

GeDiPNet Cluster 482 -- 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: 2026-10-20 00:00:46

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of sodium ion transport	GO:0002028	2	ATP1A1, NOS3	19	14	140.50	8.848e-5	2.825e-3
sensory perception of sound	GO:0007605	3	OTOGL, ESPN, SRRM4	162	14	24.72	2.170e-4	5.374e-3
glutathione metabolic process	GO:0006749	2	GSTZ1, GSTP1	49	14	54.48	6.007e-4	1.077e-2
regulation of granulocyte chemotaxis	GO:0071622	1	CAMK1D	1	14	1334.79	7.492e-4	1.230e-2
vibrational conductance of sound to the inner ear	GO:0055127	1	OTOGL	1	14	1334.79	7.492e-4	1.230e-2
nitric oxide storage	GO:0035732	1	GSTP1	1	14	1334.79	7.492e-4	1.230e-2
negative regulation of glucocorticoid biosynthetic process	GO:0031947	1	ATP1A1	1	14	1334.79	7.492e-4	1.230e-2
microvillar actin bundle assembly	GO:0030034	1	ESPN	1	14	1334.79	7.492e-4	1.230e-2
positive regulation of phagocytosis	GO:0050766	2	LYAR, CAMK1D	58	14	46.03	8.412e-4	1.325e-2
cellular oxidant detoxification	GO:0098869	2	GSTZ1, GSTP1	66	14	40.45	1.088e-3	1.529e-2
L-arabinose metabolic process	GO:0046373	1	OTOGL	2	14	667.39	1.498e-3	1.821e-2
positive regulation of striated muscle contraction	GO:0045989	1	ATP1A1	2	14	667.39	1.498e-3	1.821e-2
regulation of the force of heart contraction by chemical signal	GO:0003057	1	NOS3	2	14	667.39	1.498e-3	1.821e-2
smooth muscle hyperplasia	GO:0014806	1	NOS3	2	14	667.39	1.498e-3	1.821e-2
negative regulation of muscle hyperplasia	GO:0014740	1	NOS3	2	14	667.39	1.498e-3	1.821e-2