

HSF1-mediated gene expression

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03/05/2024

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

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Reactome database release: 88

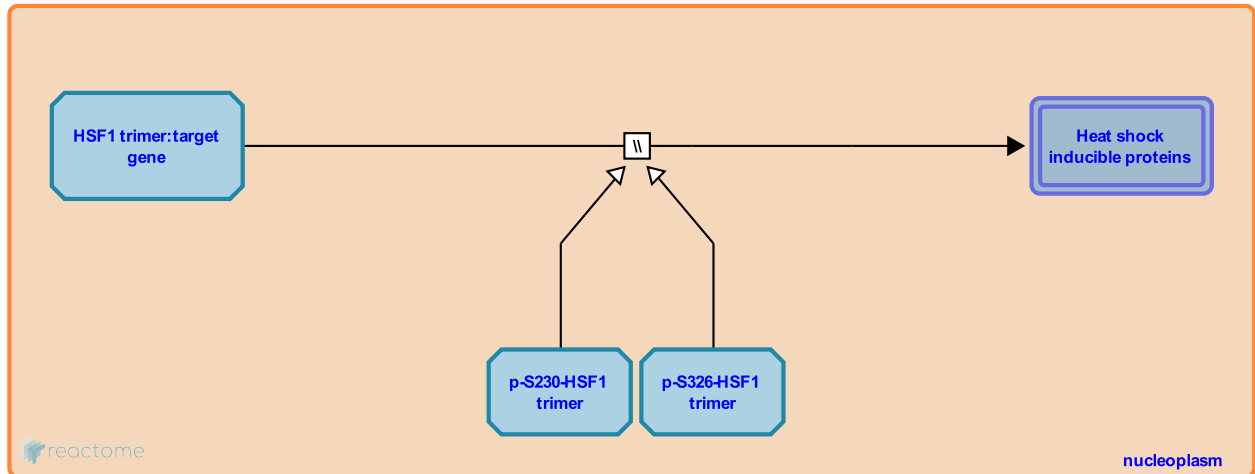
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HSF1-mediated gene expression ↗

Stable identifier: R-HSA-5082356

Type: omitted

Compartments: nucleoplasm



Combination of chromatin immunoprecipitation (ChIP) microarray analysis and time course gene expression microarray analysis with and without siRNA-mediated inhibition of HSF1 showed that human HSF1 can induce the expression of different sets of target genes to maintain a wide range of biological processes (e.g., anti-apoptosis, RNA splicing, ubiquitination)(Page TG et al. 2006; Vihervaara A. et al. 2013). However, HSF1 is best known for rapid stress-induced upregulation of certain genes related to protein folding, such as HSPA1A/HSP70, HSPC/HSP90, HSPB1/HSP27, and DNAJB1/HSP40 (Mosser DD et al. 1988; Trinklein ND et al. 2004a,b; Page TG et al. 2006; Vihervaara A. et al. 2013).

In the nucleus acetylation of Histone H3 is linked to the function of the Elongator complex in transcription (Kim JH et al. 2002). Elongator complex protein 3 (ELP3), a catalytic acetyltransferase subunit of the Elongator complex, has been reported to regulate the transcription of HSP70 gene, and the histone acetyltransferase (HAT) domain of ELP3 is essential for this function (Han Q et al. 2007; Li F et al. 2001).

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Editions

2013-10-29	Authored	Shamovsky, V.
2014-02-17	Reviewed	Pani, B.
2014-02-17	Edited	Shamovsky, V.