

GeDiPNet Cluster 166 -- 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: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-09 00:53:08

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
monoatomic ion transport	GO:0006811	6	CHRNA2, KCNQ2, KCNQ3, SCN2A, SCN8A, ATP1A2	667	12	14.01	1.555e-6	1.191e-4
monoatomic ion transmembrane transport	GO:0034220	5	CHRNA2, KCNQ2, KCNQ3, SCN2A, SCN8A	404	12	19.27	3.220e-6	2.121e-4
action potential	GO:0001508	3	KCNQ2, SCN2A, SCN8A	53	12	88.15	4.655e-6	2.861e-4
sodium ion transmembrane transport	GO:0035725	3	SCN2A, SCN8A, ATP1A2	134	12	34.86	7.565e-5	2.465e-3
sodium ion transport	GO:0006814	3	SCN2A, SCN8A, ATP1A2	144	12	32.44	9.369e-5	2.888e-3
response to auditory stimulus	GO:0010996	2	KCNQ3, ATP1A2	23	12	135.41	9.493e-5	2.915e-3
cardiac muscle cell action potential involved in contraction	GO:0086002	2	SCN2A, SCN8A	24	12	129.77	1.035e-4	3.109e-3
potassium ion transmembrane transport	GO:0071805	3	KCNQ2, KCNQ3, ATP1A2	150	12	31.15	1.058e-4	3.158e-3
potassium ion transport	GO:0006813	3	KCNQ2, KCNQ3, ATP1A2	152	12	30.74	1.100e-4	3.256e-3
membrane depolarization	GO:0051899	2	CHRNA2, ATP1A2	32	12	97.33	1.855e-4	4.796e-3
neuronal action potential	GO:0019228	2	KCNQ3, SCN2A	34	12	91.60	2.097e-4	5.219e-3
response to nicotine	GO:0035094	2	CHRNA2, ATP1A2	40	12	77.86	2.909e-4	6.606e-3
transmembrane transport	GO:0055085	4	KCNQ2, KCNQ3, SCN2A, SCN8A	557	12	11.18	3.194e-4	7.094e-3
olfactory cortex development	GO:0021989	1	ATP1A2	1	12	1557.25	6.422e-4	1.140e-2
modulation of inhibitory postsynaptic potential	GO:0098828	1	CHRNA2	1	12	1557.25	6.422e-4	1.140e-2