

GeDiPNet Cluster 521 -- 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: 10 · Generated: 2026-10-19 23:22:05

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Folate biosynthesis	KEGG	3	PTS, SPR, PAH	28	4	321.70	4.533e-8	2.794e-6
Tetrahydrobiopterin (BH4) synthesis, recycling, salvage and regulation	Reactome	2	PTS, SPR	11	4	545.91	4.572e-6	1.526e-4
Phenylketonuria	Reactome	1	PAH	1	4	3002.50	3.331e-4	4.876e-3
Biosynthesis of cofactors	KEGG	2	PTS, SPR	154	4	38.99	9.637e-4	1.102e-2
Phenylalanine, tyrosine and tryptophan biosynthesis	KEGG	1	PAH	6	4	500.42	1.997e-3	1.898e-2
Phenylalanine metabolism	Reactome	1	PAH	6	4	500.42	1.997e-3	1.898e-2
eNOS activation	Reactome	1	SPR	13	4	230.96	4.323e-3	3.305e-2
Phenylalanine metabolism	KEGG	1	PAH	16	4	187.66	5.319e-3	3.801e-2
Metabolic pathways	KEGG	3	PTS, SPR, PAH	1563	4	5.76	7.944e-3	4.940e-2
Biosynthesis of amino acids	KEGG	1	PAH	75	4	40.03	2.475e-2	9.681e-2