

MECP2 mRNA binds miR-132 RISC

Christodoulou, J., Krishnaraj, R., Orlic-Milacic, M.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references

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Reactome database release: 88

This document contains 1 reaction ([see Table of Contents](#))

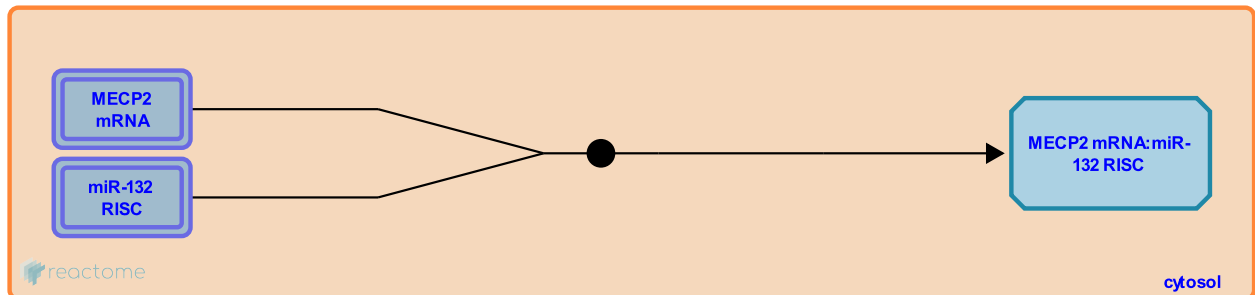
MECP2 mRNA binds miR-132 RISC ↗

Stable identifier: R-HSA-9021182

Type: binding

Compartment: cytosol

Inferred from: [Mecp2 mRNA binds miR-132 RISC \(Rattus norvegicus\)](#)



MicroRNA miR-132 is complementary to the 3'UTR of long MECP2 transcripts (>10 kb), which are predominantly expressed in the brain. Based on studies in mice and rats, miR-132 reduces both mRNA and protein levels of MECP2 and was confirmed to be specific for MECP2 mRNA by the 3'UTR-luciferase reporter gene assay (Klein et al. 2007, Su et al. 2015).

miR-132 levels increase in response to BDNF signaling in a CREB-dependent way (Vo et al. 2005, Klein et al. 2007, Lyu et al. 2016). In patients with major depressive disorder, miR-132 levels are increased while MECP2 and BDNF levels are decreased (Su et al. 2015).

Editions

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