

miRPathDB Depleted: EDAD\_cont\_10y

GO Biological  
process  
(miRPathDB)

GO Molecular  
function  
(miRPathDB)

vesicle organization  
platelet dense granule organization  
nuclear envelope organization  
morphogenesis of a polarized epithelium  
regulation of transcription from RNA  
polymerase II promoter in response to  
stress  
ribonucleoprotein complex assembly  
intracellular transport of virus  
cellular protein-containing complex  
localization  
Golgi vesicle transport  
secretory granule organization  
miRNA mediated inhibition of translation  
protein targeting to ER

structural constituent of ribosome  
basal RNA polymerase II transcription  
machinery binding  
RNA polymerase binding  
translation repressor activity mRNA  
regulatory element binding  
RNA polymerase II complex binding  
endoribonuclease activity cleaving  
miRNA-paired mRNA  
RNA helicase activity  
GTPase binding  
RNA polymerase core enzyme binding  
ATPase activity coupled  
unfolded protein binding  
nucleotidyltransferase activity

KEGG  
(miRPathDB)

Reactome  
(miRPathDB)

Ribosome  
Vasopressin-regulated water reabsorption  
Long-term depression  
RNA transport  
Metabolic pathways  
Biosynthesis of amino acids

Circadian Clock  
Regulation of PTEN localization  
Signaling by TGF-beta Receptor Complex  
in Cancer  
Competing endogenous RNAs ceRNAs  
regulate PTEN translation  
Loss of Function of SMAD23 in Cancer  
Negative regulators of DDX58IFIH1  
signaling  
Regulation of PTEN mRNA translation  
Post-transcriptional silencing by small  
RNAs  
Regulation of MECP2 expression and  
activity  
Synthesis of active ubiquitin roles of  
E1 and E2 enzymes  
Antigen processing Ubiquitination  
Proteasome degradation  
TGF-beta receptor signaling in EMT  
epithelial to mesenchymal transition

Observed  
10  
20  
30

0.6 0.9 1.2 1.5

-log10(P-adjusted)

0.6 0.9 1.2 1.5