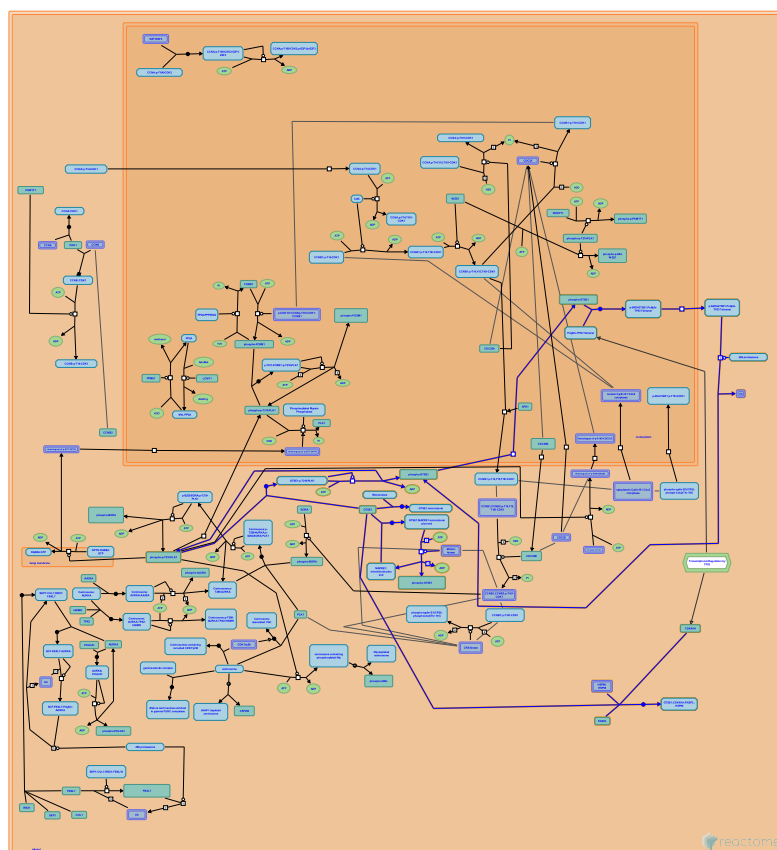


The role of GTSE1 in G2/M progression after G2 checkpoint



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](#).

03/02/2023

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. [↗](#)
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- 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. [↗](#)

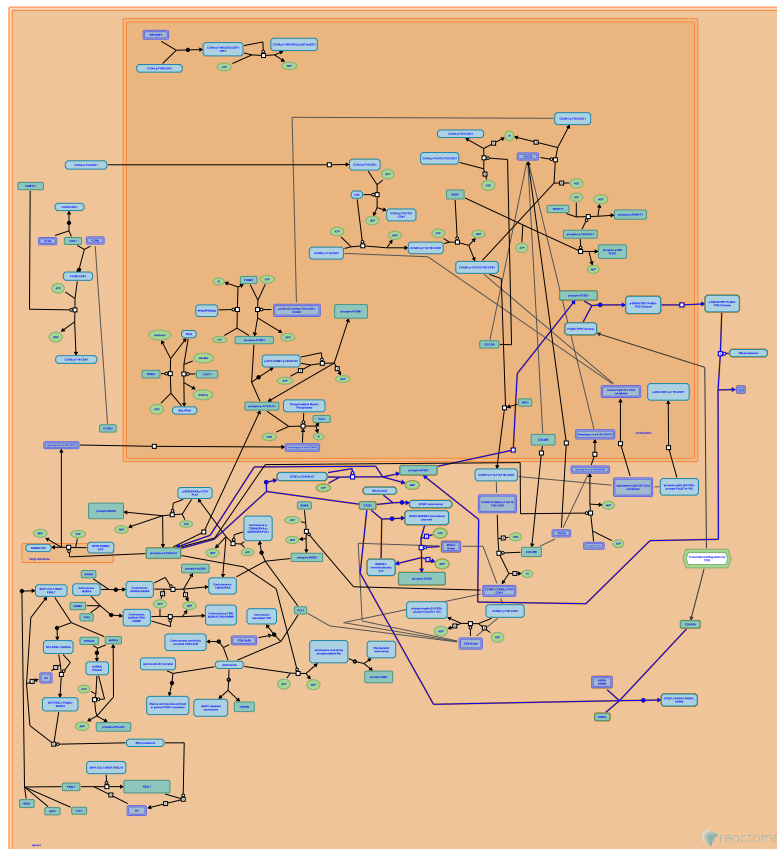
Reactome database release: 83

This document contains 1 pathway and 10 reactions ([see Table of Contents](#))

The role of GTSE1 in G2/M progression after G2 checkpoint ↗

Stable identifier: R-SSC-8852276

Inferred from: [The role of GTSE1 in G2/M progression after G2 checkpoint \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

GTSE1 binds microtubule lattice in interphase cells ↗

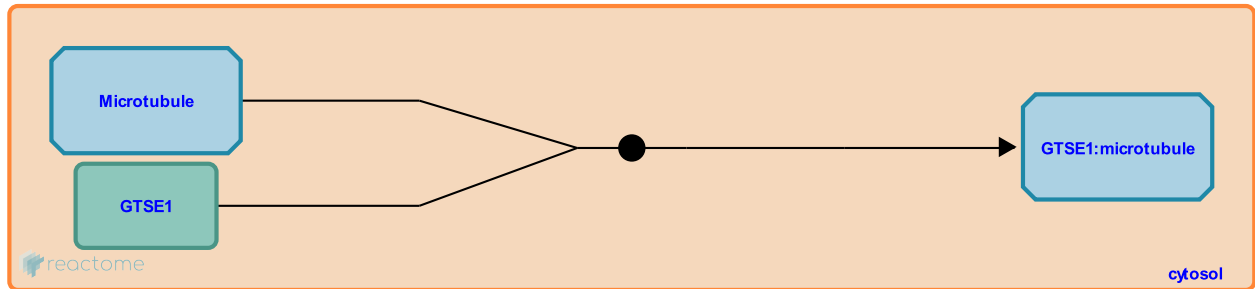
Location: [The role of GTSE1 in G2/M progression after G2 checkpoint](#)

Stable identifier: R-SSC-8852280

Type: binding

Compartments: cytosol

Inferred from: [GTSE1 binds microtubule lattice in interphase cells \(Homo sapiens\)](#)



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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GTSE1 binds MAPRE1 (EB1) at microtubule plus ends ↗

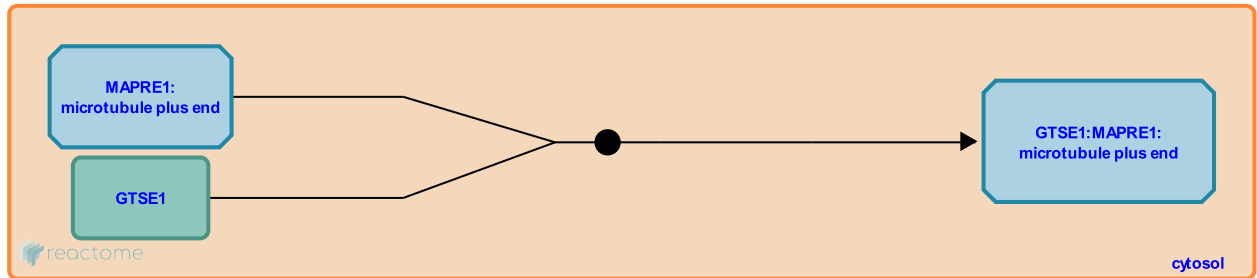
Location: [The role of GTSE1 in G2/M progression after G2 checkpoint](#)

Stable identifier: R-SSC-8852298

Type: binding

Compartments: cytosol

Inferred from: [GTSE1 binds MAPRE1 \(EB1\) at microtubule plus ends \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [Mitotic phosphorylation-induced dissociation of GTSE1 from microtubule plus ends](#)

Mitotic phosphorylation-induced dissociation of GTSE1 from microtubule plus ends



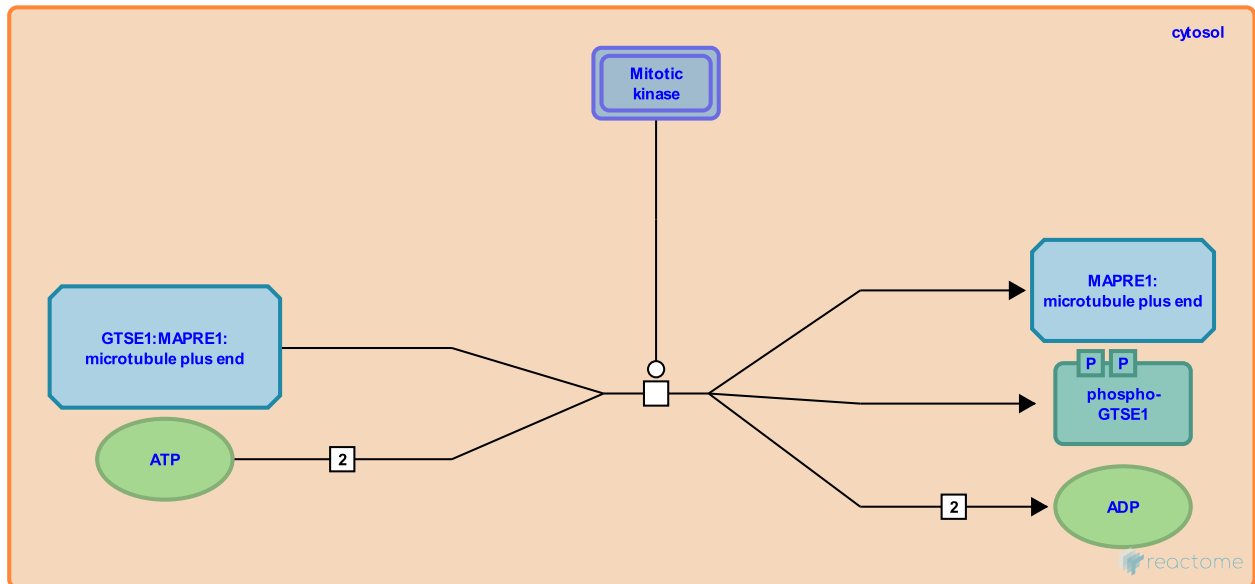
Location: [The role of GTSE1 in G2/M progression after G2 checkpoint](#)

Stable identifier: R-SSC-8852306

Type: transition

Compartments: cytosol

Inferred from: [Mitotic phosphorylation-induced dissociation of GTSE1 from microtubule plus ends \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [GTSE1 binds MAPRE1 \(EB1\) at microtubule plus ends](#)

GTSE1 binds PLK1 [↗](#)

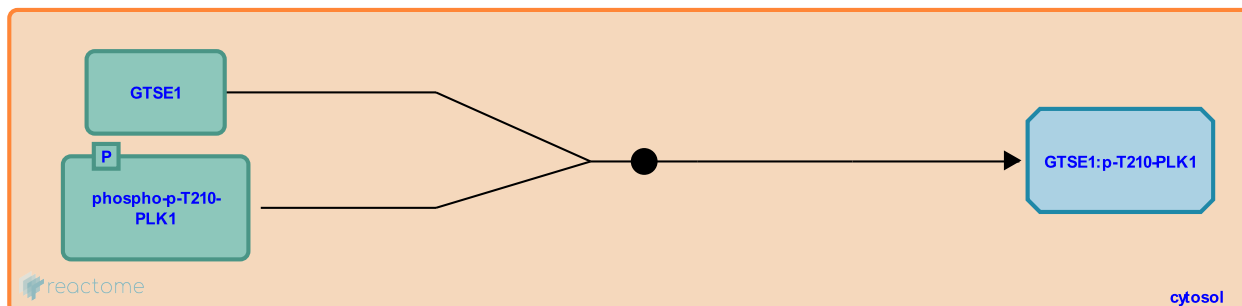
Location: [The role of GTSE1 in G2/M progression after G2 checkpoint](#)

Stable identifier: R-SSC-8852324

Type: binding

Compartments: cytosol

Inferred from: [GTSE1 binds PLK1 \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [PLK1 phosphorylates GTSE1](#)

PLK1 phosphorylates GTSE1 ↗

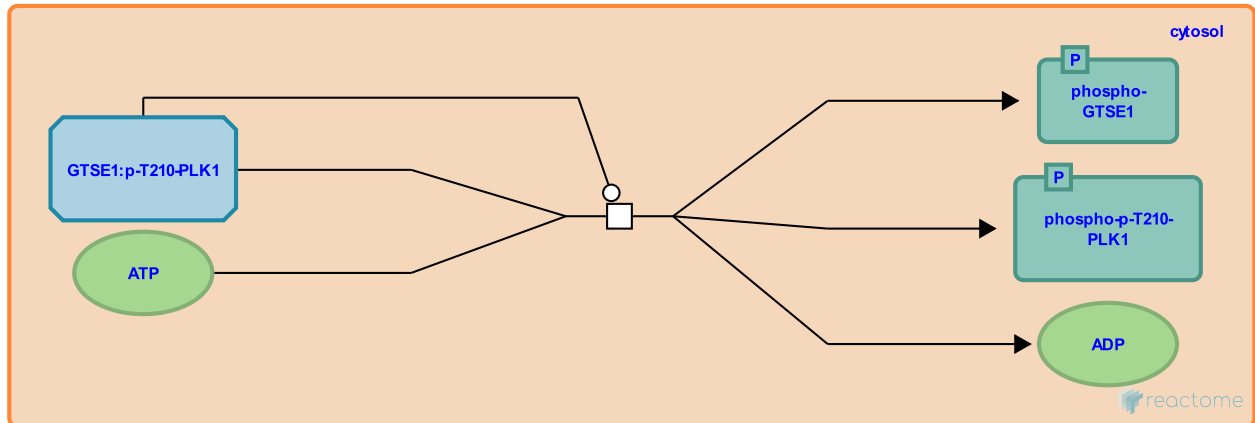
Location: [The role of GTSE1 in G2/M progression after G2 checkpoint](#)

Stable identifier: R-SSC-8852317

Type: transition

Compartments: cytosol

Inferred from: [PLK1 phosphorylates GTSE1 \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [GTSE1 binds PLK1](#)

Followed by: [GTSE1 translocates to the nucleus](#)

GTSE1 translocates to the nucleus ↗

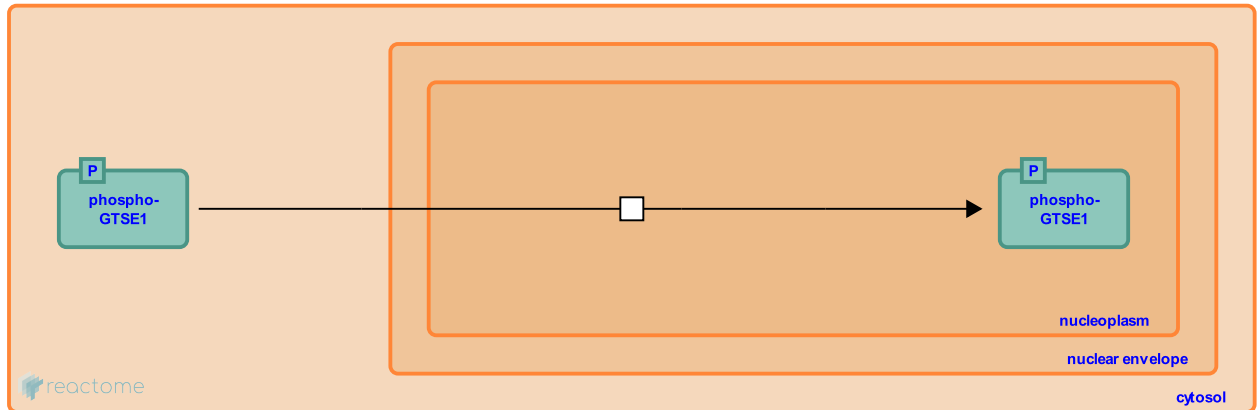
Location: [The role of GTSE1 in G2/M progression after G2 checkpoint](#)

Stable identifier: R-SSC-8852331

Type: transition

Compartments: nucleoplasm, cytosol

Inferred from: [GTSE1 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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [PLK1 phosphorylates GTSE1](#)

Followed by: [GTSE1 binds TP53](#)

GTSE1 binds TP53 ↗

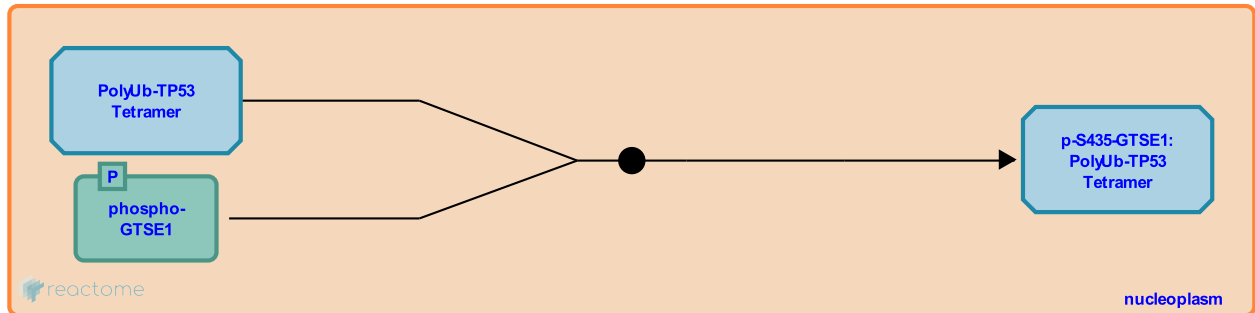
Location: [The role of GTSE1 in G2/M progression after G2 checkpoint](#)

Stable identifier: R-SSC-8852337

Type: binding

Compartments: nucleoplasm

Inferred from: [GTSE1 binds TP53 \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [GTSE1 translocates to the nucleus](#)

Followed by: [GTSE1 promotes translocation of TP53 to the cytosol](#)

GTSE1 promotes translocation of TP53 to the cytosol ↗

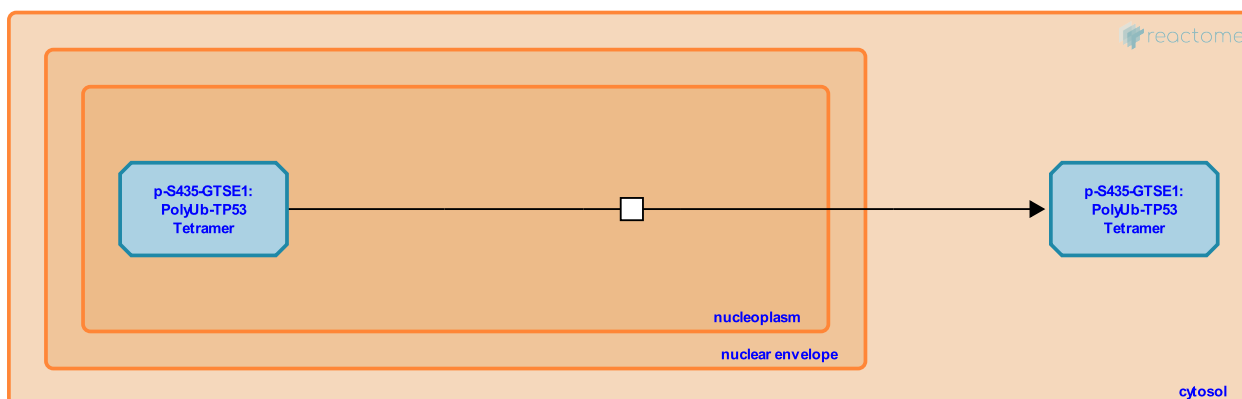
Location: [The role of GTSE1 in G2/M progression after G2 checkpoint](#)

Stable identifier: R-SSC-8852351

Type: transition

Compartments: nucleoplasm, cytosol

Inferred from: [GTSE1 promotes translocation of TP53 to the cytosol \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [GTSE1 binds TP53](#)

Followed by: [GTSE1 facilitates proteasome-mediated degradation of TP53](#)

GTSE1 facilitates proteasome-mediated degradation of TP53 ↗

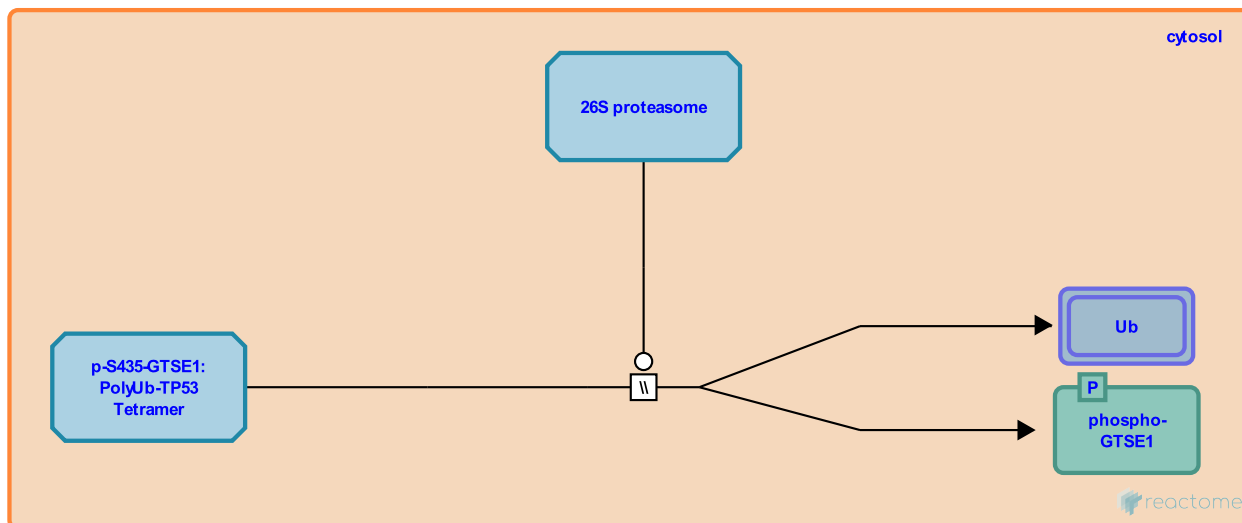
Location: [The role of GTSE1 in G2/M progression after G2 checkpoint](#)

Stable identifier: R-SSC-8852354

Type: omitted

Compartments: cytosol

Inferred from: [GTSE1 facilitates proteasome-mediated degradation of TP53 \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [GTSE1 promotes translocation of TP53 to the cytosol](#)

GTSE1 binds CDKN1A ↗

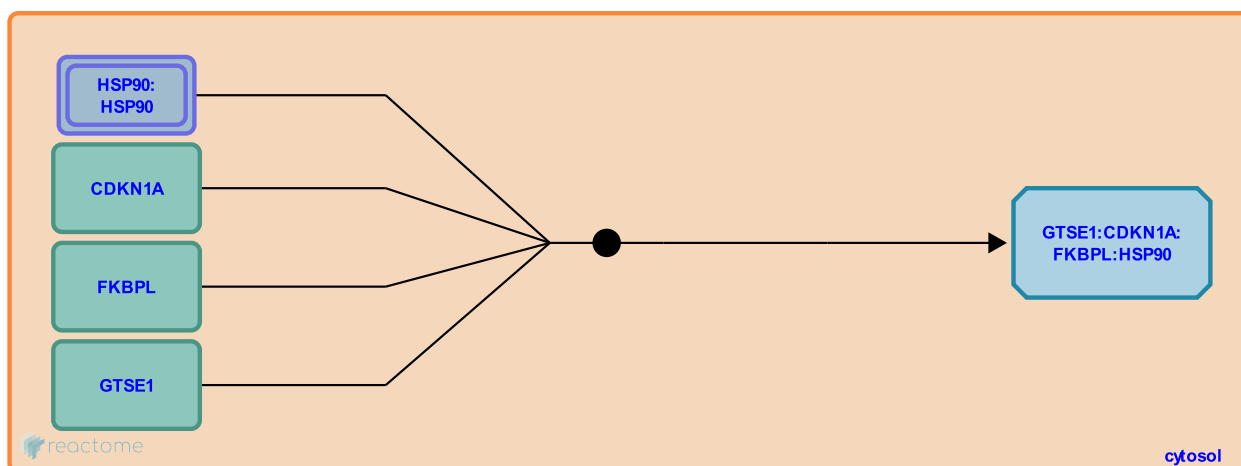
Location: [The role of GTSE1 in G2/M progression after G2 checkpoint](#)

Stable identifier: R-SSC-8852362

Type: binding

Compartments: cytosol

Inferred from: [GTSE1 binds CDKN1A \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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