HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

01/05/2024

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

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
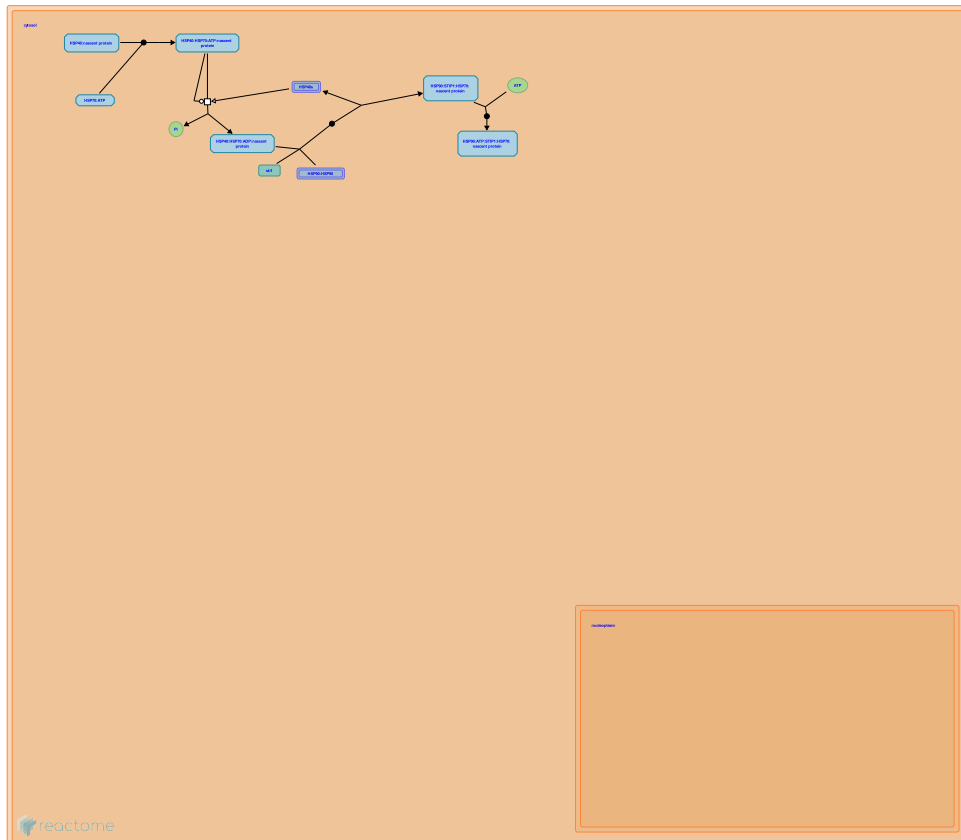
This document contains 1 pathway and 4 reactions (see Table of Contents)

HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand ↗

Stable identifier: R-SPO-3371497

Compartments: cytosol

Inferred from: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand (Homo sapiens)

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp
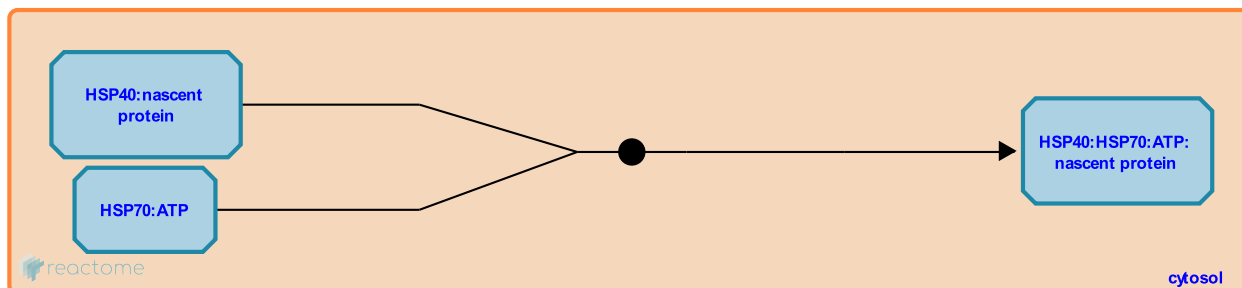
HSP70 binds to HSP40:nascent protein ↗

Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-SPO-3371590

Type: binding

Compartments: cytosol

Inferred from: HSP70 binds to HSP40:nascent protein (Homo sapiens)

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: ATP hydrolysis by HSP70
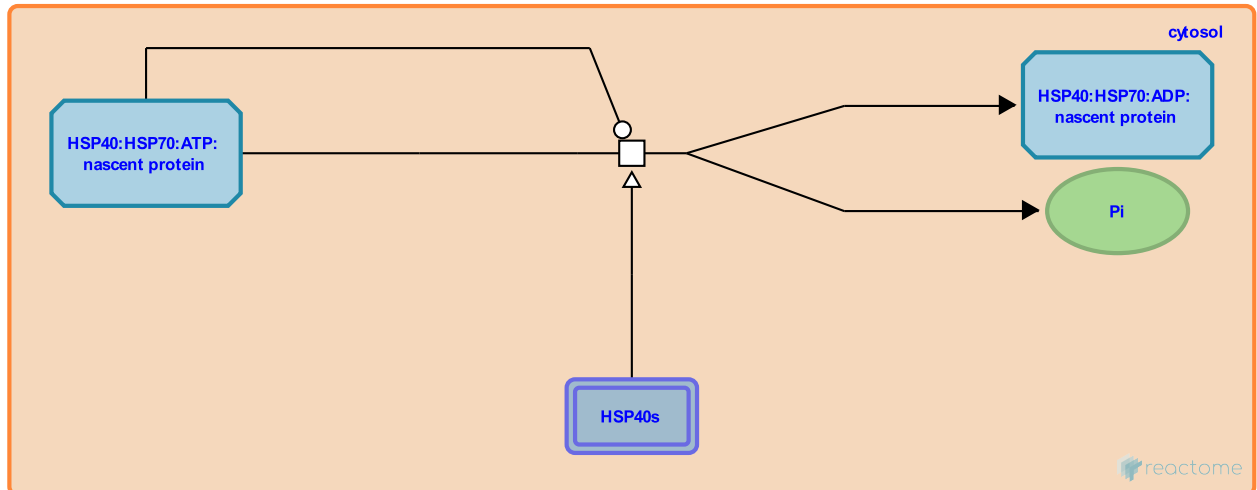
ATP hydrolysis by HSP70 ↗

Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-SPO-3371422

Type: transition

Compartments: cytosol

Inferred from: ATP hydrolysis by HSP70 (Homo sapiens)

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: HSP70 binds to HSP40:nascent protein

Followed by: STIP1(HOP) binds HSP90 and HSP70:HSP40:nascent protein

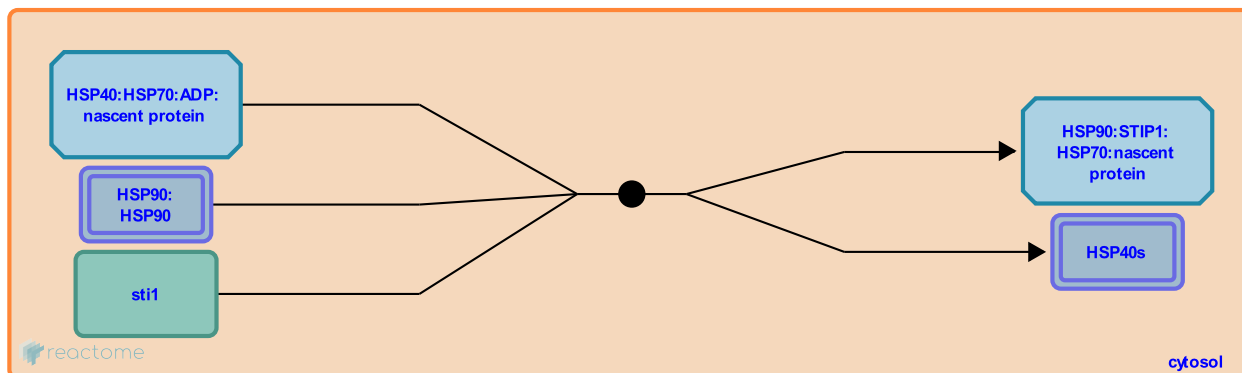## STIP1(HOP) binds HSP90 and HSP70:HSP40:nascent protein ↗

Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-SPO-3371503

Type: binding

Compartments: cytosol

Inferred from: STIP1(HOP) binds HSP90 and HSP70:HSP40:nascent protein (Homo sapiens)

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: ATP hydrolysis by HSP70

Followed by: ATP binding to HSP90 triggers conformation change

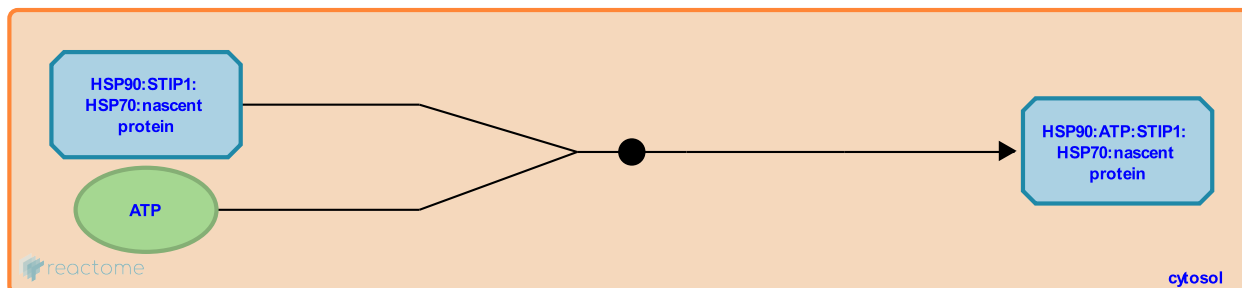# ATP binding to HSP90 triggers conformation change ↗

Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-SPO-5618107

Type: binding

Compartments: cytosol

Inferred from: ATP binding to HSP90 triggers conformation change (Homo sapiens)

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: STIP1(HOP) binds HSP90 and HSP70:HSP40:nascent protein

Table of Contents