# TP53 forms homotetramers

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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. ↗

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. ↗

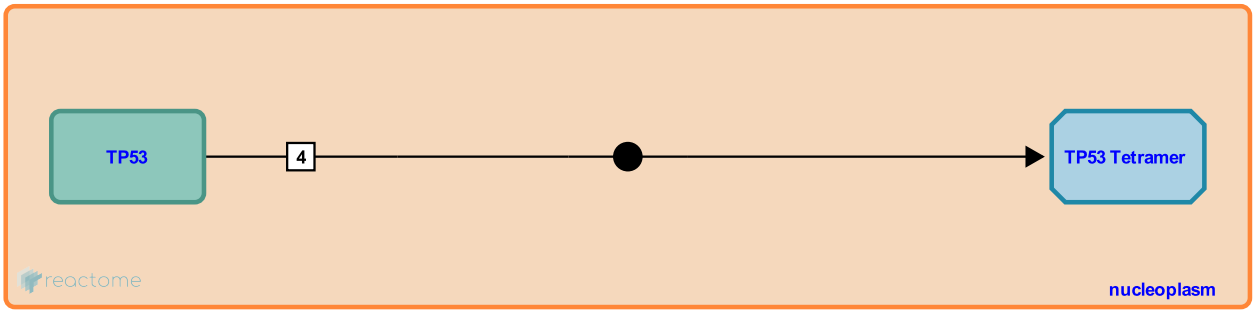
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

## TP53 forms homotetramers ↗

**Stable identifier:** R-HSA-6804762

**Type:** binding

**Compartments:** nucleoplasm




TP53 (p53) functions as a stable homotetramer. The tetramerization domain is located within the C-terminus (Stenger et al. 1994, Waterman et al. 1995, Jeffrey et al. 1995, Wang et al. 1995).

## Literature references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## Editions

| | | |
|---|---|---|
| 2015-10-14 | Authored, Edited | Orlic-Milacic, M. |
| 2016-02-04 | Reviewed | Inga, A., Zaccara, S. |
| 2021-04-30 | Reviewed | Sakaguchi, K. |