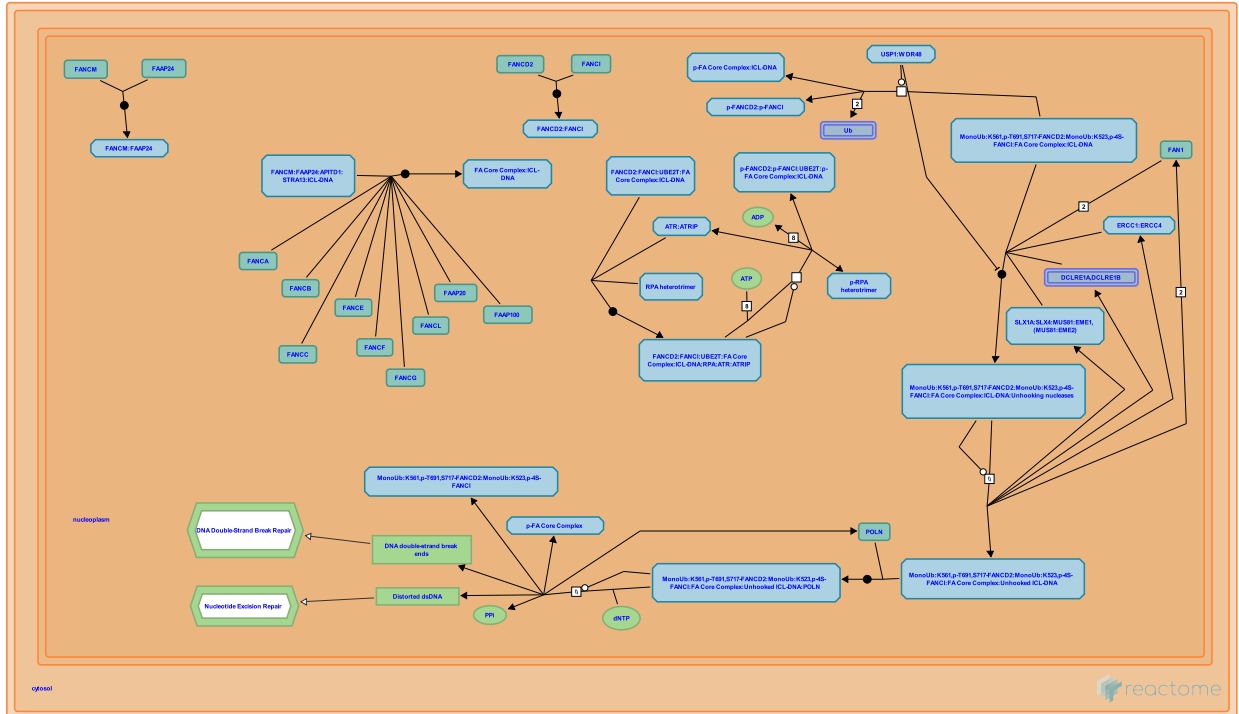


Fanconi Anemia Pathway



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](https://reactome.org/textbook/).

08/05/2024

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

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- 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: 88

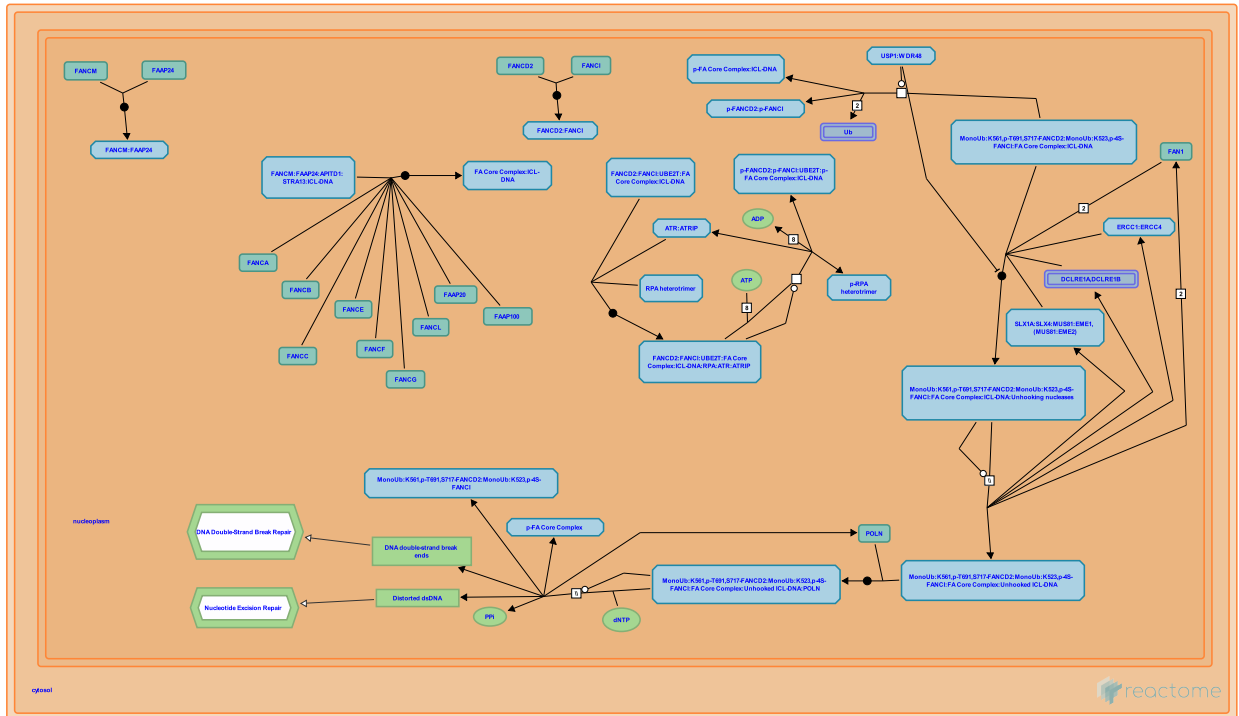
This document contains 1 pathway and 10 reactions ([see Table of Contents](#))

Fanconi Anemia Pathway ↗

Stable identifier: R-CFA-6783310

Compartments: nucleoplasm

Inferred from: Fanconi Anemia Pathway (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.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

FANCM binds FAAP24 ↗

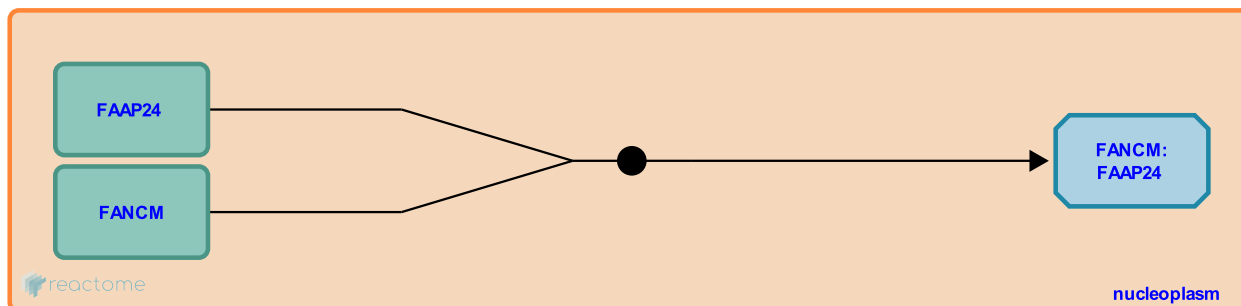
Location: [Fanconi Anemia Pathway](#)

Stable identifier: R-CFA-6785607

Type: binding

Compartments: nucleoplasm

Inferred from: [FANCM binds FAAP24 \(Homo sapiens\)](#)



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>

FA core complex assembles at DNA interstrand crosslinks (ICLs) ↗

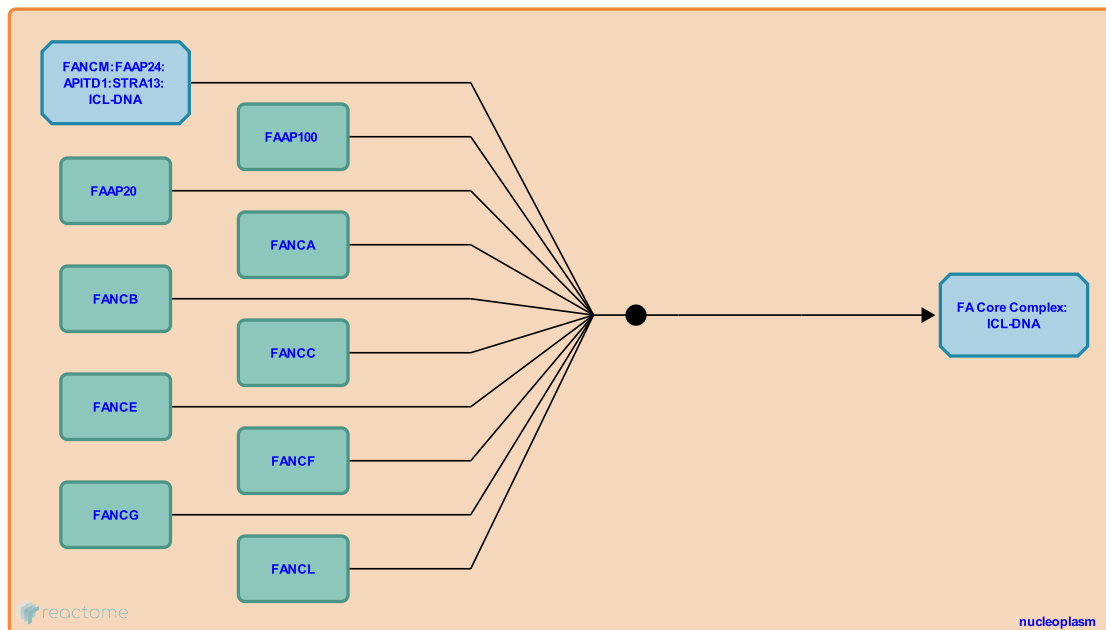
Location: Fanconi Anemia Pathway

Stable identifier: R-CFA-6785126

Type: binding

Compartments: nucleoplasm

Inferred from: FA core complex assembles at DNA interstrand crosslinks (ICLs) (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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FANCD2 binds FANCI ↗

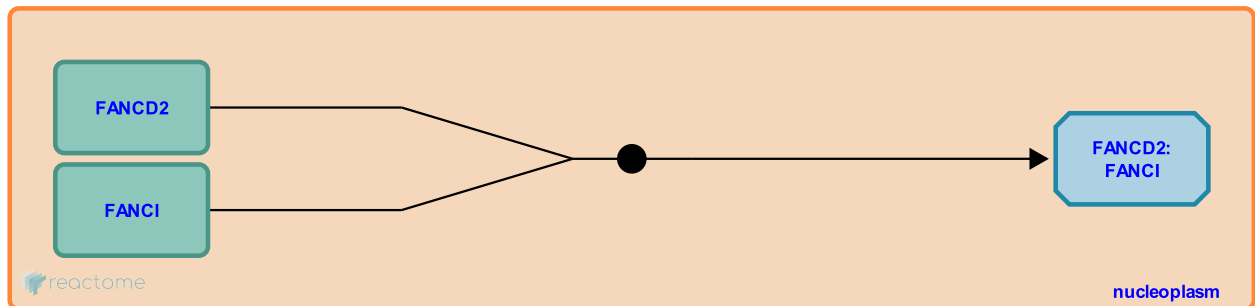
Location: [Fanconi Anemia Pathway](#)

Stable identifier: R-CFA-6785594

Type: binding

Compartments: nucleoplasm

Inferred from: [FANCD2 binds FANCI \(Homo sapiens\)](#)



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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The complex of ATR and ATRIP is recruited to ICL-DNA ↗

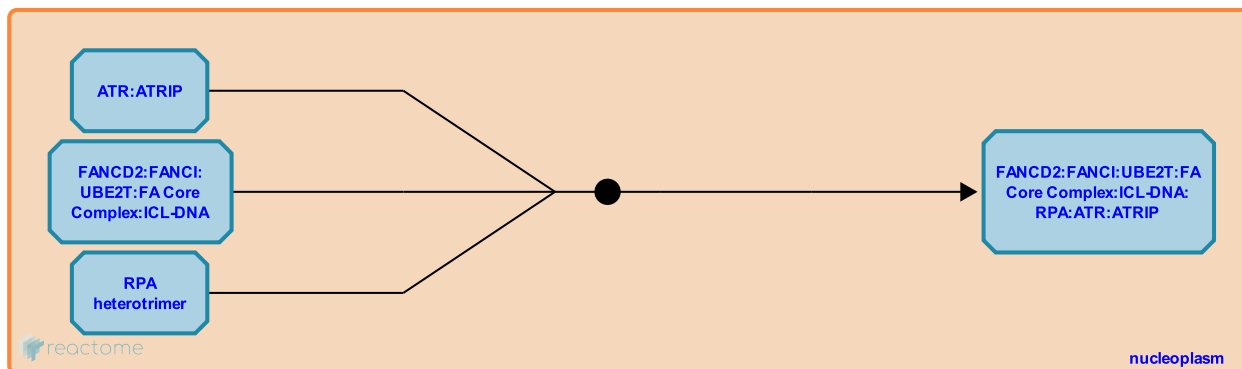
Location: Fanconi Anemia Pathway

Stable identifier: R-CFA-6788385

Type: binding

Compartments: nucleoplasm

Inferred from: The complex of ATR and ATRIP is recruited to ICL-DNA (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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Followed by: ATR phosphorylates RPA2, FANCI, FANCD2 and FANCM at ICL-DNA

ATR phosphorylates RPA2, FANCI, FANCD2 and FANCM at ICL-DNA ↗

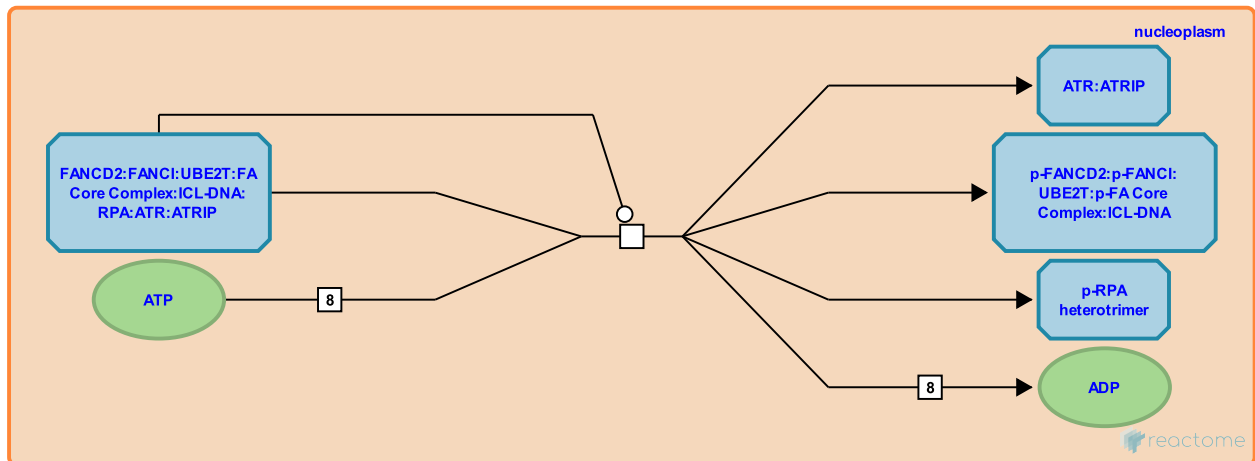
Location: Fanconi Anemia Pathway

Stable identifier: R-CFA-6788392

Type: transition

Compartments: nucleoplasm

Inferred from: ATR phosphorylates RPA2, FANCI, FANCD2 and FANCM at ICL-DNA (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: The complex of ATR and ATRIP is recruited to ICL-DNA

FANCD2 deubiquitination by USP1:WDR48 ↗

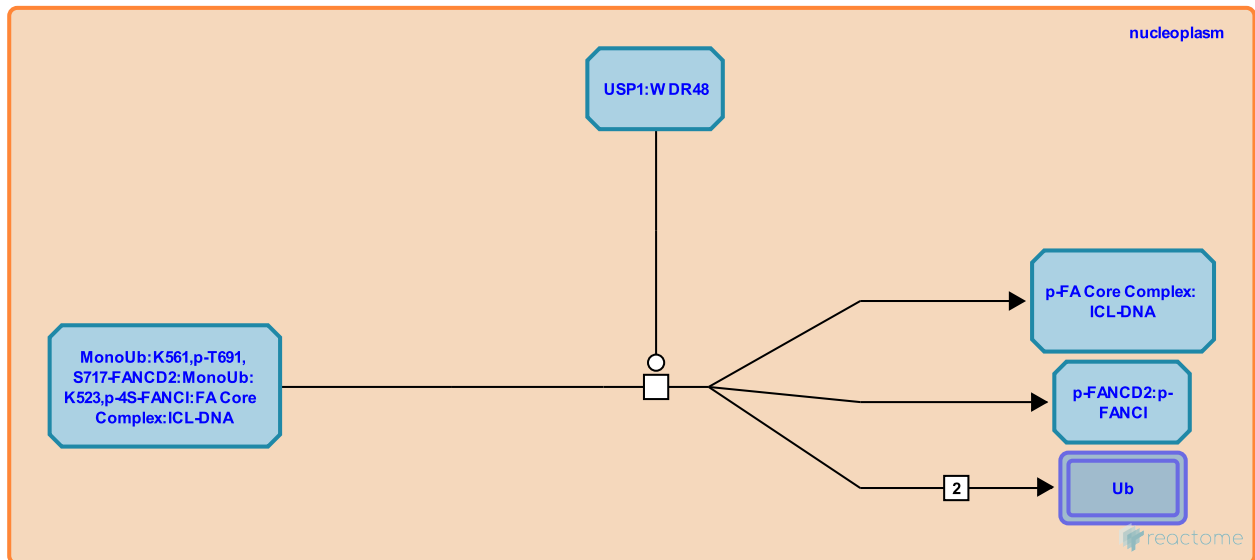
Location: [Fanconi Anemia Pathway](#)

Stable identifier: R-CFA-6786171

Type: transition

Compartments: nucleoplasm

Inferred from: [FANCD2 deubiquitination by USP1:WDR48 \(Homo sapiens\)](#)



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>

DNA nucleases bind monoubiquitinated ID2 complex ↗

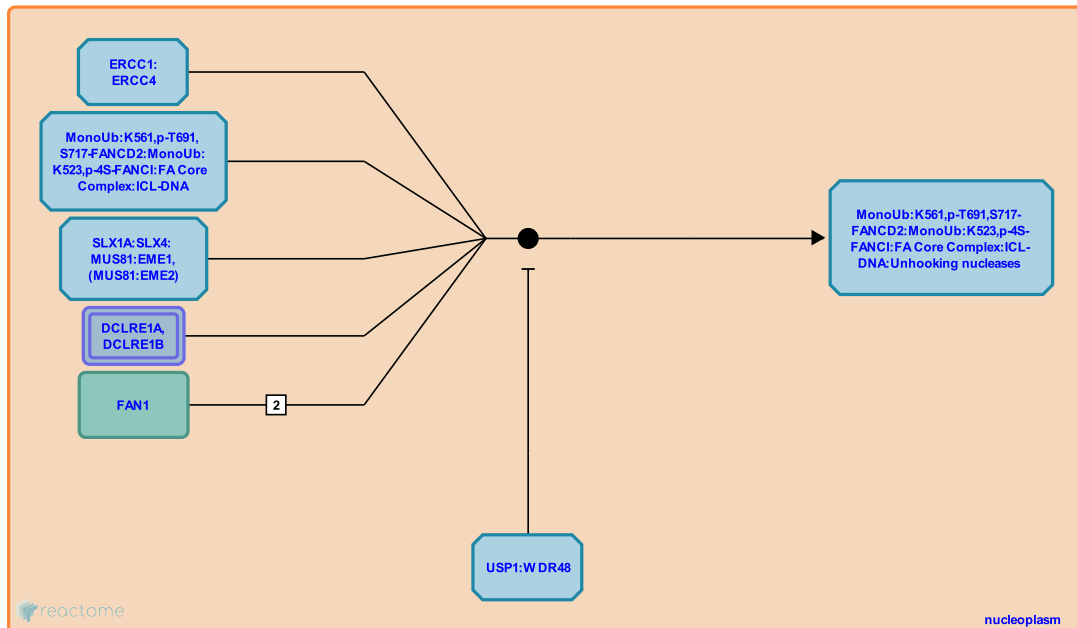
Location: Fanconi Anemia Pathway

Stable identifier: R-CFA-6785732

Type: binding

Compartments: nucleoplasm

Inferred from: DNA nucleases bind monoubiquitinated ID2 complex (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: DNA nucleases unhook the interstrand crosslink (ICL)

DNA nucleases unhook the interstrand crosslink (ICL) ↗

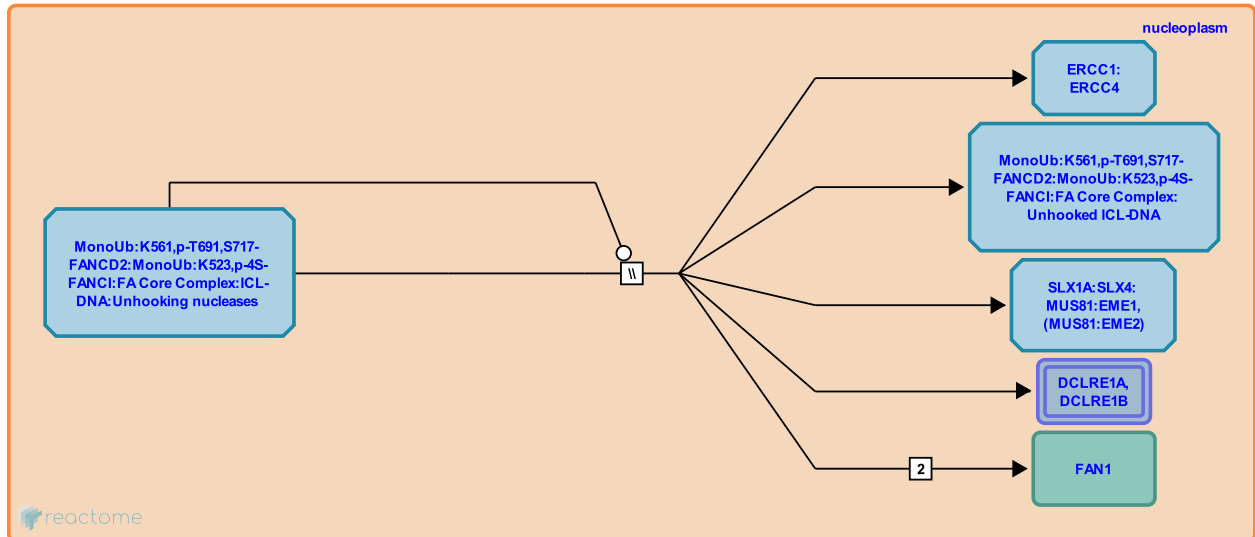
Location: Fanconi Anemia Pathway

Stable identifier: R-CFA-6785986

Type: omitted

Compartments: nucleoplasm

Inferred from: DNA nucleases unhook the interstrand crosslink (ICL) (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: DNA nucleases bind monoubiquitinated ID2 complex

Followed by: POLN binds ICL-DNA

POLN binds ICL-DNA ↗

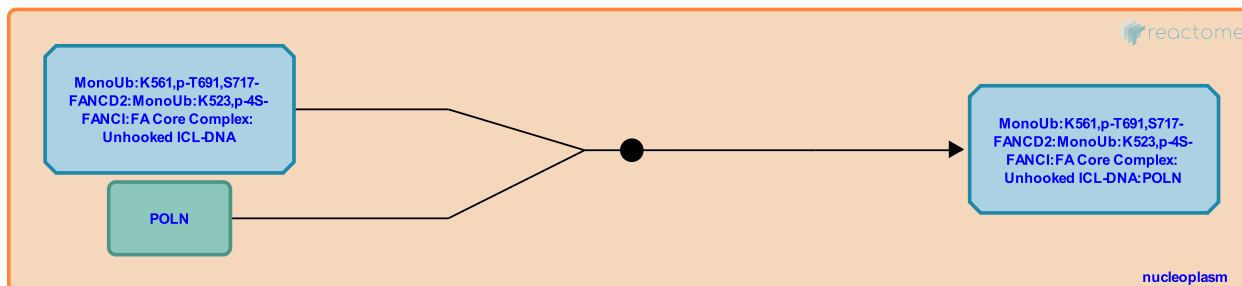
Location: [Fanconi Anemia Pathway](#)

Stable identifier: R-CFA-6786155

Type: binding

Compartments: nucleoplasm

Inferred from: [POLN binds ICL-DNA \(Homo sapiens\)](#)



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>

Preceded by: [DNA nucleases unhook the interstrand crosslink \(ICL\)](#)

Followed by: [Translesion synthesis across unhooked ICL by POLN](#)

Translesion synthesis across unhooked ICL by POLN ↗

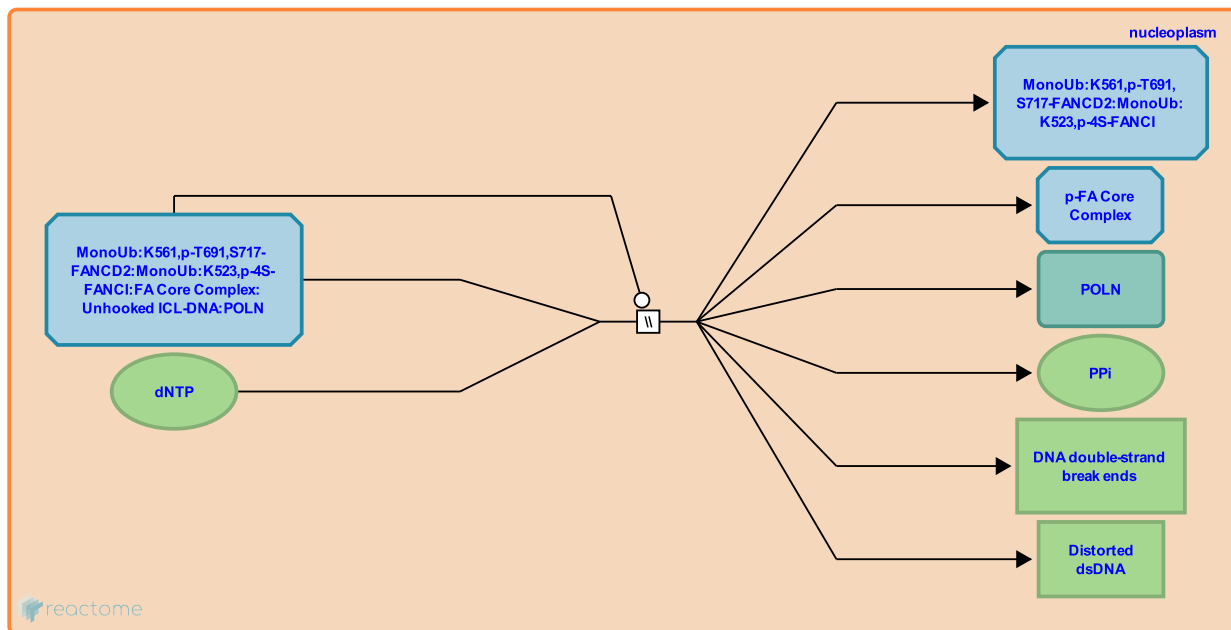
Location: Fanconi Anemia Pathway

Stable identifier: R-CFA-6786166

Type: omitted

Compartments: nucleoplasm

Inferred from: Translesion synthesis across unhooked ICL by POLN (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: POLN binds ICL-DNA

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