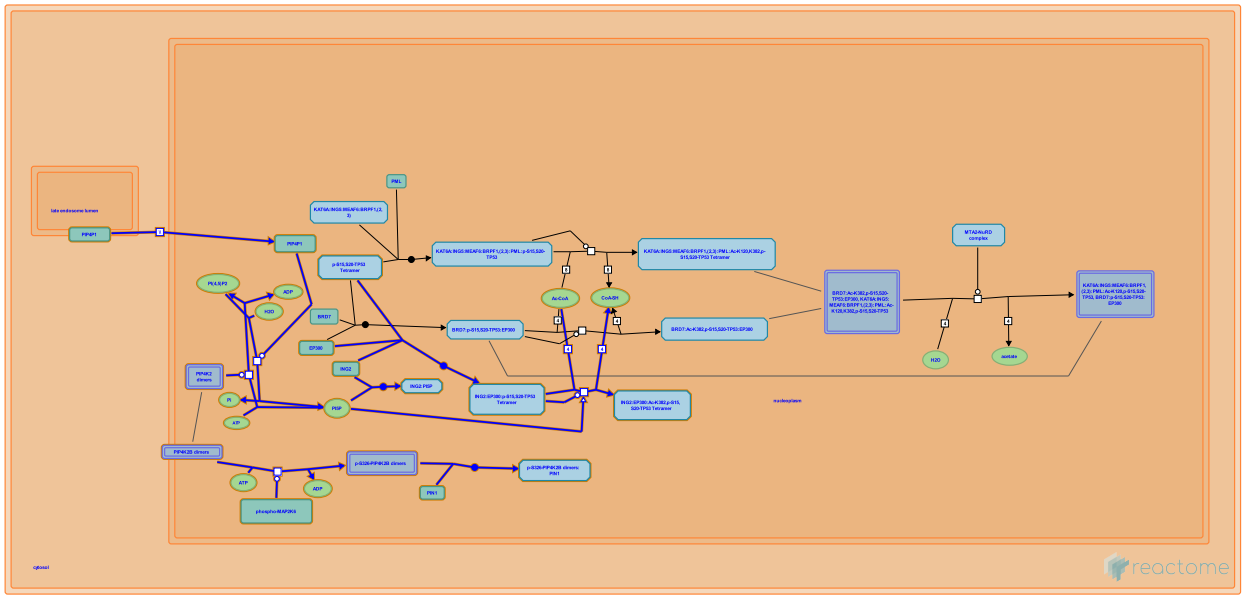
PI5P Regulates TP53 Acetylation



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

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.

20/05/2024

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. ↗

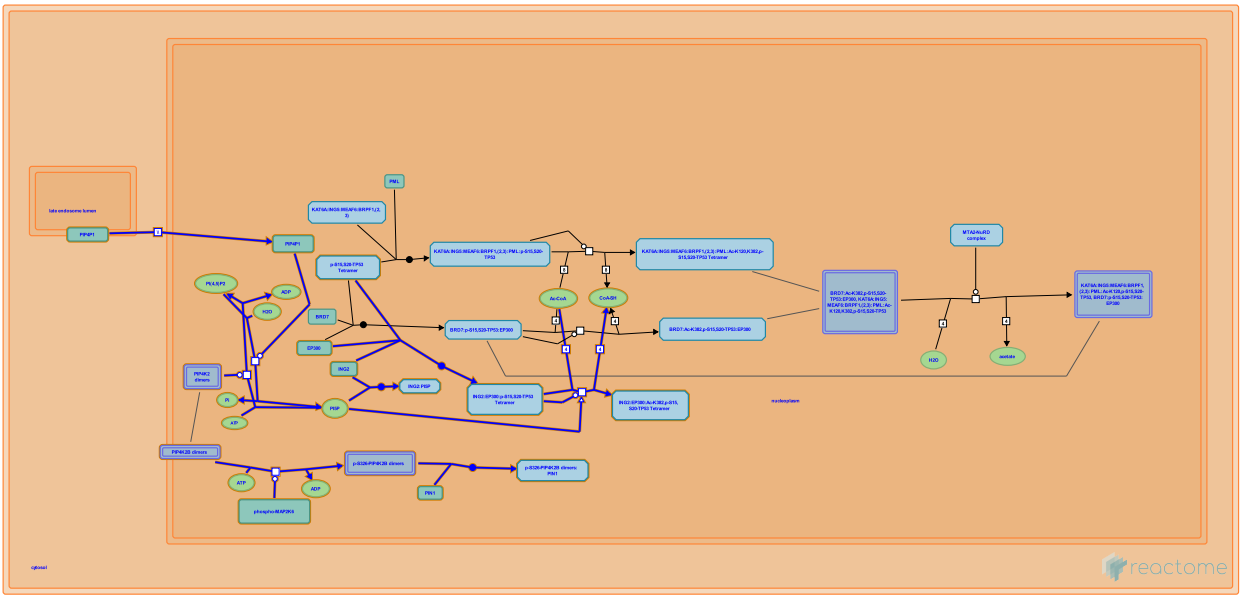
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

PI5P Regulates TP53 Acetylation ↗

Stable identifier: R-CFA-6811555

Inferred from: PI5P Regulates TP53 Acetylation (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

TMEM55B translocates to the nucleus ↗

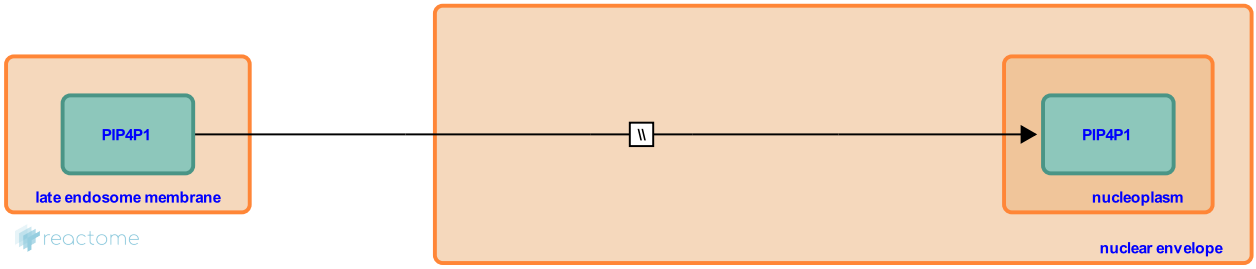
Location: PI5P Regulates TP53 Acetylation

Stable identifier: R-CFA-6810392

Type: omitted

Compartments: nuclear envelope, late endosome membrane

Inferred from: TMEM55B translocates to the nucleus (Homo sapiens)



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Followed by: PI(4,5)P2 is dephosphorylated to PI5P by TMEM55B in the nucleus

PI(4,5)P2 is dephosphorylated to PI5P by TMEM55B in the nucleus ↗

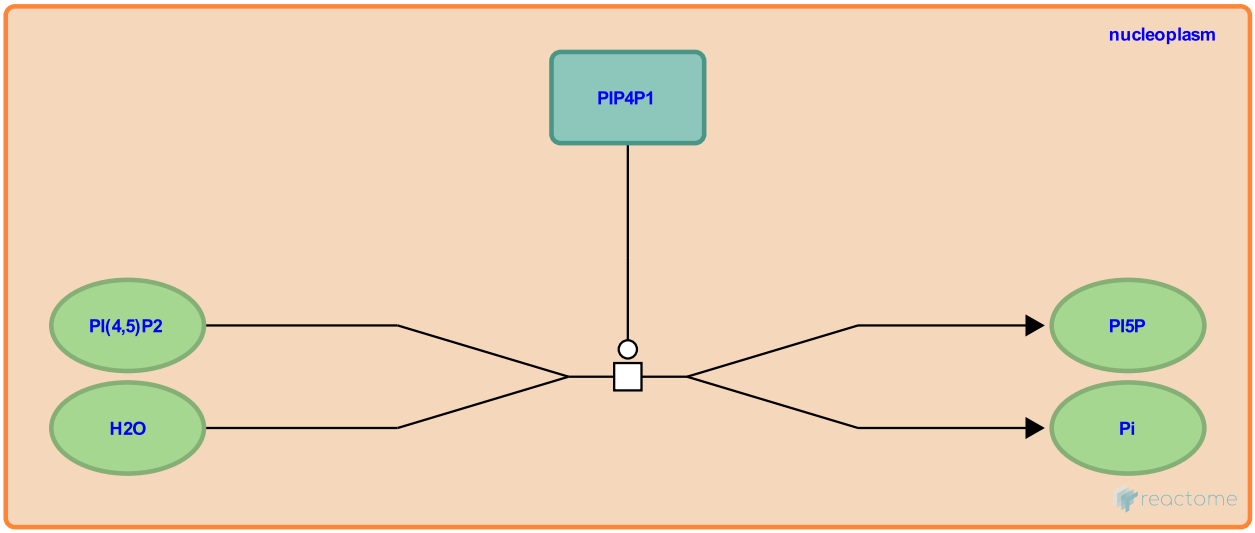
Location: PI5P Regulates TP53 Acetylation

Stable identifier: R-CFA-6810410

Type: transition

Compartments: nucleoplasm

Inferred from: PI(4,5)P2 is dephosphorylated to PI5P by TMEM55B in the nucleus (Homo sapiens)



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Preceded by: TMEM55B translocates to the nucleus

Followed by: ING2 binds PI5P

PI5P is phosphorylated to PI(4,5)P2 by PIP4K2 dimers in the nucleus ↗

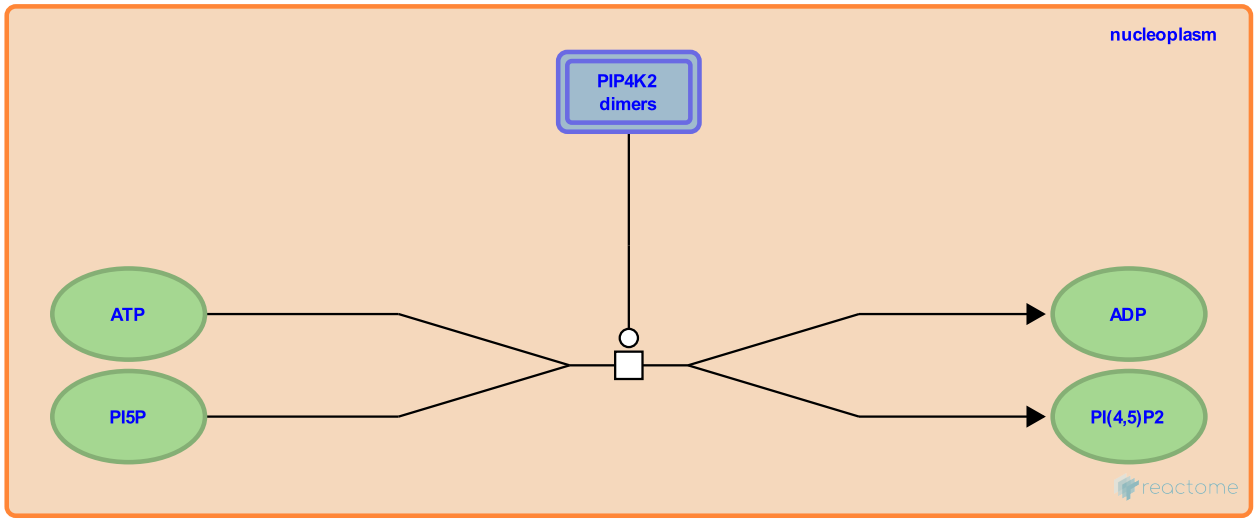
Location: PI5P Regulates TP53 Acetylation

Stable identifier: R-CFA-6811522

Type: transition

Compartments: nucleoplasm

Inferred from: PI5P is phosphorylated to PI(4,5)P2 by PIP4K2 dimers in the nucleus (Homo sapiens)



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ING2 binds PI5P ↗

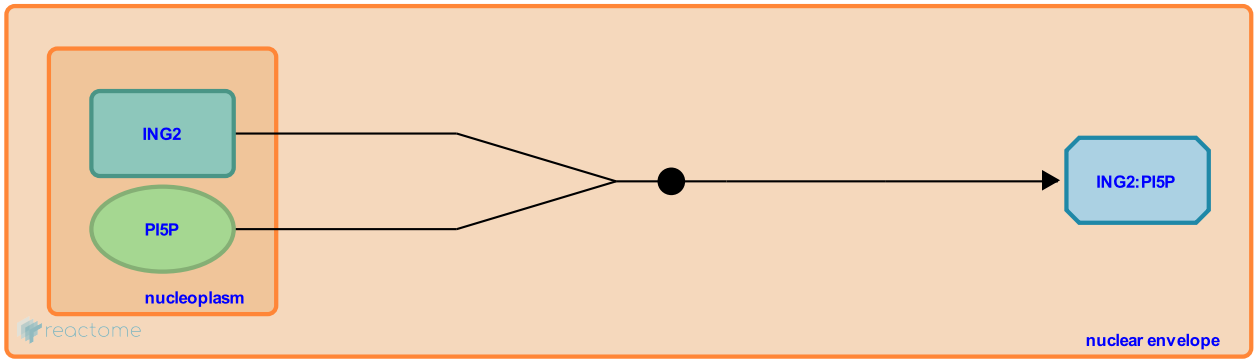
Location: PI5P Regulates TP53 Acetylation

Stable identifier: R-CFA-6810376

Type: binding

Compartments: nuclear envelope, nucleoplasm

Inferred from: ING2 binds PI5P (Homo sapiens)



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Preceded by: PI(4,5)P2 is dephosphorylated to PI5P by TMEM55B in the nucleus

ING2 recruits EP300 to TP53 ↗

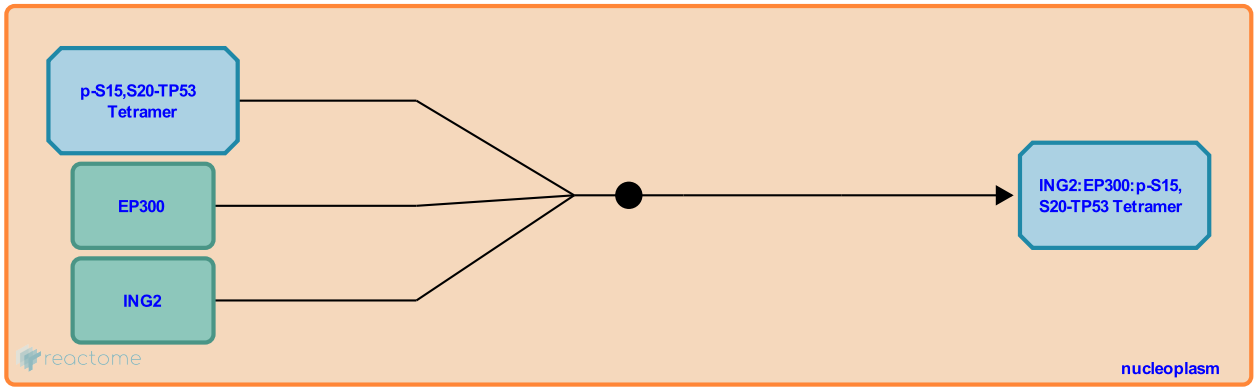
Location: PI5P Regulates TP53 Acetylation

Stable identifier: R-CFA-6811479

Type: binding

Compartments: nucleoplasm

Inferred from: ING2 recruits EP300 to TP53 (Homo sapiens)



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Followed by: ING2-bound EP300 acetylates TP53

ING2-bound EP300 acetylates TP53 ↗

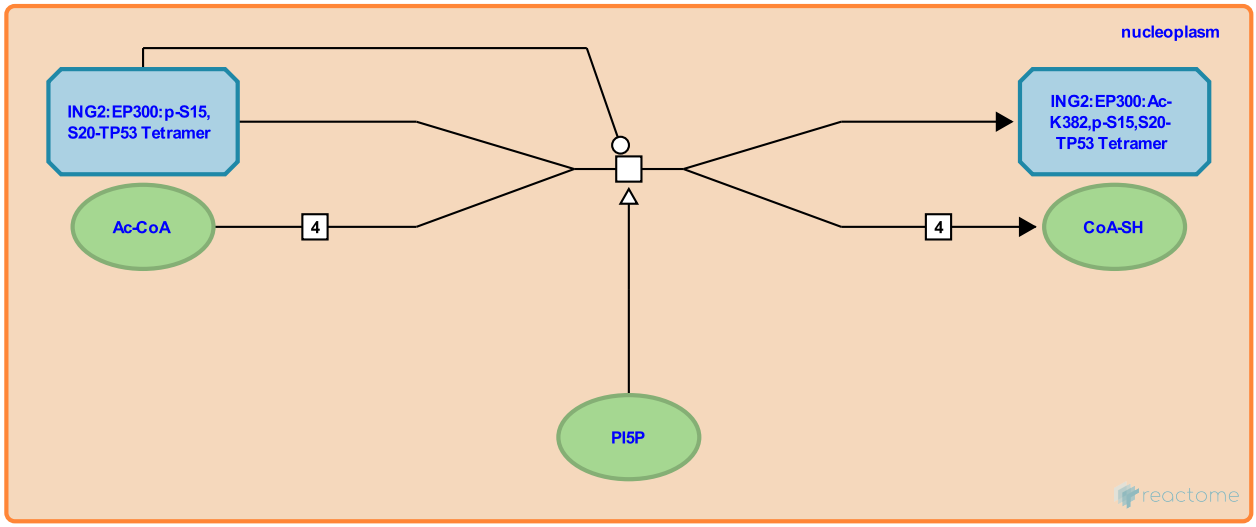
Location: PI5P Regulates TP53 Acetylation

Stable identifier: R-CFA-6811508

Type: transition

Compartments: nucleoplasm

Inferred from: ING2-bound EP300 acetylates TP53 (Homo sapiens)



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Preceded by: ING2 recruits EP300 to TP53

MAP2K6 phosphorylates PIP4K2B ↗

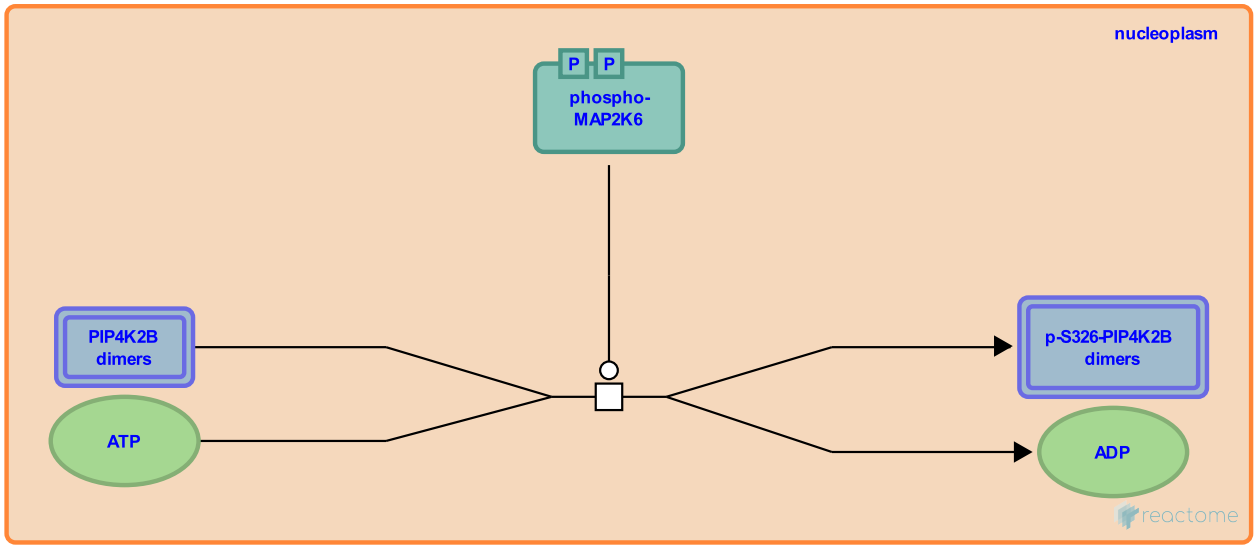
Location: PI5P Regulates TP53 Acetylation

Stable identifier: R-CFA-8877691

Type: transition

Compartments: nucleoplasm

Inferred from: MAP2K6 phosphorylates PIP4K2B (Homo sapiens)



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

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

Followed by: PIN1 binds phosphorylated PIP4K2B

PIN1 binds phosphorylated PIP4K2B ↗

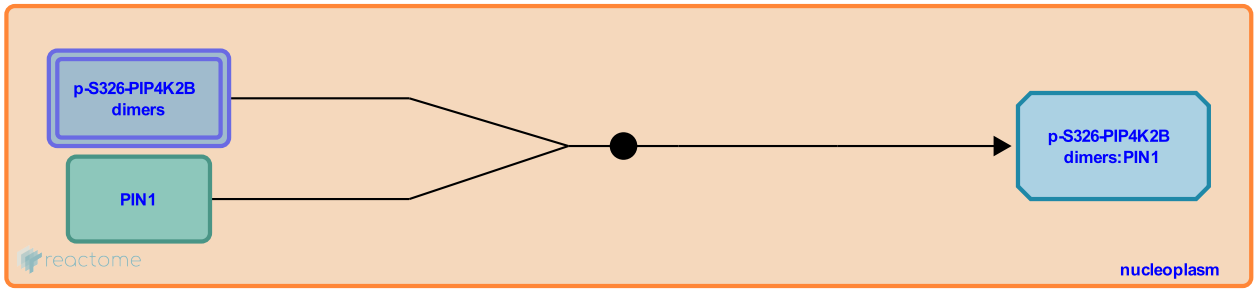
Location: PI5P Regulates TP53 Acetylation

Stable identifier: R-CFA-8877692

Type: binding

Compartments: nucleoplasm

Inferred from: PIN1 binds phosphorylated PIP4K2B (Homo sapiens)



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Preceded by: MAP2K6 phosphorylates PIP4K2B

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