

GeDiPNet Cluster 528 -- 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: 2026-10-20 00:02:38

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Heme biosynthesis	Reactome	3	CPOX, UROD, ALAD	14	7	367.65	4.402e-8	2.727e-6
Biosynthesis of protectins	Reactome	2	CYP1A1, CYP1A2	4	7	857.86	1.746e-6	6.757e-5
Porphyrin metabolism	KEGG	3	CPOX, UROD, ALAD	46	7	111.89	1.821e-6	6.984e-5
Chemical carcinogenesis - DNA adducts	KEGG	3	CYP1A1, CYP1A2, GSTM1	70	7	73.53	6.527e-6	2.044e-4
Synthesis of epoxy (EET) and dihydroxyeicosatrienoic acids (DHET)	Reactome	2	CYP1A1, CYP1A2	8	7	428.93	8.140e-6	2.457e-4
Metabolism of xenobiotics by cytochrome P450	KEGG	3	CYP1A1, CYP1A2, GSTM1	79	7	65.15	9.408e-6	2.767e-4
Synthesis of (16-20)-hydroxyeicosatetraenoic acids (HETE)	Reactome	2	CYP1A1, CYP1A2	9	7	381.27	1.046e-5	3.021e-4
Metabolic pathways	KEGG	6	CPOX, UROD, ALAD, CYP1A1, CYP1A2, GSTM1	1563	7	6.59	2.998e-5	7.241e-4
Biosynthesis of cofactors	KEGG	3	CPOX, UROD, ALAD	154	7	33.42	6.969e-5	1.420e-3
Chemical carcinogenesis - receptor activation	KEGG	3	CYP1A1, CYP1A2, GSTM1	215	7	23.94	1.878e-4	3.123e-3
Chemical carcinogenesis - reactive oxygen species	KEGG	3	CYP1A1, CYP1A2, GSTM1	227	7	22.67	2.205e-4	3.549e-3
Tryptophan metabolism	KEGG	2	CYP1A1, CYP1A2	42	7	81.70	2.480e-4	3.888e-3
Steroid hormone biosynthesis	KEGG	2	CYP1A1, CYP1A2	63	7	54.47	5.592e-4	7.285e-3
Aromatic amines can be N-hydroxylated or N-dealkylated by CYP1A2	Reactome	1	CYP1A2	1	7	1715.71	5.828e-4	7.518e-3
Retinol metabolism	KEGG	2	CYP1A1, CYP1A2	68	7	50.46	6.513e-4	8.190e-3