# GTSE1 facilitates proteasome-mediated degradation of TP53

Bird, AW., Orlic-Milacic, M.

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



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# 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.

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## Literature references

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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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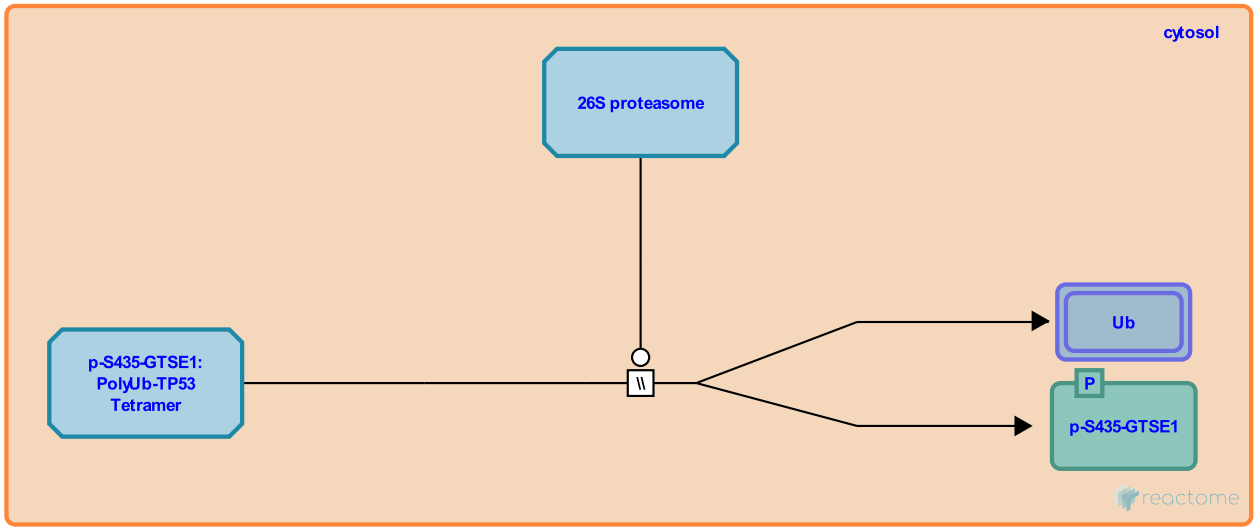
**Stable identifier:** R-HSA-8852354

**Type:** omitted

**Compartments:** cytosol




GTSE1 promotes down-regulation of TP53 in a proteasome-dependent way. Nuclear export of TP53 facilitated by GTSE1 and MDM2likely makes ubiquitinated TP53 available to the proteasome machinery. GTSE1-mediated decrease of TP53 levels is needed for the G2 checkpoint recovery (cell cycle re-entry after DNA damage induced G2 arrest) and rescues cells from DNA damage induced apoptosis during S/G2 phase (Monte et al. 2003, Monte et al. 2004).

## Literature references

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## Editions

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