

# IGF2BP2 binds specific RNAs

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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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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.

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This document contains 1 reaction (see Table of Contents)

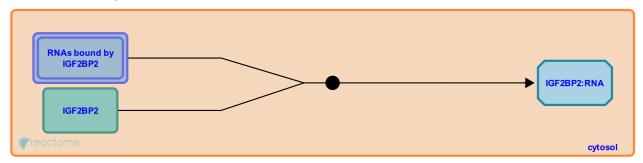
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Stable identifier: R-HSA-428293

**Type:** binding

**Compartments:** cytosol



Insulin-like Growth Factor mRNA Binding Factor-2 (IGF2BP2, also known as IMP2 and VICKZ2) binds several specific RNAs containing the sequence motif CAUH (where H is A, C, or U). Binding causes stabilization and subcellular localization of the RNA.

Isoforms of IGF2 mRNA containing leader-3 are bound by IGF2BP2 at the 5' UTR, repressing translation (Other isoforms of IGF2 are constitutive).

IGF2BP2 may be a causal factor in type 2 diabetes.

#### Literature references

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#### **Editions**

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