

GeDiPNet Cluster 278 -- 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 13:26:20

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
protein localization to membrane	GO:0072657	2	ANO1, NMT1	33	15	75.50	3.130e-4	6.929e-3
negative regulation of cardiac muscle tissue development	GO:0055026	1	FGF3	2	15	622.90	1.605e-3	1.983e-2
N-terminal peptidyl-glycine N-myristoylation	GO:0018008	1	NMT1	2	15	622.90	1.605e-3	1.983e-2
otic placode development	GO:1905040	1	FOXI3	2	15	622.90	1.605e-3	1.983e-2
cellular pigment accumulation	GO:0043482	1	SHROOM3	2	15	622.90	1.605e-3	1.983e-2
glial cell projection elongation	GO:0106091	1	ANO1	3	15	415.27	2.406e-3	2.497e-2
ketone metabolic process	GO:0042180	1	NMT1	3	15	415.27	2.406e-3	2.497e-2
myoblast fate commitment	GO:0048625	1	EPAS1	3	15	415.27	2.406e-3	2.497e-2
positive regulation of establishment of protein localization to mitochondrion	GO:1903749	1	NMT1	5	15	249.16	4.007e-3	3.280e-2
epidermal cell fate specification	GO:0009957	1	FOXI3	5	15	249.16	4.007e-3	3.280e-2
positive regulation of protein localization to lysosome	GO:0150032	1	NMT1	6	15	207.63	4.807e-3	3.579e-2
parathyroid gland development	GO:0060017	1	FOXI3	7	15	177.97	5.606e-3	3.882e-2
iodide transport	GO:0015705	1	ANO1	8	15	155.73	6.405e-3	4.146e-2
cellular response to peptide	GO:1901653	1	ANO1	8	15	155.73	6.405e-3	4.146e-2
anatomical structure morphogenesis	GO:0009653	2	FGF3, FOXI3	160	15	15.57	7.110e-3	4.375e-2