

GeDiPNet Cluster 456 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-19 23:18:39

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
mitochondrial proton-transporting ATP synthase complex assembly	GO:0033615	2	TMEM70, ATPAF2	8	5	934.35	1.603e-6	1.267e-4
regulation of translation by machinery localization	GO:0043143	1	PADI6	1	5	3737.40	2.676e-4	6.245e-3
proton-transporting ATP synthase complex assembly	GO:0043461	1	ATPAF2	1	5	3737.40	2.676e-4	6.245e-3
hydroxylysine biosynthetic process	GO:0046947	1	PLOD3	2	5	1868.70	5.351e-4	9.880e-3
intracellular protein localization	GO:0008104	2	PADI6, PLOD3	194	5	38.53	1.050e-3	1.514e-2
basement membrane assembly	GO:0070831	1	PLOD3	5	5	747.48	1.337e-3	1.709e-2
protein storage	GO:0140089	1	PADI6	5	5	747.48	1.337e-3	1.709e-2
cytoplasm organization	GO:0007028	1	PADI6	6	5	622.90	1.605e-3	1.885e-2
in utero embryonic development	GO:0001701	2	PADI6, PLOD3	252	5	29.66	1.763e-3	1.990e-2
epidermis morphogenesis	GO:0048730	1	PLOD3	7	5	533.91	1.872e-3	2.050e-2
peptidyl-lysine hydroxylation	GO:0017185	1	PLOD3	7	5	533.91	1.872e-3	2.050e-2
epigenetic programming in the zygotic pronuclei	GO:0044725	1	PADI6	9	5	415.27	2.406e-3	2.324e-2
embryonic cleavage	GO:0040016	1	PADI6	9	5	415.27	2.406e-3	2.324e-2
endothelial cell morphogenesis	GO:0001886	1	PLOD3	15	5	249.16	4.007e-3	3.008e-2
negative regulation of protein processing	GO:0010955	1	NLRP7	15	5	249.16	4.007e-3	3.008e-2