

GeDiPNet Cluster 319 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 15:49:23

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Nitric oxide stimulates guanylate cyclase	Reactome	2	NOS3, NOS1	3	12	667.22	2.744e-6	1.168e-4
Arginine biosynthesis	KEGG	2	NOS3, NOS1	23	12	87.03	2.289e-4	4.391e-3
ROS and RNS production in phagocytes	Reactome	2	NOS3, NOS1	34	12	58.87	5.044e-4	8.181e-3
Arginine and proline metabolism	KEGG	2	NOS3, NOS1	50	12	40.03	1.092e-3	1.484e-2
NOSIP mediated eNOS trafficking	Reactome	1	NOS3	2	12	500.42	1.997e-3	2.322e-2
NOSTRIN mediated eNOS trafficking	Reactome	1	NOS3	5	12	200.17	4.987e-3	4.437e-2
Synthesis of 5-eicosatetraenoic acids	Reactome	1	PON1	6	12	166.81	5.981e-3	5.030e-2
Platelet activation	KEGG	2	TLN1, NOS3	126	12	15.89	6.728e-3	5.441e-2
Phase 1 - inactivation of fast Na+ channels	Reactome	1	KCNIP1	7	12	142.98	6.975e-3	5.567e-2
Relaxin signaling pathway	KEGG	2	NOS3, NOS1	130	12	15.40	7.148e-3	5.656e-2
Apelin signaling pathway	KEGG	2	NOS3, NOS1	140	12	14.30	8.248e-3	6.205e-2
Ca2+ activated K+ channels	Reactome	1	KCNMB1	9	12	111.20	8.960e-3	6.534e-2
SEMA3A-Plexin repulsion signaling by inhibiting Integrin adhesion	Reactome	1	TLN1	10	12	100.08	9.951e-3	6.966e-2
Tetrahydrobiopterin (BH4) synthesis, recycling, salvage and regulation	Reactome	1	NOS3	11	12	90.98	1.094e-2	7.412e-2
cGMP-PKG signaling pathway	KEGG	2	NOS3, KCNMB1	166	12	12.06	1.144e-2	7.597e-2