

GeDiPNet Cluster 486 -- 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: 2026-10-19 23:21:12

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Selenocompound metabolism	KEGG	1	SEPHS1	17	21	33.64	2.933e-2	1.069e-1
Signaling by cytosolic FGFR1 fusion mutants	Reactome	1	ZMYM2	18	21	31.77	3.103e-2	1.102e-1
Regulation of TP53 Activity through Acetylation	Reactome	1	BRPF1	23	21	24.87	3.949e-2	1.264e-1
Deadenylation of mRNA	Reactome	1	PAN2	24	21	23.83	4.117e-2	1.295e-1
TRP channels	Reactome	1	TRPM3	28	21	20.43	4.787e-2	1.413e-1
Signaling by FGFR1 in disease	Reactome	1	ZMYM2	33	21	17.33	5.619e-2	1.548e-1
Lysine degradation	KEGG	1	ASH1L	63	21	9.08	1.046e-1	2.221e-1
PKMTs methylate histone lysines	Reactome	1	ASH1L	71	21	8.05	1.172e-1	2.376e-1
RNA degradation	KEGG	1	PAN2	78	21	7.33	1.280e-1	2.503e-1
Viral mRNA Translation	Reactome	1	RPL10L	89	21	6.43	1.447e-1	2.700e-1
HATs acetylate histones	Reactome	1	BRPF1	93	21	6.15	1.507e-1	2.765e-1
SRP-dependent cotranslational protein targeting to membrane	Reactome	1	RPL10L	93	21	6.15	1.507e-1	2.765e-1
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	Reactome	1	RPL10L	95	21	6.02	1.537e-1	2.799e-1
Formation of a pool of free 40S subunits	Reactome	1	RPL10L	101	21	5.66	1.626e-1	2.903e-1
L13a-mediated translational silencing of Ceruloplasmin expression	Reactome	1	RPL10L	111	21	5.15	1.773e-1	3.068e-1