miR-19a microRNA binds PTEN mRNA

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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

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

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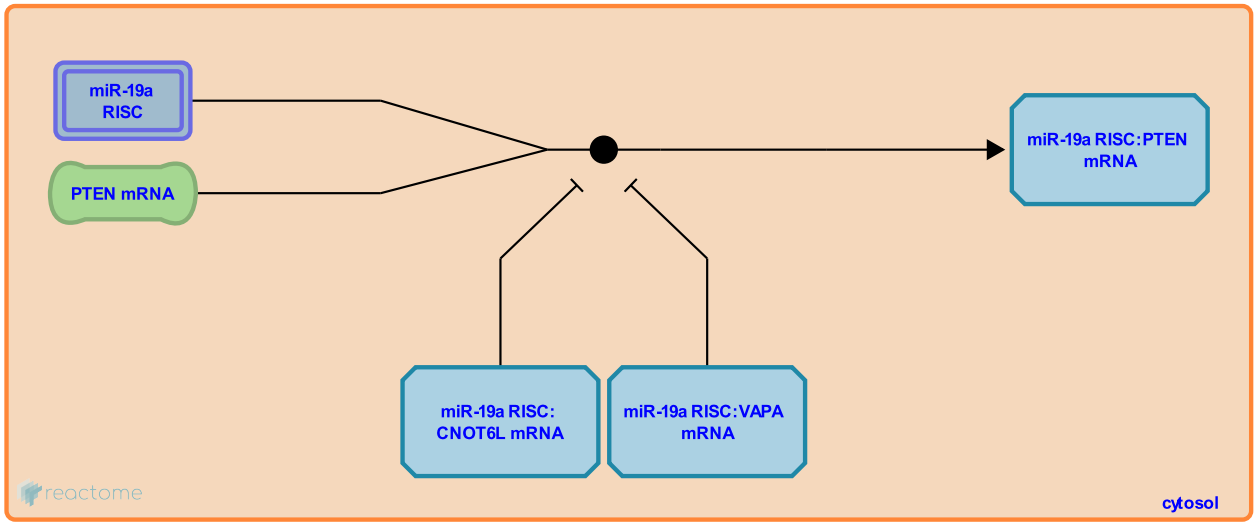
Stable identifier: R-HSA-8944522

Type: binding

Compartments: cytosol



MicroRNA miR-19a-3p, one of the two mature products of miR-19a, binds the 3'UTR of PTEN mRNA (Xiao et al. 2008, Poliseno, Salmena, Riccardi et al. 2010). miR-19a microRNA causes reduction in both PTEN mRNA and protein levels and is thus shown to function as a part of the endonucleolytic RISC. It is possible that miR-19a microRNA also functions as a part of the nonendonucleolytic RISC.

Literature references

Rameh, L., Varmeh, S., Sportoletti, P., Fornari, A., Loda, M., Poliseno, L. et al. (2010). Identification of the miR-106b~25 microRNA cluster as a proto-oncogenic PTEN-targeting intron that cooperates with its host gene MCM7 in transformation. *Sci Signal, 3,* ra29. ↗

Zhang, B., Xiao, C., Kutok, JL., Henderson, JM., Wang, J., Calado, DP. et al. (2008). Lymphoproliferative disease and autoimmunity in mice with increased miR-17-92 expression in lymphocytes. *Nat. Immunol., 9,* 405-14. ↗

Editions

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