

miRPathDB Enriched: SINAPTOFISINA_1_vs_0

GO Biological process (miRPathDB)

keratinocyte migration

trachea formation

receptor-mediated endocytosis

thymus development

microtubule polymerization or depolymerization

mRNA cleavage involved in gene silencing by miRNA

artery morphogenesis

negative regulation of stem cell differentiation

positive regulation of vasoconstriction

regulation of RNA polymerase II transcriptional preinitiation complex assembly

calcium ion import into sarcoplasmic reticulum

vesicle cargo loading

GO Molecular function (miRPathDB)

protein N-terminus binding

endoribonuclease activity cleaving miRNA-paired mRNA

insulin-like growth factor receptor binding

cyclin-dependent protein serine/threonine kinase inhibitor activity

structural molecule activity

MAP kinase kinase activity

endoribonuclease activity producing 5-phosphomonoesters

histone deacetylase regulator activity

signaling receptor activity

single-stranded DNA binding

BH3 domain binding

BH domain binding

KEGG (miRPathDB)

Protein processing in endoplasmic reticulum

Aldosterone-regulated sodium reabsorption

Fc gamma R-mediated phagocytosis

Arrhythmogenic right ventricular cardiomyopathy ARVC

Viral myocarditis

Alcoholism

Amyotrophic lateral sclerosis ALS

Prion diseases

Dorso-ventral axis formation

B cell receptor signaling pathway

DNA replication

Natural killer cell mediated cytotoxicity

Reactome (miRPathDB)

Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimers disease models

Neurodegenerative Diseases

Transport to the Golgi and subsequent modification

E3 ubiquitin ligases ubiquitinate target proteins

Protein ubiquitination

Asparagine N-linked glycosylation

CaMK IV-mediated phosphorylation of CREB

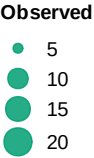
NOTCH2 intracellular domain regulates transcription

NOTCH4 Intracellular Domain Regulates Transcription

Phosphate bond hydrolysis by NTPDase proteins

Negative regulation of FGFR3 signaling

Neddylation



-log10(P-adjusted)