

GeDiPNet Cluster 478 -- 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 00:02:53

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Choline catabolism	Reactome	1	ALDH7A1	6	6	333.61	2.994e-3	2.538e-2
InlB-mediated entry of Listeria monocytogenes into host cell	Reactome	1	CBL	7	6	285.95	3.493e-3	2.829e-2
PTK6 Regulates RTKs and Their Effectors AKT1 and DOK1	Reactome	1	CBL	9	6	222.41	4.489e-3	3.394e-2
Interleukin-6 signaling	Reactome	1	CBL	11	6	181.97	5.484e-3	3.872e-2
Lysine catabolism	Reactome	1	ALDH7A1	12	6	166.81	5.981e-3	4.097e-2
TGF-beta receptor signaling activates SMADs	Reactome	1	CBL	12	6	166.81	5.981e-3	4.097e-2
Regulation of KIT signaling	Reactome	1	CBL	14	6	142.98	6.975e-3	4.528e-2
Constitutive Signaling by EGFRvIII	Reactome	1	CBL	15	6	133.44	7.472e-3	4.730e-2
Spry regulation of FGF signaling	Reactome	1	CBL	16	6	125.10	7.968e-3	4.940e-2
Class B/2 (Secretin family receptors)	Reactome	1	ADGRE3	18	6	111.20	8.961e-3	5.313e-2
Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	Reactome	1	CBL	19	6	105.35	9.457e-3	5.493e-2
Negative regulation of MET activity	Reactome	1	CBL	21	6	95.32	1.045e-2	5.837e-2
Regulation of signaling by CBL	Reactome	1	CBL	21	6	95.32	1.045e-2	5.837e-2
Histidine metabolism	KEGG	1	ALDH7A1	22	6	90.98	1.094e-2	6.008e-2
Negative regulation of FGFR3 signaling	Reactome	1	CBL	22	6	90.98	1.094e-2	6.008e-2