

GeDiPNet Cluster 417 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 07:27:26

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
CYP2E1 reactions	Reactome	2	CYP2A6, CYP2C9	11	5	436.73	7.615e-6	2.666e-4
Ubiquinone and other terpenoid-quinone biosynthesis	KEGG	2	GGCX, VKORC1	12	5	400.33	9.137e-6	3.116e-4
Biosynthesis of cofactors	KEGG	3	GGCX, VKORC1, MAT2A	154	5	46.79	2.029e-5	6.045e-4
Metabolic pathways	KEGG	5	GGCX, CYP2A6, CYP2C9, VKORC1, MAT2A	1563	5	7.68	3.712e-5	9.981e-4
Xenobiotics	Reactome	2	CYP2A6, CYP2C9	24	5	200.17	3.813e-5	1.022e-3
Retinol metabolism	KEGG	2	CYP2A6, CYP2C9	68	5	70.65	3.124e-4	5.536e-3
Chemical carcinogenesis - DNA adducts	KEGG	2	CYP2A6, CYP2C9	70	5	68.63	3.311e-4	5.793e-3
Drug metabolism - cytochrome P450	KEGG	2	CYP2A6, CYP2C9	73	5	65.81	3.601e-4	6.183e-3
Metabolism of xenobiotics by cytochrome P450	KEGG	2	CYP2A6, CYP2C9	79	5	60.81	4.218e-4	6.975e-3
Metabolism of vitamin K	Reactome	1	VKORC1	3	5	800.67	1.249e-3	1.600e-2
Caffeine metabolism	KEGG	1	CYP2A6	6	5	400.33	2.496e-3	2.686e-2
Biosynthesis of maresin-like SPMs	Reactome	1	CYP2C9	6	5	400.33	2.496e-3	2.686e-2
Lipid and atherosclerosis	KEGG	2	CYP2A6, CYP2C9	216	5	22.24	3.107e-3	3.152e-2
Synthesis of epoxy (EET) and dihydroxyeicosatrienoic acids (DHET)	Reactome	1	CYP2C9	8	5	300.25	3.327e-3	3.313e-2
Synthesis of (16-20)-hydroxyeicosatetraenoic acids (HETE)	Reactome	1	CYP2C9	9	5	266.89	3.742e-3	3.593e-2