

AUF1 binds translation and heat shock proteins

May, B., Wilusz, J.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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: 74

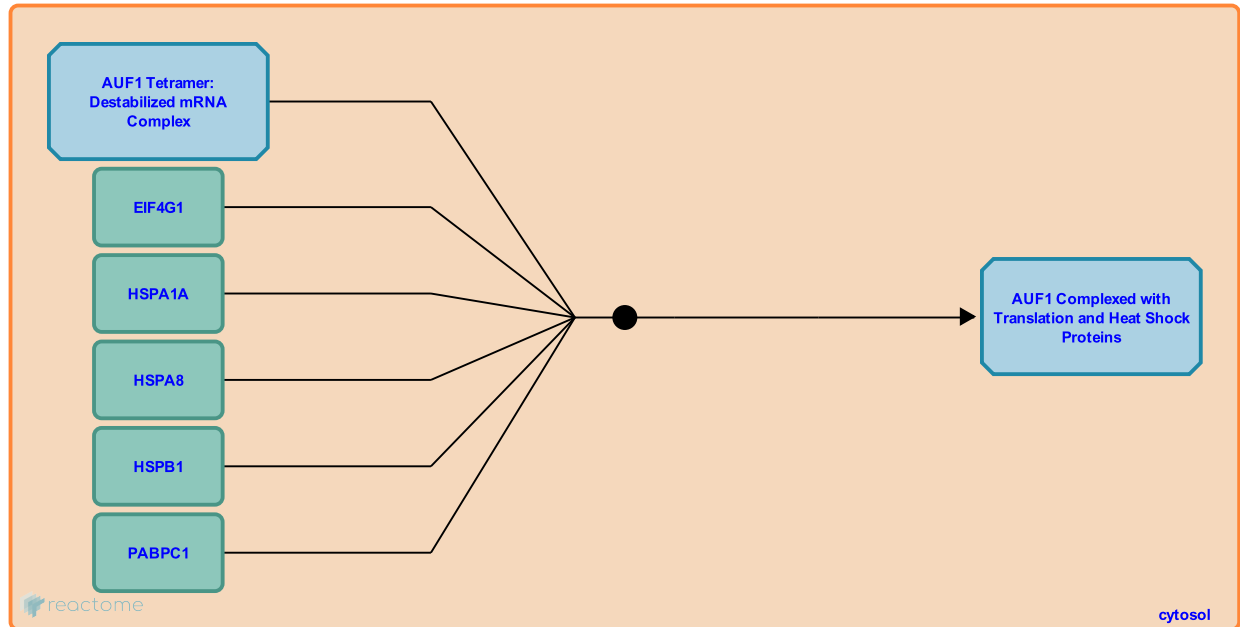
This document contains 1 reaction ([see Table of Contents](#))

AUF1 binds translation and heat shock proteins ↗

Stable identifier: R-HSA-450551

Type: binding

Compartments: cytosol



Tetrameric AUF1 bound to RNA forms a complex with other proteins, including elongation factor eIF4G, polyA-binding protein PABP, Hsp, Hsc70, and Hsp27. AUF1 also directly interacts with polyadenylate.

Literature references

- Wilson, GM., Lu, J., Sutphen, K., Sun, Y., Huynh, Y., Brewer, G. (2003). Regulation of A + U-rich element-directed mRNA turnover involving reversible phosphorylation of AUF1. *J Biol Chem*, 278, 33029-38. ↗
- Sinsimer, KS., Gratacos, FM., Knapinska, AM., Lu, J., Krause, CD., Wierzbowski, AV. et al. (2008). Chaperone Hsp27, a novel subunit of AUF1 protein complexes, functions in AU-rich element-mediated mRNA decay. *Mol Cell Biol*, 28, 5223-37. ↗
- Laroia, G., Cuesta, R., Brewer, G., Schneider, RJ. (1999). Control of mRNA decay by heat shock-ubiquitin-proteasome pathway. *Science*, 284, 499-502. ↗
- Lu, JY., Bergman, N., Sadri, N., Schneider, RJ. (2006). Assembly of AUF1 with eIF4G-poly(A) binding protein complex suggests a translation function in AU-rich mRNA decay. *RNA*, 12, 883-93. ↗

Editions

2009-12-29	Authored, Edited	May, B.
2010-06-29	Reviewed	Wilusz, J.