

GeDiPNet Cluster 307 -- 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 05:00:21

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
muscle cell apoptotic process	GO:0010657	2	COL6A1, DMPK	2	9	2076.33	2.062e-7	2.227e-5
response to UV	GO:0009411	3	COL6A1, COL6A2, COL6A3	54	9	115.35	1.893e-6	1.376e-4
cell adhesion	GO:0007155	5	COL12A1, COL6A1, COL6A2, COL6A3, COL4A3	665	9	15.61	6.290e-6	3.602e-4
glomerular basement membrane development	GO:0032836	2	COL4A3, COL4A4	10	9	415.27	9.260e-6	4.920e-4
phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0043491	3	COL6A1, COL6A2, COL6A3	92	9	67.71	9.495e-6	5.018e-4
neuron apoptotic process	GO:0051402	3	COL6A1, COL6A2, COL6A3	98	9	63.56	1.148e-5	5.796e-4
collagen-activated tyrosine kinase receptor signaling pathway	GO:0038063	2	COL4A3, COL4A5	12	9	346.06	1.357e-5	6.620e-4
muscle organ development	GO:0007517	3	COL6A1, COL6A3, LMNA	114	9	54.64	1.808e-5	8.291e-4
nuclear envelope organization	GO:0006998	2	DMPK, LMNA	24	9	173.03	5.660e-5	1.972e-3
endodermal cell differentiation	GO:0035987	2	COL12A1, COL6A1	36	9	115.35	1.288e-4	3.661e-3
tissue development	GO:0009888	2	COL12A1, COL6A1	51	9	81.42	2.597e-4	6.076e-3
collagen fibril organization	GO:0030199	2	COL12A1, COL6A1	65	9	63.89	4.222e-4	8.545e-3
response to glucose	GO:0009749	2	COL6A2, COL6A3	68	9	61.07	4.620e-4	9.072e-3
response to polyamine macromolecule	GO:1904583	1	COL6A1	1	9	2076.33	4.816e-4	9.305e-3
regulation of excitatory postsynaptic membrane potential involved in skeletal muscle contraction	GO:0014853	1	DMPK	1	9	2076.33	4.816e-4	9.305e-3