

GeDiPNet Cluster 154 -- 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 00:28:45

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
glycogen metabolic process	GO:0005977	13	AGL, G6PC1, GAA, GBE1, GYS1, PHKA1, PHKA2, PHKG2, PRKAG2, PYGL, PYGM, PHKB	40	37	164.14	7.660e-27	2.912e-23
glycogen catabolic process	GO:0005980	7	AGL, G6PC1, GAA, PFKM, PHKG2, PYGL, PYGM	11	37	321.40	2.142e-17	2.364e-14
carbohydrate metabolic process	GO:0005975	11	AGL, GAA, GBE1, PHKA1, PHKA2, PYGL, PYGM, SLC2A2, PHKB, PHKG1, PGM1	175	37	31.75	2.450e-14	1.488e-11
glycolytic process	GO:0006096	7	PGAM2, PFKM, ALDOA, LDHA, ENO3, PGK1, PGM1	49	37	72.15	5.286e-12	2.066e-9
glycogen biosynthetic process	GO:0005978	5	AGL, GBE1, GYG1, GYS1, GYS2	18	37	140.29	1.932e-10	5.177e-8
gluconeogenesis	GO:0006094	6	PGAM2, G6PC1, SLC37A4, ENO3, PGK1, PGM1	56	37	54.11	1.190e-9	2.620e-7
generation of precursor metabolites and energy	GO:0006091	5	GBE1, PHKA1, PHKA2, PHKG2, PHKB	49	37	51.54	4.113e-8	5.745e-6
canonical glycolysis	GO:0061621	4	PGAM2, PFKM, ENO3, PGK1	22	37	91.83	9.272e-8	1.130e-5
striated muscle contraction	GO:0006941	4	PGAM2, GAA, ALDOA, TNNT2	24	37	84.18	1.343e-7	1.546e-5
muscle cell cellular homeostasis	GO:0046716	4	LAMP2, GAA, PFKM, ALDOA	26	37	77.70	1.884e-7	2.059e-5
glucose metabolic process	GO:0006006	4	GAA, SLC37A4, PIK3CA, PGM1	66	37	30.61	8.585e-6	4.630e-4
positive regulation of glycogen catabolic process	GO:0045819	2	PHKA1, PHKG2	4	37	252.53	2.283e-5	9.938e-4
glucose-6-phosphate transport	GO:0015760	2	G6PC1, SLC37A4	7	37	144.30	7.961e-5	2.550e-3
cardiac muscle contraction	GO:0060048	3	GAA, PIK3CA, TNNT2	43	37	35.24	8.350e-5	2.643e-3
fructose 1,6-bisphosphate metabolic process	GO:0030388	2	PFKM, ALDOA	8	37	126.26	1.060e-4	3.158e-3