

GeDiPNet Cluster 578 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See scripts/build_cluster_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-19 23:22:18

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Highly sodium permeable postsynaptic acetylcholine nicotinic receptors	Reactome	1	CHRNA3	7	3	571.90	1.748e-3	1.725e-2
Nef and signal transduction	Reactome	1	ELMO1	8	3	500.42	1.997e-3	1.898e-2
Highly calcium permeable nicotinic acetylcholine receptors	Reactome	1	CHRNA3	9	3	444.81	2.247e-3	2.074e-2
Highly calcium permeable postsynaptic nicotinic acetylcholine receptors	Reactome	1	CHRNA3	12	3	333.61	2.995e-3	2.538e-2
PTK6 Regulates RHO GTPases, RAS GTPase and MAP kinases	Reactome	1	ELMO1	14	3	285.95	3.493e-3	2.829e-2
FCGR3A-mediated phagocytosis	Reactome	1	ELMO1	59	3	67.85	1.467e-2	7.167e-2
Regulation of actin dynamics for phagocytic cup formation	Reactome	1	ELMO1	60	3	66.72	1.491e-2	7.221e-2
VEGFA-VEGFR2 Pathway	Reactome	1	ELMO1	62	3	64.57	1.541e-2	7.381e-2
Bacterial invasion of epithelial cells	KEGG	1	ELMO1	78	3	51.32	1.936e-2	8.409e-2
Peptide ligand-binding receptors	Reactome	1	ECE1	106	3	37.77	2.625e-2	1.004e-1
Cholinergic synapse	KEGG	1	CHRNA3	115	3	34.81	2.845e-2	1.049e-1
Yersinia infection	KEGG	1	ELMO1	138	3	29.01	3.408e-2	1.164e-1
Efferocytosis	KEGG	1	ELMO1	157	3	25.50	3.871e-2	1.252e-1
Chemokine signaling pathway	KEGG	1	ELMO1	193	3	20.74	4.744e-2	1.405e-1
Chemical carcinogenesis - receptor activation	KEGG	1	CHRNA3	215	3	18.62	5.275e-2	1.490e-1