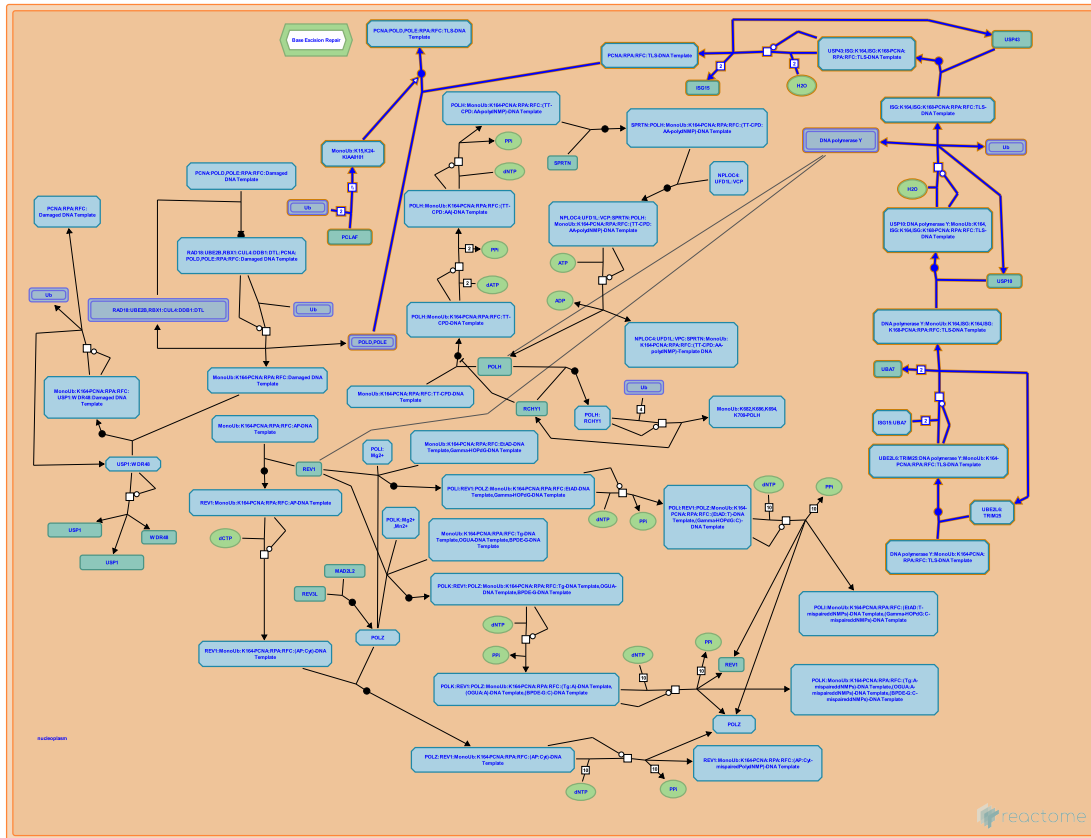


# Termination of translesion DNA synthesis



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.

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

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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. [↗](#)

Reactome database release: 81

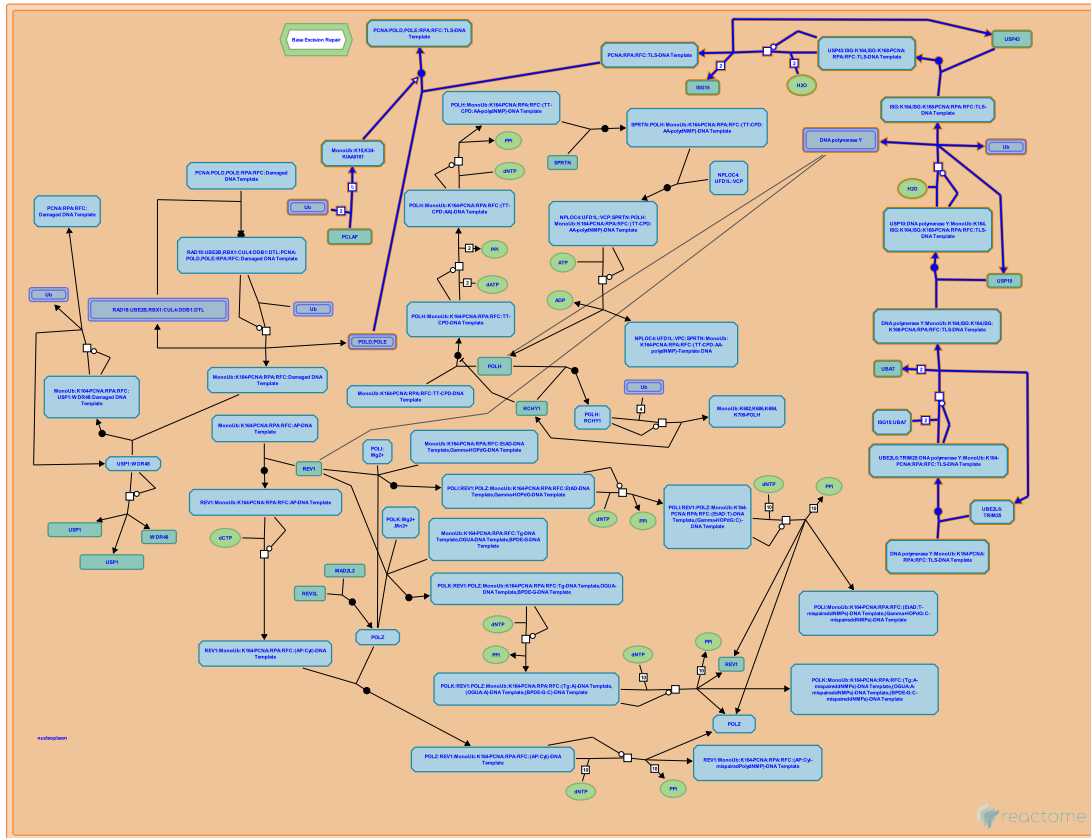
This document contains 1 pathway and 8 reactions ([see Table of Contents](#))

# Termination of translesion DNA synthesis ↗

Stable identifier: R-SSC-5656169

Compartments: nucleoplasm

Inferred from: Termination of translesion DNA synthesis (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>

## TRIM25 binds monoUb:164-PCNA ↗

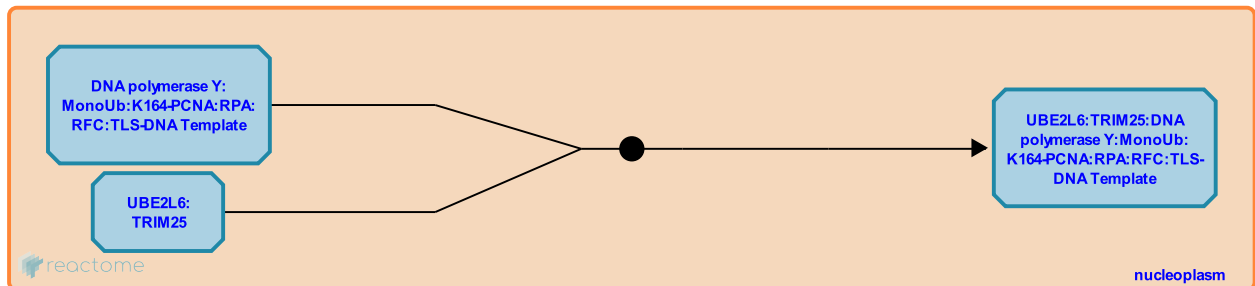
**Location:** Termination of translesion DNA synthesis

**Stable identifier:** R-SSC-5653756

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** TRIM25 binds monoUb:164-PCNA (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:** UBE2L6:TRIM25 ISGylates monoUb:K164-PCNA

## UBE2L6:TRIM25 ISGylates monoUb:K164-PCNA ↗

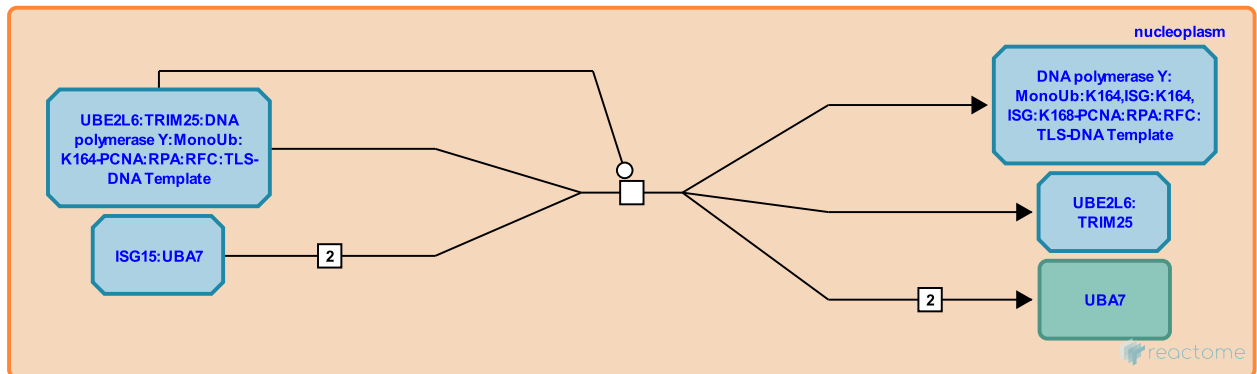
**Location:** [Termination of translesion DNA synthesis](#)

**Stable identifier:** R-SSC-5653754

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [UBE2L6:TRIM25 ISGylates monoUb:K164-PCNA \(Homo sapiens\)](#)



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:** [TRIM25 binds monoUb:164-PCNA](#)

**Followed by:** [USP10 binds monoUb:K164,ISG:K164,ISG:K168-PCNA](#)

## USP10 binds monoUb:K164,ISG:K164,ISG:K168-PCNA [↗](#)

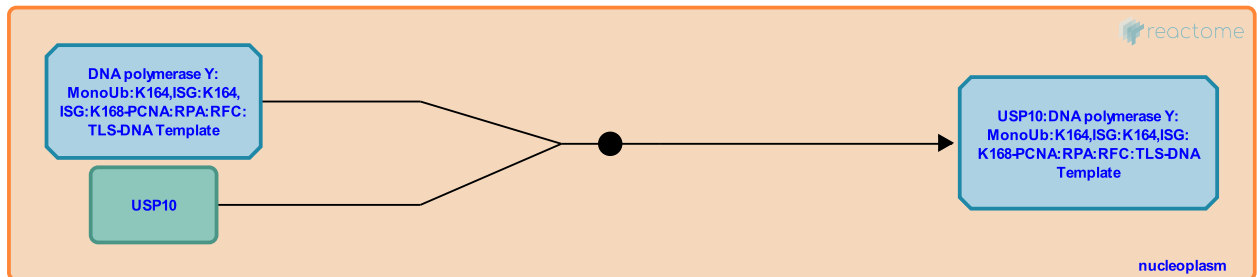
**Location:** [Termination of translesion DNA synthesis](#)

**Stable identifier:** R-SSC-5653766

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [USP10 binds monoUb:K164,ISG:K164,ISG:K168-PCNA \(Homo sapiens\)](#)



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:** [UBE2L6:TRIM25 ISGylates monoUb:K164-PCNA](#)

**Followed by:** [USP10 deubiquitinates monoUb:K164,ISG:K164,ISG:K168-PCNA](#)

## USP10 deubiquitinates monoUb:K164,ISG:K164,ISG:K168-PCNA ↗

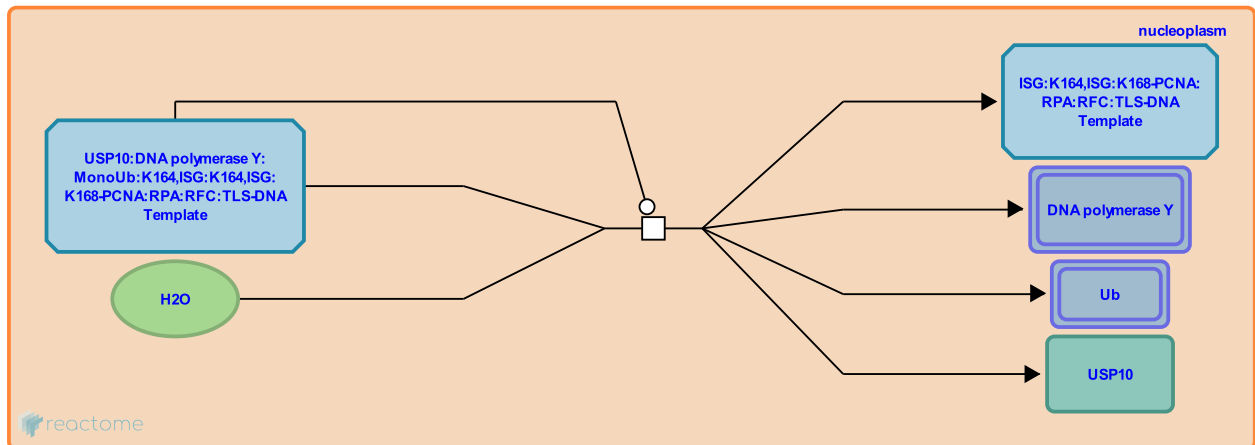
**Location:** [Termination of translesion DNA synthesis](#)

**Stable identifier:** R-SSC-5653770

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [USP10 deubiquitinates monoUb:K164,ISG:K164,ISG:K168-PCNA \(Homo sapiens\)](#)



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:** [USP10 binds monoUb:K164,ISG:K164,ISG:K168-PCNA](#)

**Followed by:** [USP43 binds ISG:K164,ISG:K168-PCNA](#)

## USP43 binds ISG:K164,ISG:K168-PCNA ↗

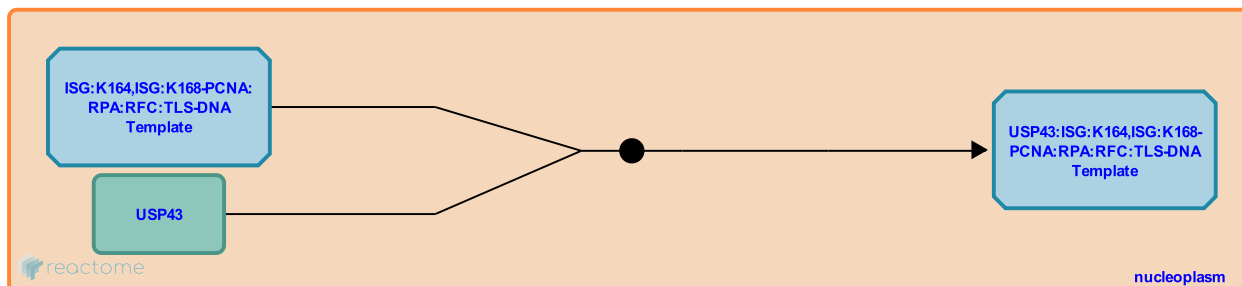
**Location:** [Termination of translesion DNA synthesis](#)

**Stable identifier:** R-SSC-5653780

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [USP43 binds ISG:K164,ISG:K168-PCNA \(Homo sapiens\)](#)



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:** [USP10 deubiquitinates monoUb:K164,ISG:K164,ISG:K168-PCNA](#)

**Followed by:** [USP43 deISGylates ISG:K164,ISG:K168-PCNA](#)



## USP43 deISGylates ISG:K164,ISG:K168-PCNA ↗

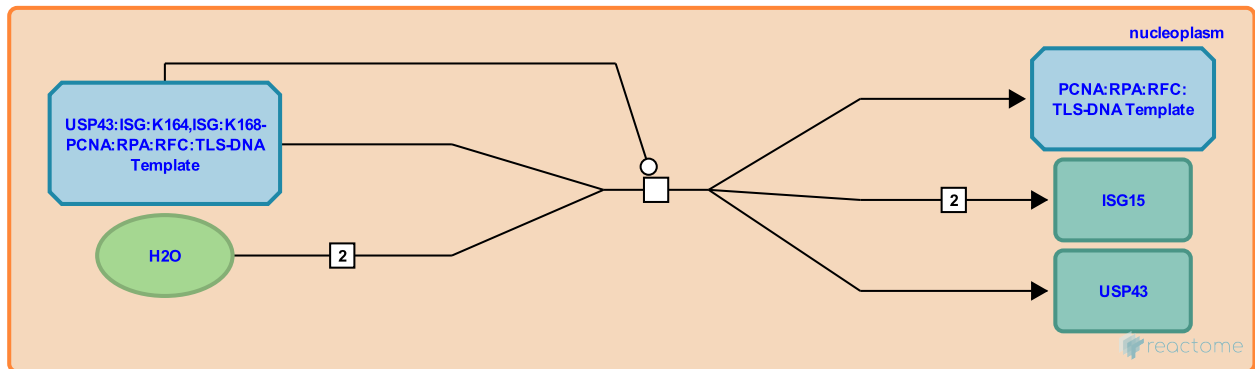
**Location:** [Termination of translesion DNA synthesis](#)

**Stable identifier:** R-SSC-5653786

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [USP43 deISGylates ISG:K164,ISG:K168-PCNA \(Homo sapiens\)](#)



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:** [USP43 binds ISG:K164,ISG:K168-PCNA](#)

**Followed by:** [POLD,POLE binds deISGylated PCNA after TLS](#)

## POLD,POLE binds deISGylated PCNA after TLS ↗

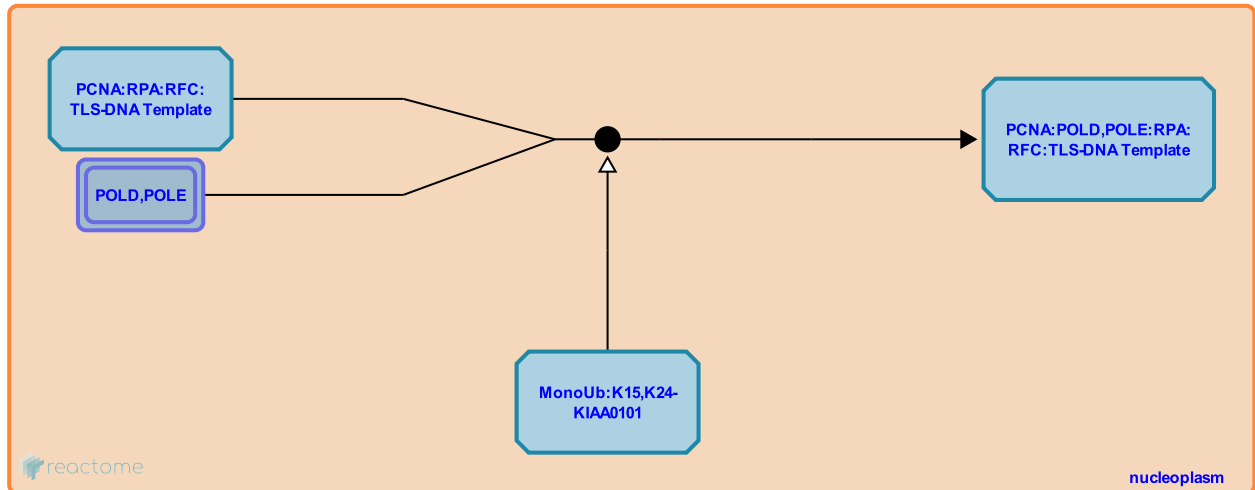
**Location:** Termination of translesion DNA synthesis

**Stable identifier:** R-SSC-5653838

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** POLD,POLE binds deISGylated PCNA after TLS (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:** USP43 deISGylates ISG:K164,ISG:K168-PCNA

## KIAA0101 double monoubiquitination ↗

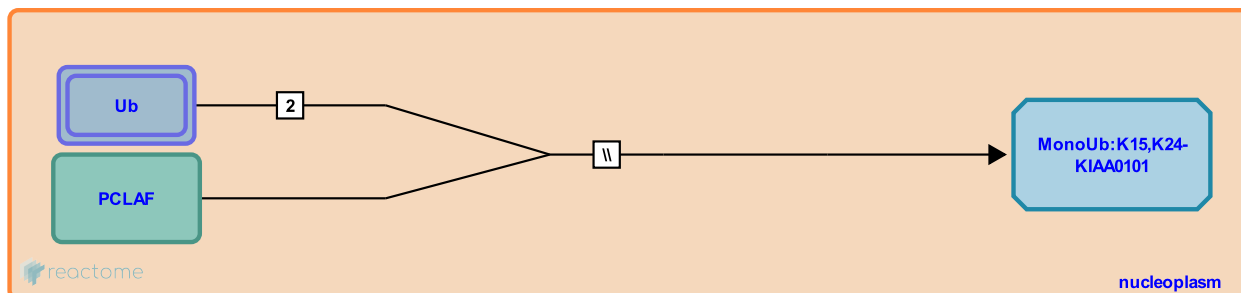
**Location:** [Termination of translesion DNA synthesis](#)

**Stable identifier:** R-SSC-5655193

**Type:** omitted

**Compartments:** nucleoplasm

**Inferred from:** [KIAA0101 double monoubiquitination \(Homo sapiens\)](#)



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>

# Table of Contents

Introduction	1
☒ Termination of translesion DNA synthesis	2
↳ TRIM25 binds monoUb:164-PCNA	3
↳ UBE2L6:TRIM25 ISGylates monoUb:K164-PCNA	4
↳ USP10 binds monoUb:K164,ISG:K164,ISG:K168-PCNA	5
↳ USP10 deubiquitinates monoUb:K164,ISG:K164,ISG:K168-PCNA	6
↳ USP43 binds ISG:K164,ISG:K168-PCNA	7
↳ USP43 deISGylates ISG:K164,ISG:K168-PCNA	8
↳ POLD,POLE binds deISGylated PCNA after TLS	9
☒ KIAA0101 double monoubiquitination	10
Table of Contents	11