

GeDiPNet Cluster 272 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-07 23:57:28

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Signaling by Insulin receptor	Reactome	1	INSR	2	2	3002.50	3.330e-4	5.910e-3
IRS activation	Reactome	1	INSR	5	2	1201.00	8.325e-4	1.209e-2
Insulin receptor signalling cascade	Reactome	1	INSR	6	2	1000.83	9.990e-4	1.390e-2
Signal attenuation	Reactome	1	INSR	10	2	600.50	1.665e-3	2.040e-2
Maturity onset diabetes of the young	KEGG	1	HNF1A	26	2	230.96	4.325e-3	4.039e-2
Insulin receptor recycling	Reactome	1	INSR	26	2	230.96	4.325e-3	4.039e-2
Aldosterone-regulated sodium reabsorption	KEGG	1	INSR	38	2	158.03	6.318e-3	5.221e-2
Type II diabetes mellitus	KEGG	1	INSR	47	2	127.77	7.812e-3	5.994e-2
Ovarian steroidogenesis	KEGG	1	INSR	52	2	115.48	8.641e-3	6.399e-2
Regulation of lipolysis in adipocytes	KEGG	1	INSR	59	2	101.78	9.801e-3	6.920e-2
Longevity regulating pathway - multiple species	KEGG	1	INSR	62	2	96.85	1.030e-2	7.140e-2
Longevity regulating pathway	KEGG	1	INSR	90	2	66.72	1.493e-2	8.921e-2
Adherens junction	KEGG	1	INSR	93	2	64.57	1.543e-2	9.123e-2
PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	Reactome	1	INSR	103	2	58.30	1.708e-2	9.709e-2
Insulin resistance	KEGG	1	INSR	109	2	55.09	1.807e-2	1.003e-1