

GeDiPNet Cluster 246 -- 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 14:41:49

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Aromatic amines can be N-hydroxylated or N-dealkylated by CYP1A2	Reactome	1	CYP1A2	1	16	750.63	1.332e-3	1.681e-2
APC truncation mutants are not K63 polyubiquitinated	Reactome	1	APC	1	16	750.63	1.332e-3	1.681e-2
Influenza A	KEGG	3	PLG, FAS, JAK2	173	16	13.02	1.433e-3	1.780e-2
Chemical carcinogenesis - receptor activation	KEGG	3	JAK2, AHR, CYP1A2	215	16	10.47	2.667e-3	2.828e-2
Leishmaniasis	KEGG	2	ITGB2, JAK2	78	16	19.25	4.711e-3	4.215e-2
Biosynthesis of protectins	Reactome	1	CYP1A2	4	16	187.66	5.319e-3	4.557e-2
Complement and coagulation cascades	KEGG	2	PLG, ITGB2	88	16	17.06	5.958e-3	4.923e-2
FasL/ CD95L signaling	Reactome	1	FAS	5	16	150.13	6.644e-3	5.278e-2
Staphylococcus aureus infection	KEGG	2	PLG, ITGB2	99	16	15.16	7.487e-3	5.693e-2
Caffeine metabolism	KEGG	1	CYP1A2	6	16	125.10	7.968e-3	5.956e-2
Biosynthesis of maresin-like SPMs	Reactome	1	CYP1A2	6	16	125.10	7.968e-3	5.956e-2
Interleukin-4 and Interleukin-13 signaling	Reactome	2	ITGB2, JAK2	108	16	13.90	8.855e-3	6.375e-2
Th17 cell differentiation	KEGG	2	JAK2, AHR	109	16	13.77	9.014e-3	6.445e-2
Aryl hydrocarbon receptor signalling	Reactome	1	AHR	7	16	107.23	9.291e-3	6.561e-2
Synthesis of epoxy (EET) and dihydroxyeicosatrienoic acids (DHET)	Reactome	1	CYP1A2	8	16	93.83	1.061e-2	7.123e-2