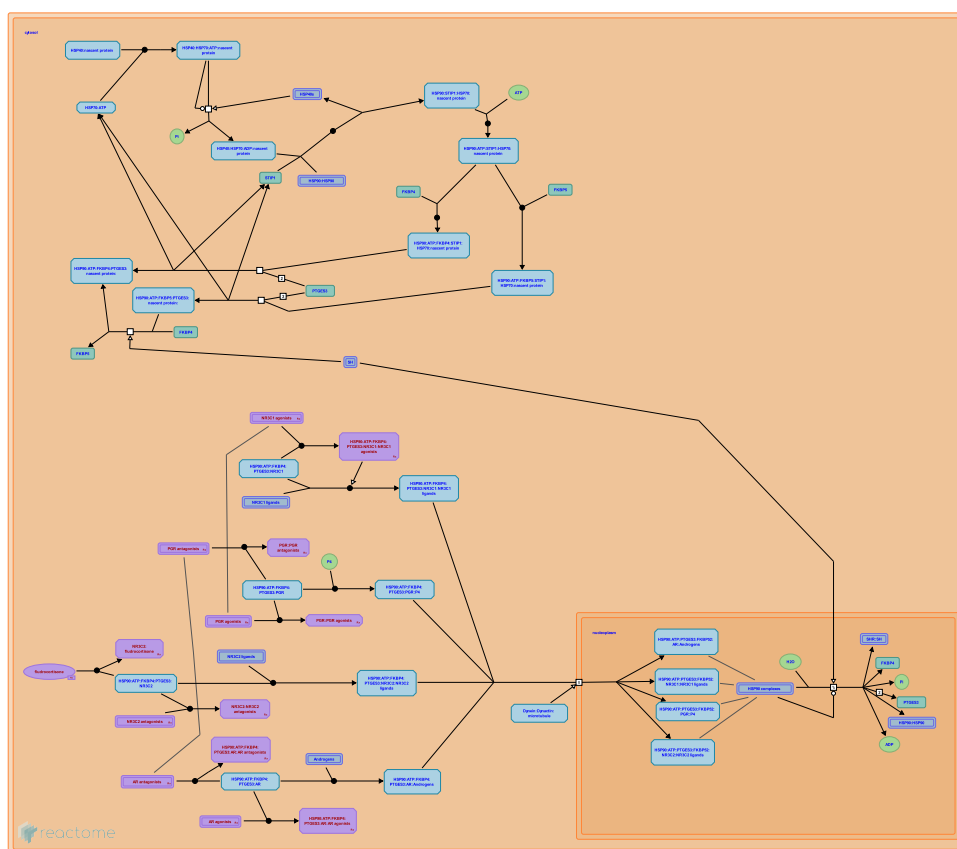


HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand



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

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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](https://reactome.org/page/faq).

16/05/2024

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

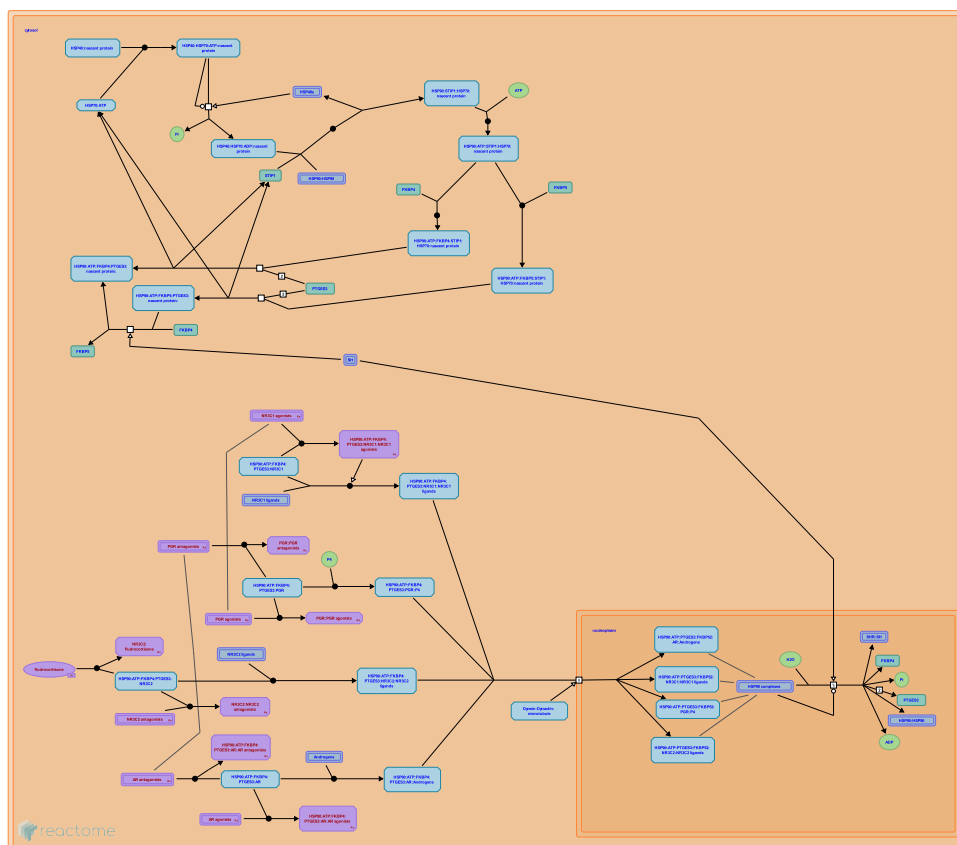
This document contains 1 pathway and 22 reactions ([see Table of Contents](#))

HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of lig- and ↗

Stable identifier: R-BTA-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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

HSP70 binds to HSP40:nascent protein ↗

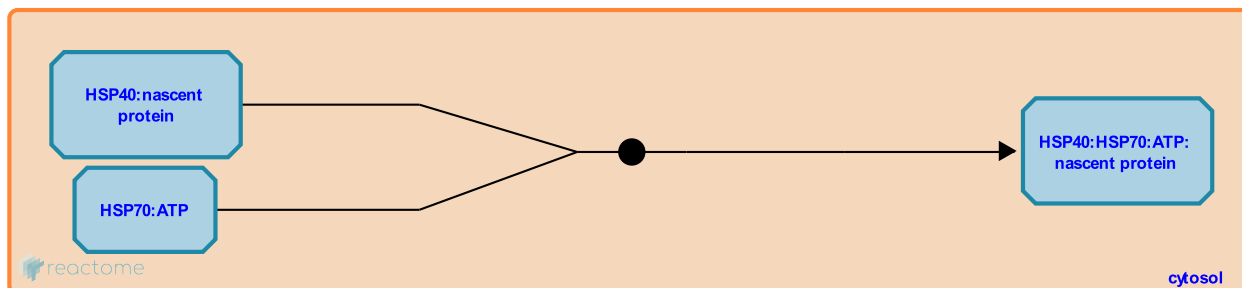
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: ATP hydrolysis by HSP70

ATP hydrolysis by HSP70 ↗

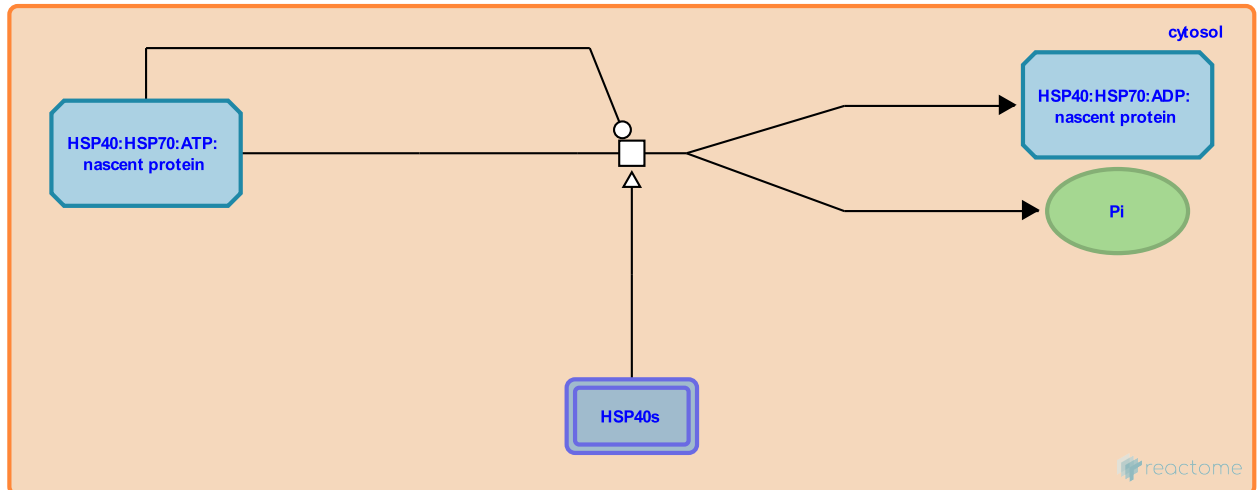
Location: [HSP90 chaperone cycle for steroid hormone receptors \(SHR\) in the presence of ligand](#)

Stable identifier: R-BTA-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 ↗

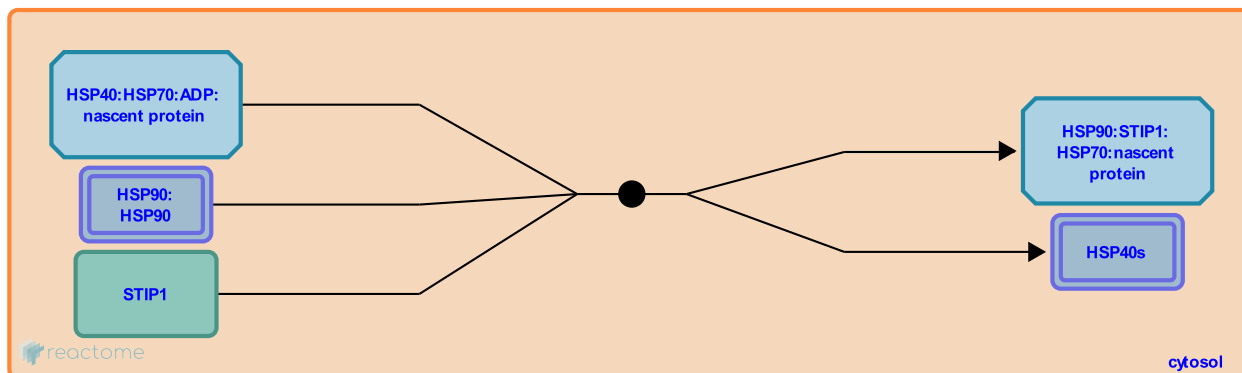
Location: [HSP90 chaperone cycle for steroid hormone receptors \(SHR\) in the presence of ligand](#)

Stable identifier: R-BTA-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 ↗

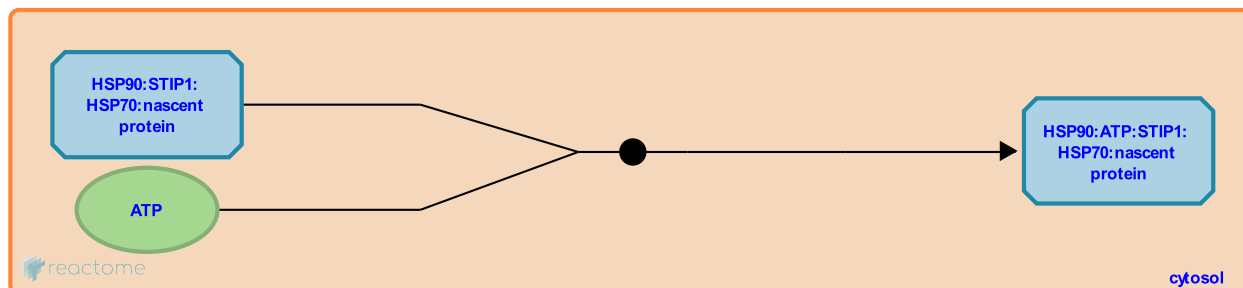
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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

Followed by: FKBP5 binds HSP90:ATP:STIP1:HSP70:nascent protein, FKBP4 binds HSP90:ATP:STIP1:HSP70:nascent protein

FKBP5 binds HSP90:ATP:STIP1:HSP70:nascent protein ↗

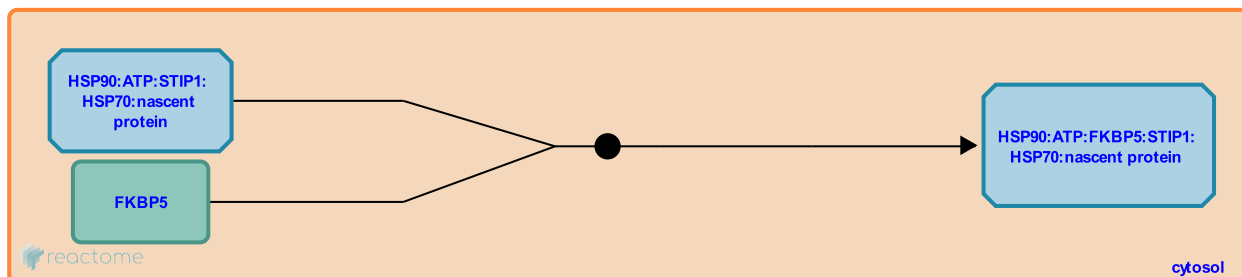
Location: [HSP90 chaperone cycle for steroid hormone receptors \(SHR\) in the presence of ligand](#)

Stable identifier: R-BTA-5618105

Type: binding

Compartments: cytosol

Inferred from: [FKBP5 binds HSP90:ATP:STIP1:HSP70: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 binding to HSP90 triggers conformation change](#)

Followed by: [p23 \(PTGES3\) binds HSP90:ATP:FKBP5:nascent protein](#)

FKBP4 binds HSP90:ATP:STIP1:HSP70:nascent protein ↗

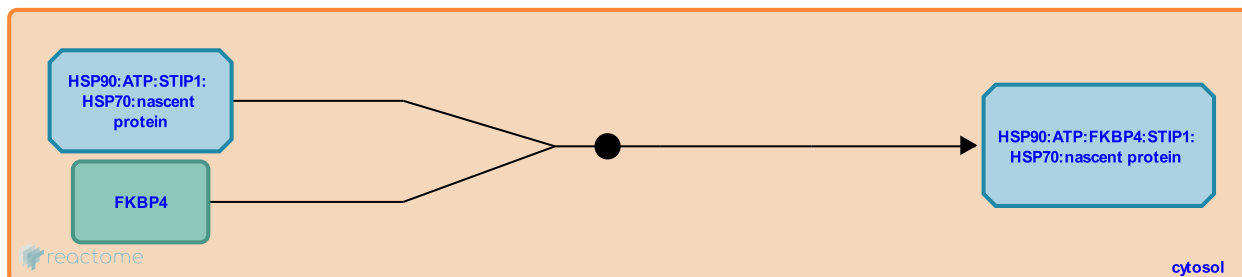
Location: [HSP90 chaperone cycle for steroid hormone receptors \(SHR\) in the presence of ligand](#)

Stable identifier: R-BTA-5618085

Type: binding

Compartments: cytosol

Inferred from: [FKBP4 binds HSP90:ATP:STIP1:HSP70: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 binding to HSP90 triggers conformation change](#)

Followed by: [p23 \(PTGES3\) binds HSP90:ATP:FKBP4:nascent protein](#)

p23 (PTGES3) binds HSP90:ATP:FKBP4:nascent protein ↗

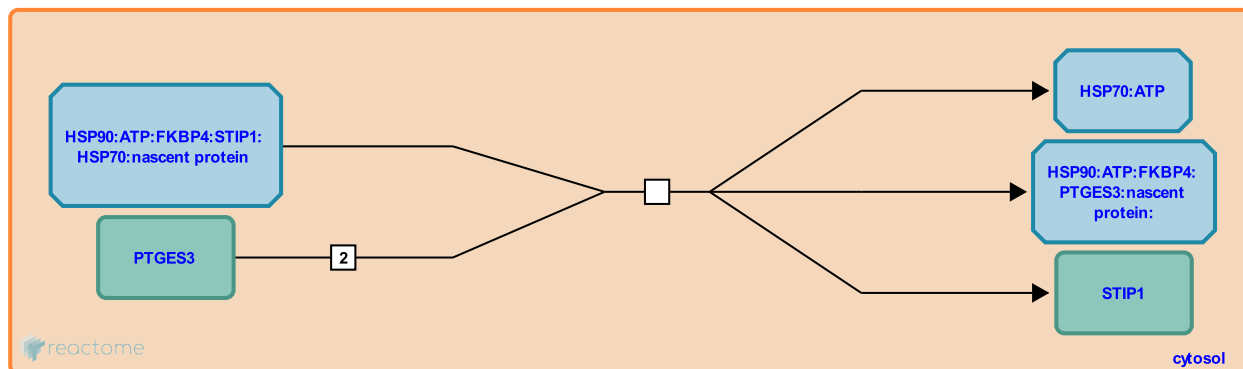
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-5618110

Type: transition

Compartments: cytosol

Inferred from: p23 (PTGES3) binds HSP90:ATP:FKBP4: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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: FKBP4 binds HSP90:ATP:STIP1:HSP70:nascent protein

Followed by: NR3C1 ligands bind NR3C1 (in the HSP90 chaperone complex), P4 bind PGR (in the HSP90 chaperone complex), NR3C2 ligands bind NR3C2 (in the HSP90 chaperone complex)

p23 (PTGES3) binds HSP90:ATP:FKBP5:nascent protein ↗

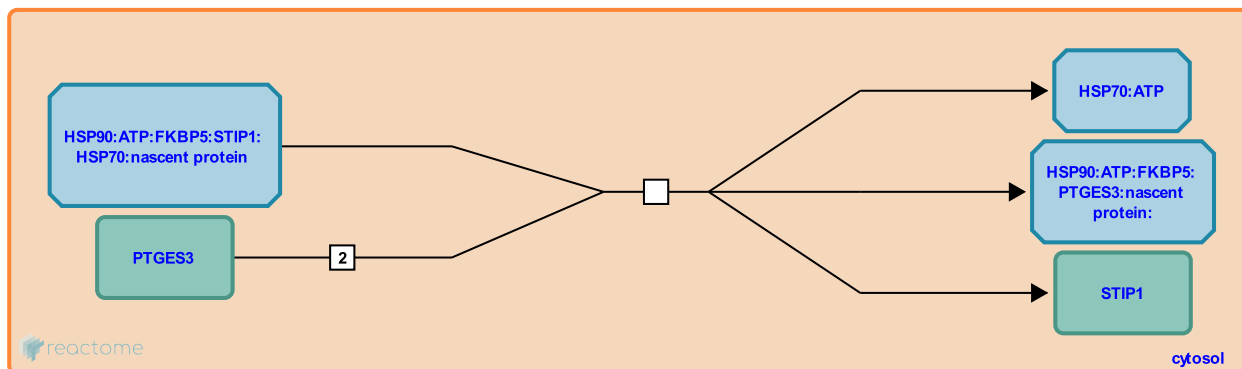
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-5618098

Type: transition

Compartments: cytosol

Inferred from: p23 (PTGES3) binds HSP90:ATP:FKBP5: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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: FKBP5 binds HSP90:ATP:STIP1:HSP70:nascent protein

Followed by: FKBP4 replaces FKBP5 within HSP90:ATP:FKBP5:unfolded protein

FKBP4 replaces FKBP5 within HSP90:ATP:FKBP5:unfolded protein ↗

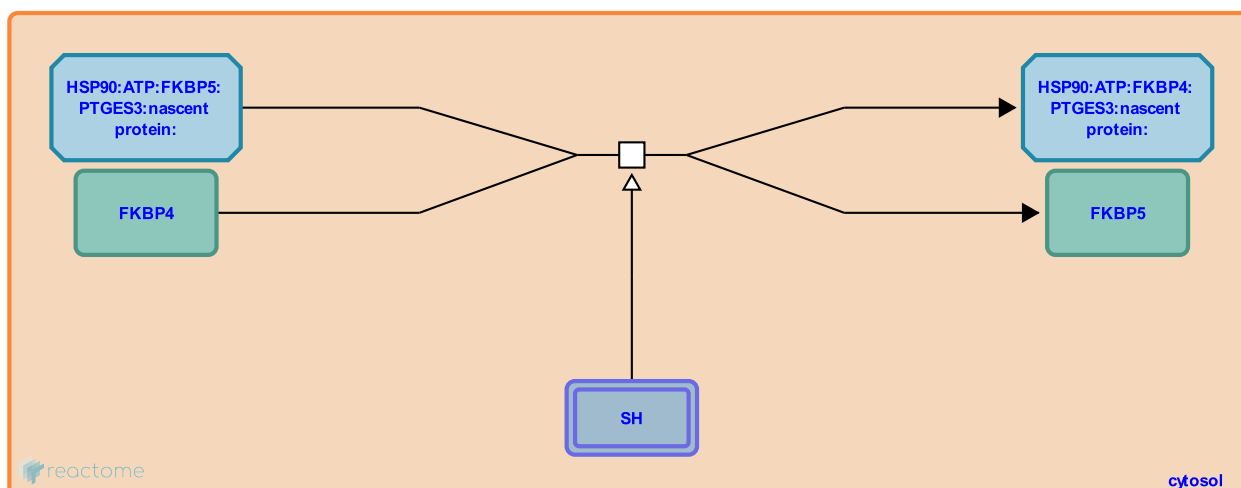
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-5618073

Type: transition

Compartments: cytosol

Inferred from: FKBP4 replaces FKBP5 within HSP90:ATP:FKBP5:unfolded 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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: p23 (PTGES3) binds HSP90:ATP:FKBP5: nascent protein

Followed by: NR3C1 ligands bind NR3C1 (in the HSP90 chaperone complex), P4 bind PGR (in the HSP90 chaperone complex), NR3C2 ligands bind NR3C2 (in the HSP90 chaperone complex)

Androgens binds AR (in the HSP90 chaperone complex) ↗

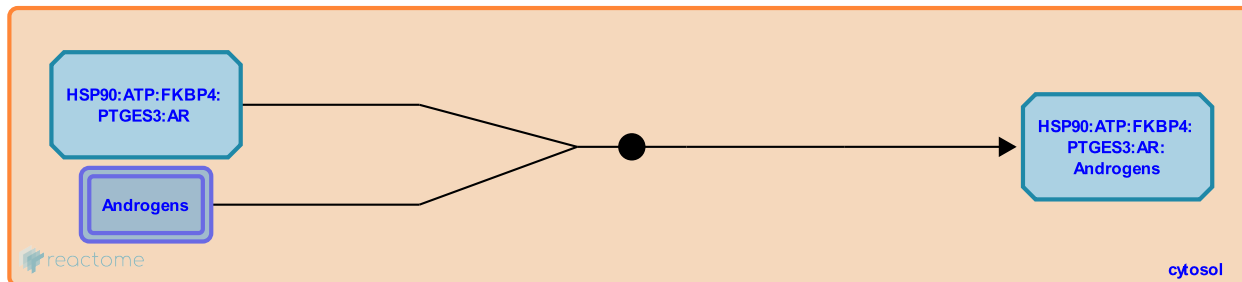
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-9705925

Type: binding

Compartments: cytosol

Inferred from: Androgens binds AR (in the HSP90 chaperone complex) (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: HSP90:ATP:p23:FKBP52:SHR:SH translocates to the nucleus

AR binds AR agonists ↗

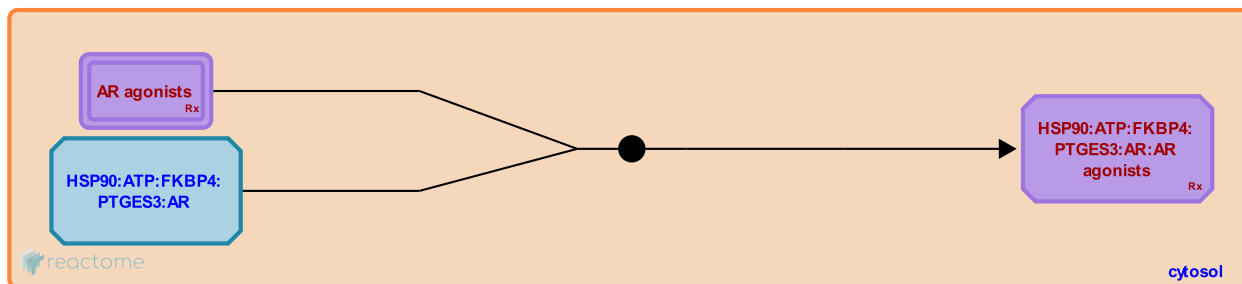
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-9705926

Type: binding

Compartments: cytosol

Inferred from: AR binds AR agonists (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.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

AR binds AR antagonists ↗

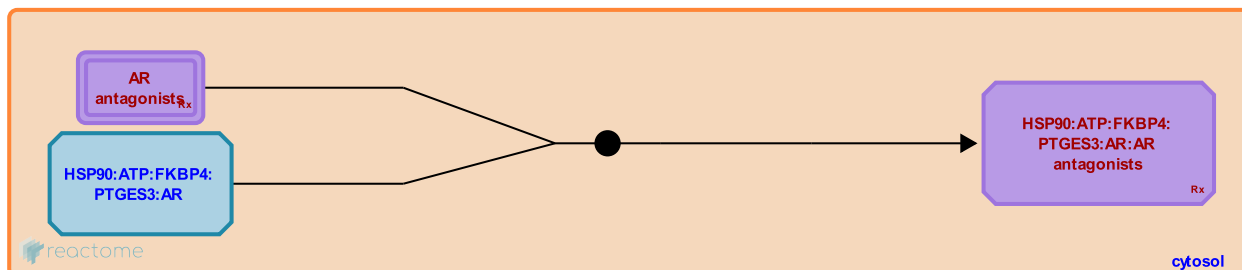
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-9706837

Type: binding

Compartments: cytosol

Inferred from: AR binds AR antagonists (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

P4 bind PGR (in the HSP90 chaperone complex) ↗

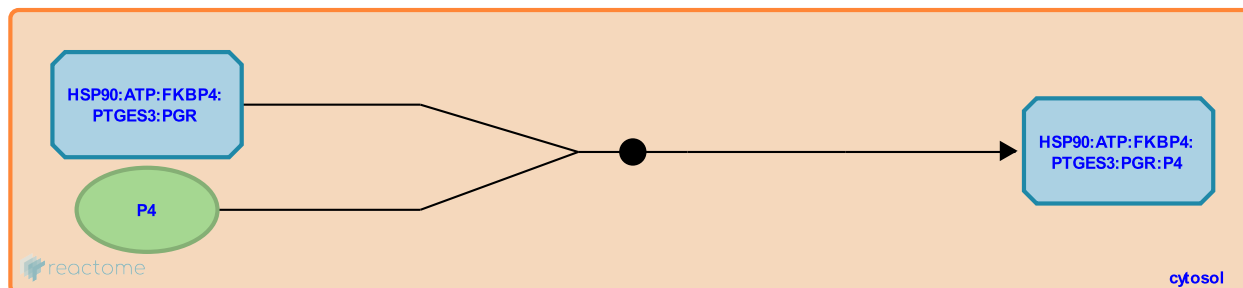
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-9725885

Type: binding

Compartments: cytosol

Inferred from: P4 bind PGR (in the HSP90 chaperone complex) (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: FKBP4 replaces FKBP5 within HSP90:ATP:FKBP5:unfolded protein, p23 (PTGES3) binds HSP90:ATP:FKBP4:nascent protein

Followed by: HSP90:ATP:p23:FKBP52:SHR:SH translocates to the nucleus

PGR binds PGR agonists ↗

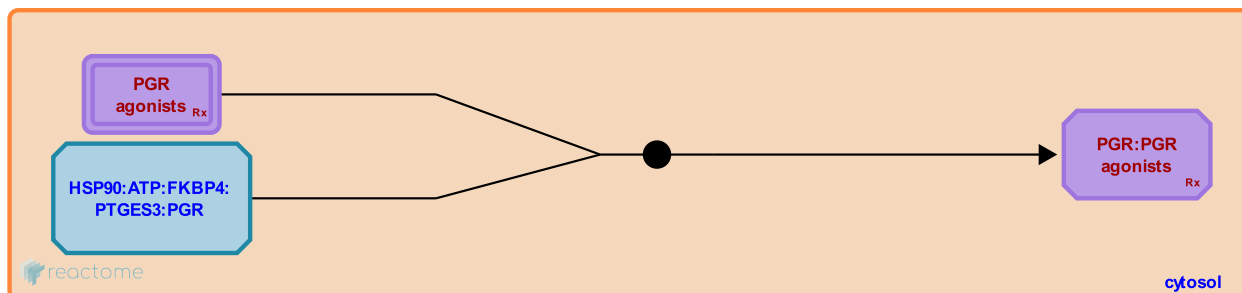
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-9726580

Type: binding

Compartments: cytosol

Inferred from: PGR binds PGR agonists (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.

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PGR binds PGR antagonists ↗

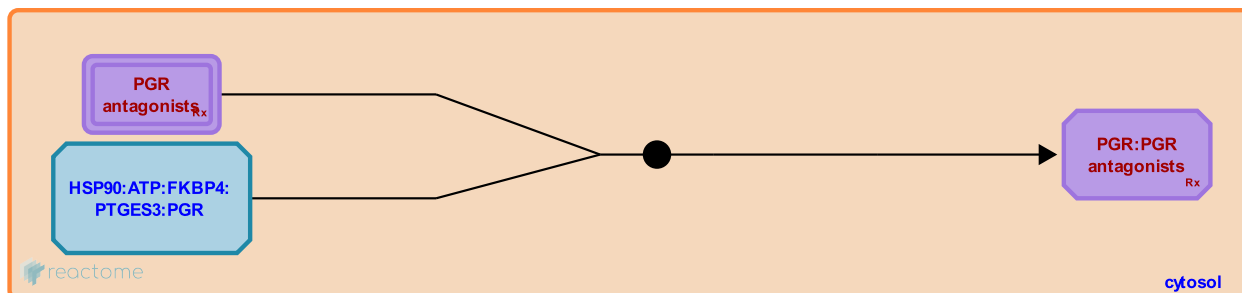
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-9726621

Type: binding

Compartments: cytosol

Inferred from: PGR binds PGR antagonists (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

NR3C1 ligands bind NR3C1 (in the HSP90 chaperone complex) ↗

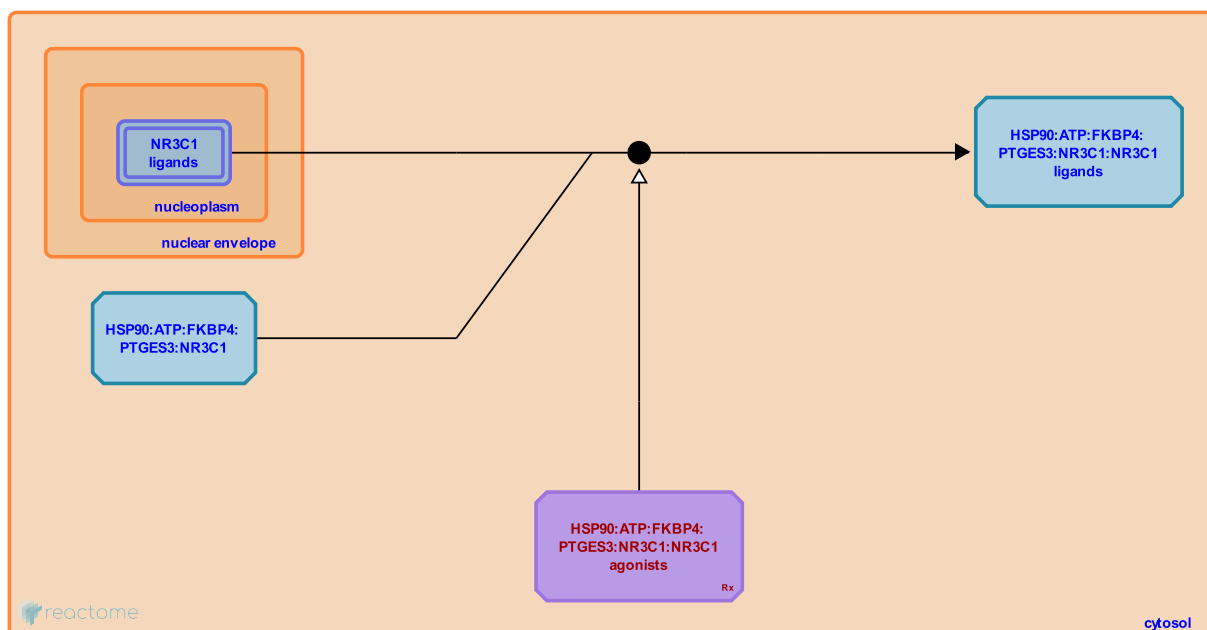
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-9690534

Type: binding

Compartments: cytosol

Inferred from: NR3C1 ligands bind NR3C1 (in the HSP90 chaperone complex) (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: FKBP4 replaces FKBP5 within HSP90:ATP:FKBP5:unfolded protein, p23 (PTGES3) binds HSP90:ATP:FKBP4:nascent protein

Followed by: HSP90:ATP:p23:FKBP52:SHR:SH translocates to the nucleus

NR3C1 binds NR3C1 agonists ↗

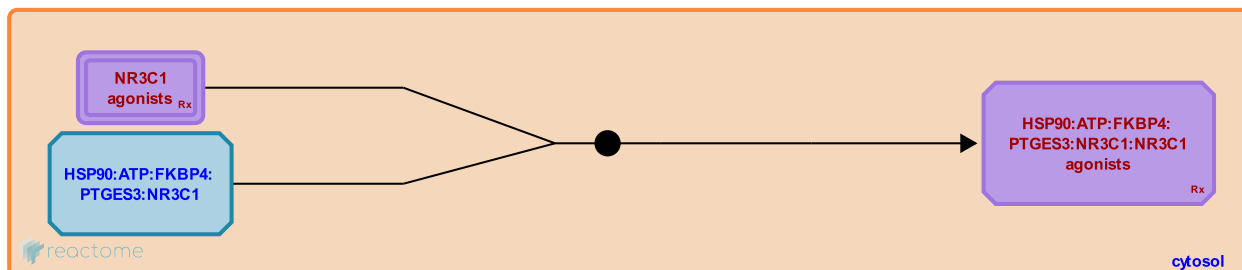
Location: [HSP90 chaperone cycle for steroid hormone receptors \(SHR\) in the presence of ligand](#)

Stable identifier: R-BTA-9678925

Type: binding

Compartments: cytosol

Inferred from: [NR3C1 binds NR3C1 agonists \(Homo sapiens\)](#)



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>

NR3C2 ligands bind NR3C2 (in the HSP90 chaperone complex) ↗

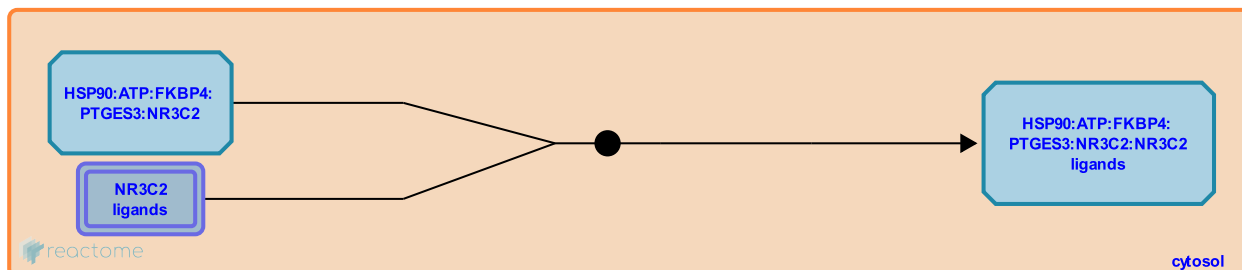
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-5618099

Type: binding

Compartments: cytosol

Inferred from: NR3C2 ligands bind NR3C2 (in the HSP90 chaperone complex) (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: FKBP4 replaces FKBP5 within HSP90:ATP:FKBP5:unfolded protein, p23 (PTGES3) binds HSP90:ATP:FKBP4:nascent protein

Followed by: HSP90:ATP:p23:FKBP52:SHR:SH translocates to the nucleus

NR3C2 binds NR3C2 antagonists ↗

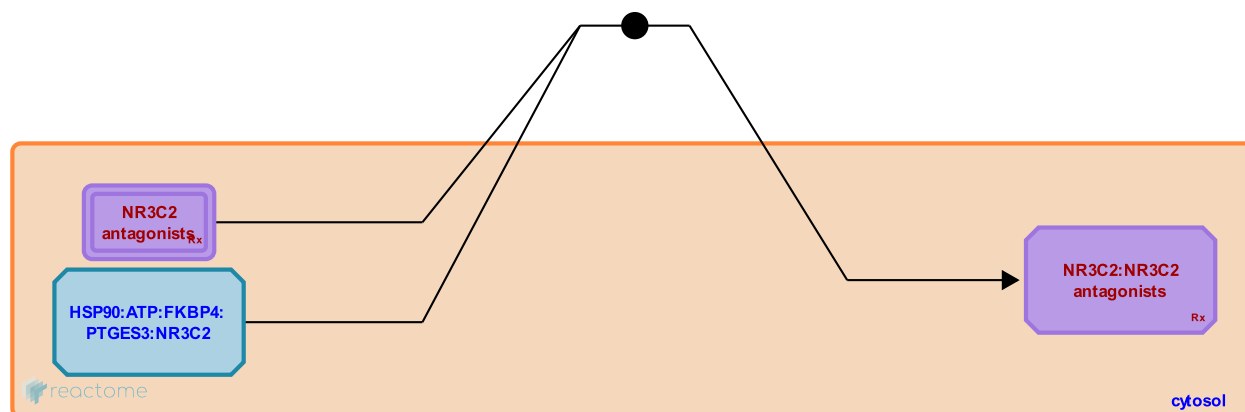
Location: [HSP90 chaperone cycle for steroid hormone receptors \(SHR\) in the presence of ligand](#)

Stable identifier: R-BTA-9725855

Type: binding

Compartments: extracellular region, cytosol

Inferred from: [NR3C2 binds NR3C2 antagonists \(Homo sapiens\)](#)



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>

NR3C2 binds fludrocortisone ↗

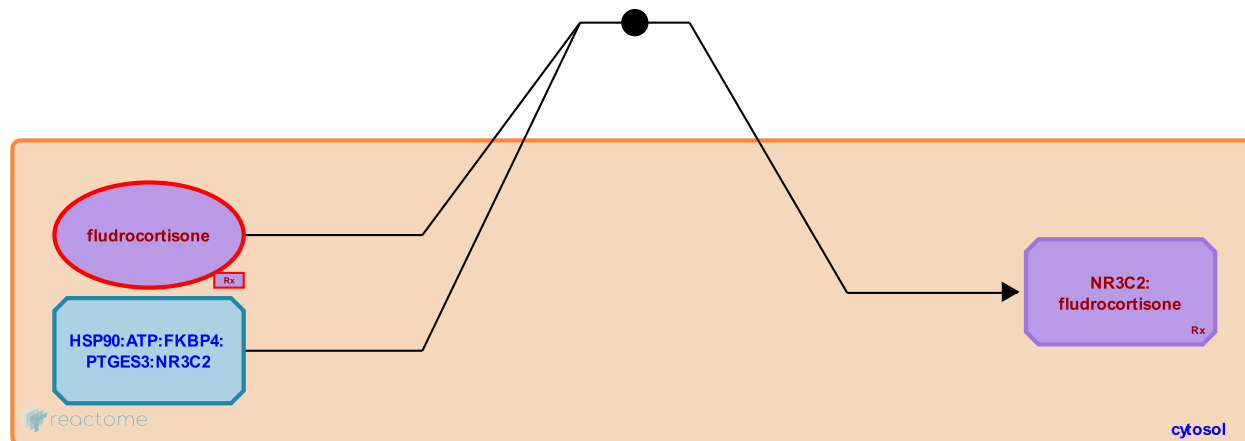
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-9726509

Type: binding

Compartments: extracellular region, cytosol

Inferred from: NR3C2 binds fludrocortisone (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.](https://www.reactome.org/docs/event_inference.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

HSP90:ATP:p23:FKBP52:SHR:SH translocates to the nucleus ↗

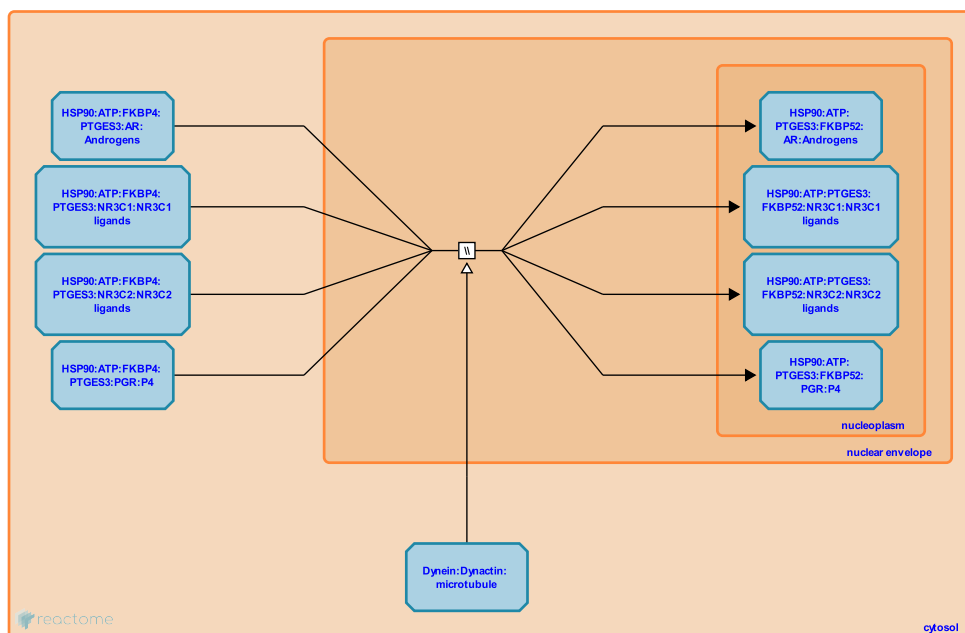
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-5618080

Type: omitted

Compartments: nuclear envelope, nucleoplasm, cytosol

Inferred from: HSP90:ATP:p23:FKBP52:SHR:SH translocates to the nucleus (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: NR3C1 ligands bind NR3C1 (in the HSP90 chaperone complex), P4 bind PGR (in the HSP90 chaperone complex), NR3C2 ligands bind NR3C2 (in the HSP90 chaperone complex), Androgens binds AR (in the HSP90 chaperone complex)

Followed by: ATP hydrolysis by HSP90

ATP hydrolysis by HSP90 ↗

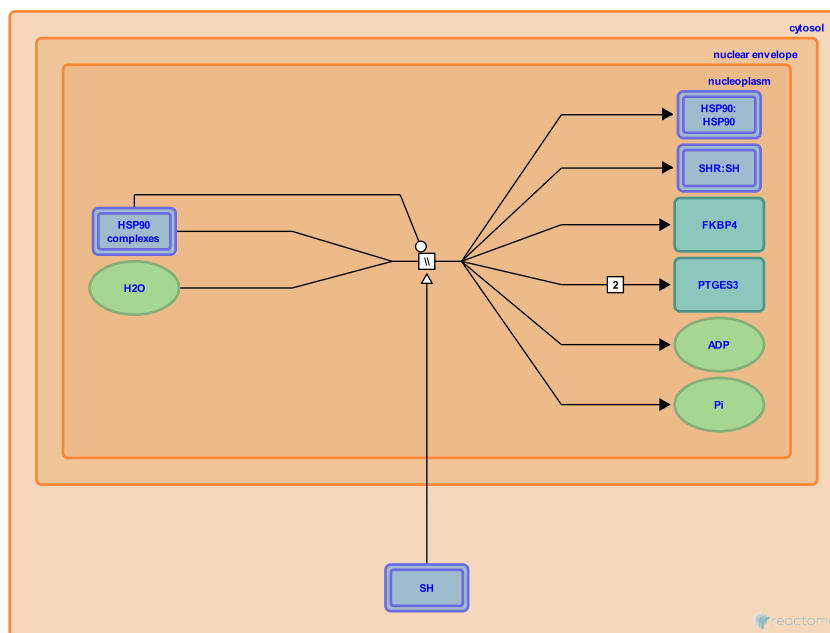
Location: HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand

Stable identifier: R-BTA-5618093

Type: omitted

Compartments: nucleoplasm

Inferred from: ATP hydrolysis by HSP90 (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: HSP90:ATP:p23:FKBP52:SHR:SH translocates to the nucleus

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