

GeDiPNet Cluster 522 -- 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 23:21:06

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Regulation of lipolysis in adipocytes	KEGG	5	AKT2, CIDEC, LIPE, PLIN1, PLAAT3	59	22	46.26	5.945e-8	3.553e-6
Apoptosis	KEGG	4	AKT2, LMNA, PARP2, LMNB2	137	22	15.94	1.011e-4	1.911e-3
Apelin signaling pathway	KEGG	4	AKT2, LIPE, PLIN1, NOTCH3	140	22	15.60	1.099e-4	2.045e-3
Glycerophospholipid metabolism	KEGG	3	AGPAT2, PCYT1A, PLAAT3	102	22	16.06	8.145e-4	9.688e-3
VEGFR2 mediated vascular permeability	Reactome	2	AKT2, CAV1	29	22	37.65	1.262e-3	1.353e-2
AMPK signaling pathway	KEGG	3	AKT2, LIPE, PPARG	122	22	13.42	1.368e-3	1.436e-2
Dual Incision in GG-NER	Reactome	2	PARP2, POLD1	41	22	26.63	2.515e-3	2.243e-2
Base excision repair	KEGG	2	PARP2, POLD1	44	22	24.81	2.892e-3	2.485e-2
Adrenaline signalling through Alpha-2 adrenergic receptor	Reactome	1	ADRA2A	3	22	181.97	5.486e-3	3.872e-2
Inhibition of TSC complex formation by PKB	Reactome	1	AKT2	3	22	181.97	5.486e-3	3.872e-2
Breakdown of the nuclear lamina	Reactome	1	LMNA	3	22	181.97	5.486e-3	3.872e-2
Transcriptional regulation of white adipocyte differentiation	Reactome	2	PLIN1, PPARG	67	22	16.30	6.590e-3	4.373e-2
AKT-mediated inactivation of FOXO1A	Reactome	1	AKT2	4	22	136.48	7.308e-3	4.669e-2
Activation of AKT2	Reactome	1	AKT2	4	22	136.48	7.308e-3	4.669e-2
PPAR signaling pathway	KEGG	2	PLIN1, PPARG	76	22	14.37	8.411e-3	5.110e-2