mannose biosynthetic process	GO:0009298	2	HK1, MPI	6	10	622.90	3.862e-6	2.440e-4
glucose metabolic process	GO:0006006	3	GCK, HK1, TPI1	66	10	84.94	4.961e-6	2.985e-4
fructose 6-phosphate metabolic process	GO:0006002	2	HK1, TALDO1	13	10	287.49	2.004e-5	8.990e-4
regulation of glycolytic process	GO:0006110	2	GCK, PRKAG3	13	10	287.49	2.004e-5	8.990e-4
carbohydrate phosphorylation	GO:0046835	2	GCK, HK1	24	10	155.73	7.069e-5	2.335e-3
intracellular glucose homeostasis	GO:0001678	2	GCK, HK1	27	10	138.42	8.982e-5	2.794e-3
regulation of insulin secretion	GO:0050796	2	G6PC2, GCK	46	10	81.25	2.634e-4	6.139e-3
gluconeogenesis	GO:0006094	2	G6PC2, TPI1	56	10	66.74	3.909e-4	8.069e-3
methylglyoxal biosynthetic process	GO:0019242	1	TPI1	1	10	1868.70	5.351e-4	9.981e-3