LIN28 binds POU5F1 (OCT4) 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. ↗

Reactome database release: 88

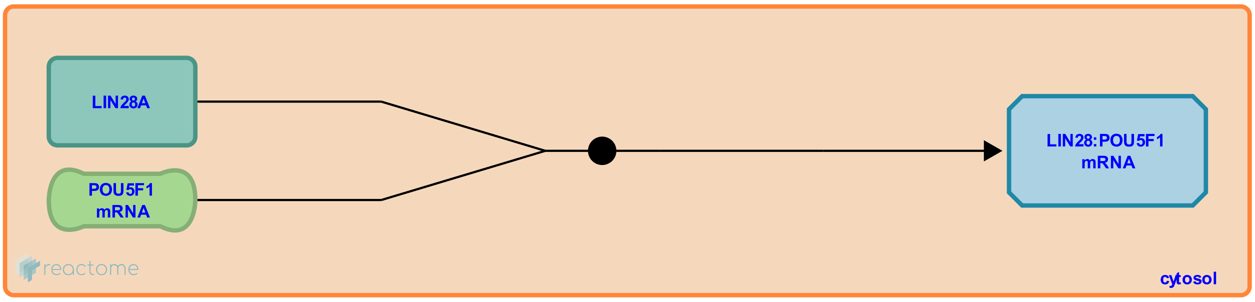
This document contains 1 reaction (see Table of Contents)

LIN28 binds POU5F1 (OCT4) mRNA ↗

Stable identifier: R-HSA-500366

Type: binding

Compartments: cytosol



LIN28 binds the R2 region of the POU5F1 (OCT4) mRNA and increases translation of a luciferase reporter mRNA containing the binding site (Qiu et al. 2009, Lei et al. 2012). Reduction of LIN28 levels in embryonic stem cells causes a reduction in POU5F1 protein (Qiu et al. 2009).

Literature references

Peng, S., Huang, Y., Qiu, C., Wang, J., Ma, Y. (2009). Lin28-mediated post-transcriptional regulation of Oct4 expression in human embryonic stem cells. *Nucleic Acids Res, 38*, 1240-8. ↗

Qiao, C., Lei, XX., Hammond, SM., Huang, Y., Newman, MA., Ma, W. et al. (2012). Determinants of mRNA recognition and translation regulation by Lin28. *Nucleic Acids Res., 40*, 3574-84. ↗

Editions

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