Alpha-protein kinase 1 signaling pathway

25/08/2021

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

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. ↗
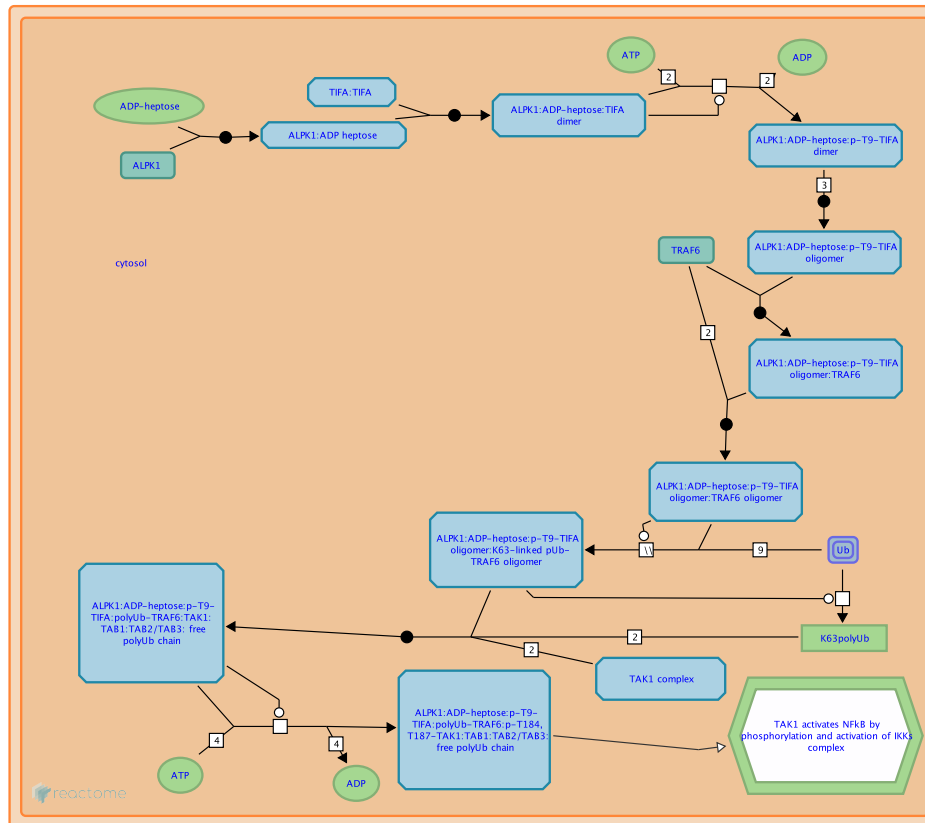
Reactome database release: 77

This document contains 1 pathway and 10 reactions ()

Alpha-protein kinase 1 signaling pathway ↗

Stable identifier: R-CFA-9645460

Compartments: cytosol

Inferred from: Alpha-protein kinase 1 signaling 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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp
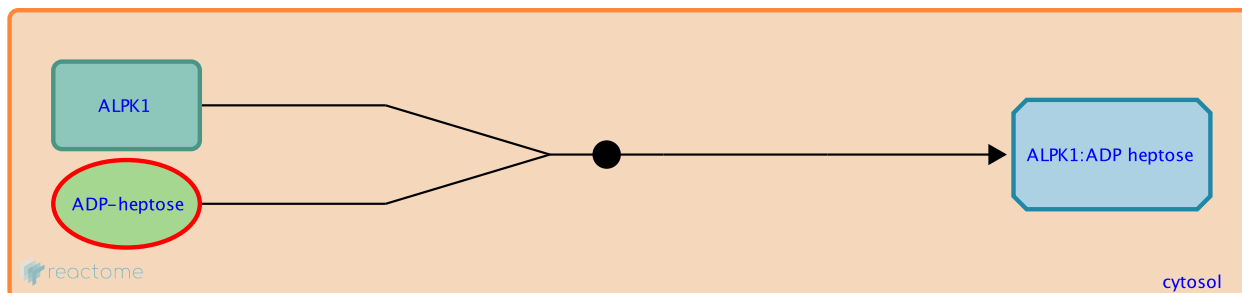
ALPK1 binds ADP-heptose ↗

Location: Alpha-protein kinase 1 signaling pathway

Stable identifier: R-CFA-9645428

Type: binding

Compartments: cytosol

Inferred from: ALPK1 binds ADP-heptose (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: ALPK1:ADP-heptose binds TIFA
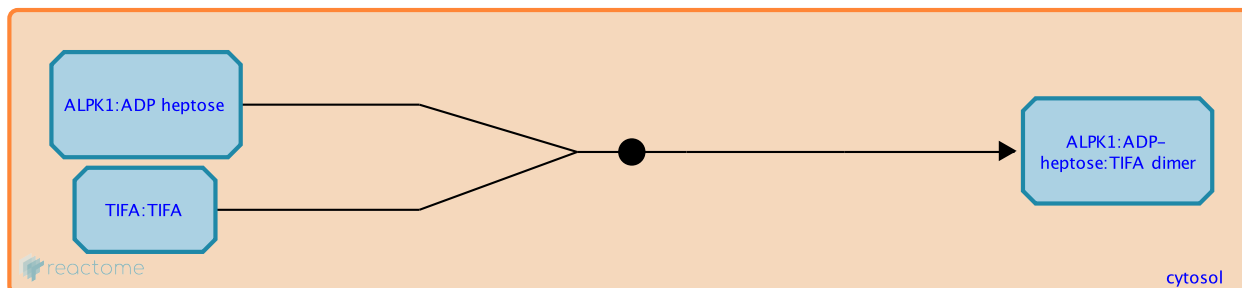
ALPK1:ADP-heptose binds TIFA ↗

Location: Alpha-protein kinase 1 signaling pathway

Stable identifier: R-CFA-9645524

Type: binding

Compartments: cytosol

Inferred from: ALPK1:ADP-heptose binds TIFA (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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Preceded by: ALPK1 binds ADP-heptose

Followed by: ALPK1 phosphorylates TIFA
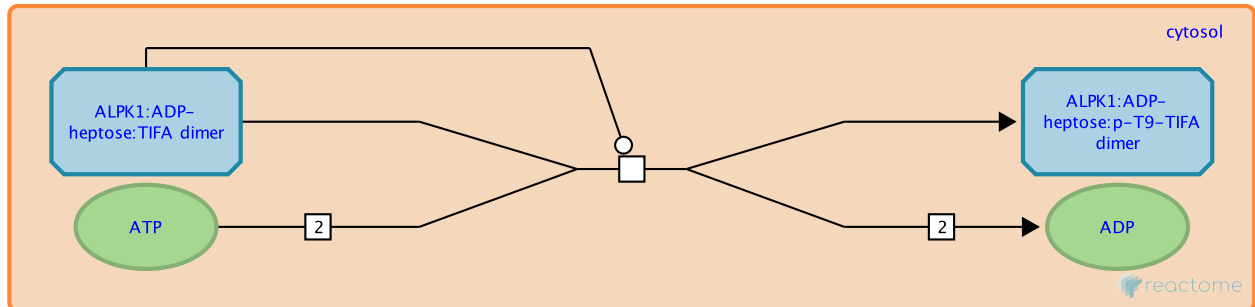
ALPK1 phosphorylates TIFA ↗

Location: Alpha-protein kinase 1 signaling pathway

Stable identifier: R-CFA-9645535

Type: transition

Compartments: cytosol

Inferred from: ALPK1 phosphorylates TIFA (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: ALPK1:ADP-heptose binds TIFA

Followed by: TIFA oligomerization
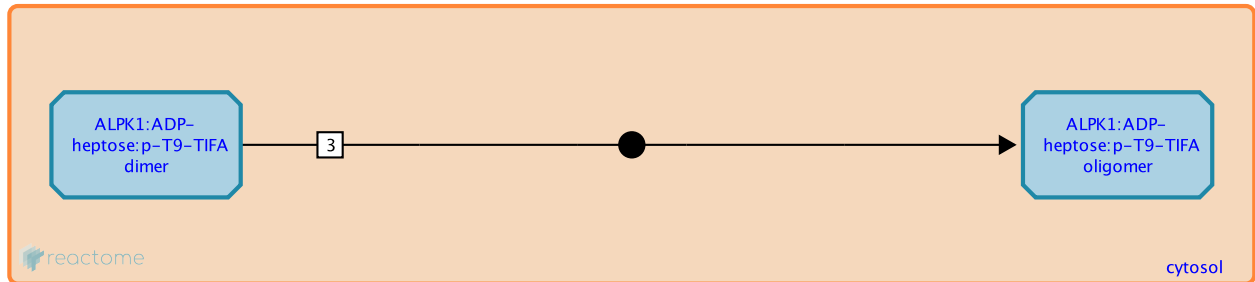
TIFA oligomerization ↗

Location: Alpha-protein kinase 1 signaling pathway

Stable identifier: R-CFA-9645481

Type: binding

Compartments: cytosol

Inferred from: TIFA oligomerization (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: ALPK1 phosphorylates TIFA

Followed by: ALPK1:ADP-heptose:TIFA oligomer recruits TRAF6
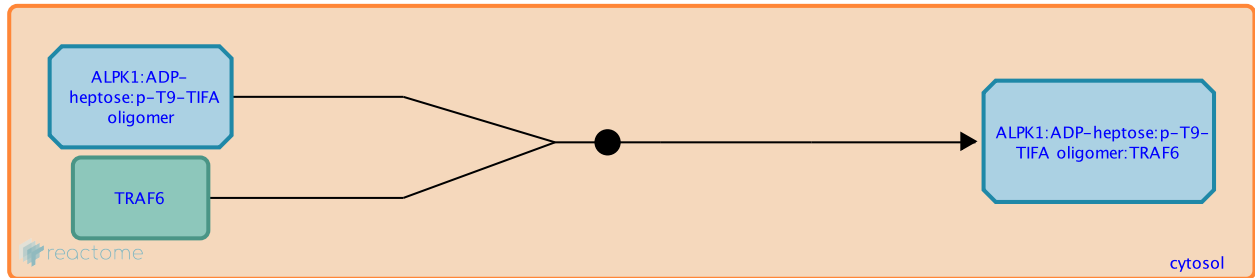
ALPK1:ADP-heptose:TIFA oligomer recruits TRAF6 ↗

Location: Alpha-protein kinase 1 signaling pathway

Stable identifier: R-CFA-9645520

Type: binding

Compartments: cytosol

Inferred from: ALPK1:ADP-heptose:TIFA oligomer recruits TRAF6 (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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Preceded by: TIFA oligomerization

Followed by: TRAF6 oligomerizes within the ALPK1:ADP-heptose:TIFA oligomer complex

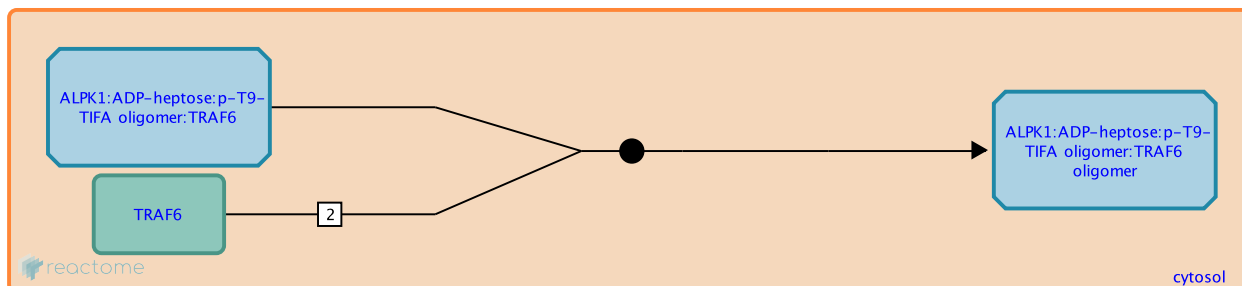## TRAF6 oligomerizes within the ALPK1:ADP-heptose:TIFA oligomer complex ↗

Location: Alpha-protein kinase 1 signaling pathway

Stable identifier: R-CFA-9645501

Type: binding

Compartments: cytosol

Inferred from: TRAF6 oligomerizes within the ALPK1:ADP-heptose:TIFA oligomer 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.

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Preceded by: ALPK1:ADP-heptose:TIFA oligomer recruits TRAF6

Followed by: Auto ubiquitination of TRAF6 bound to ALPK1:ADP-heptose:TIFA oligomer

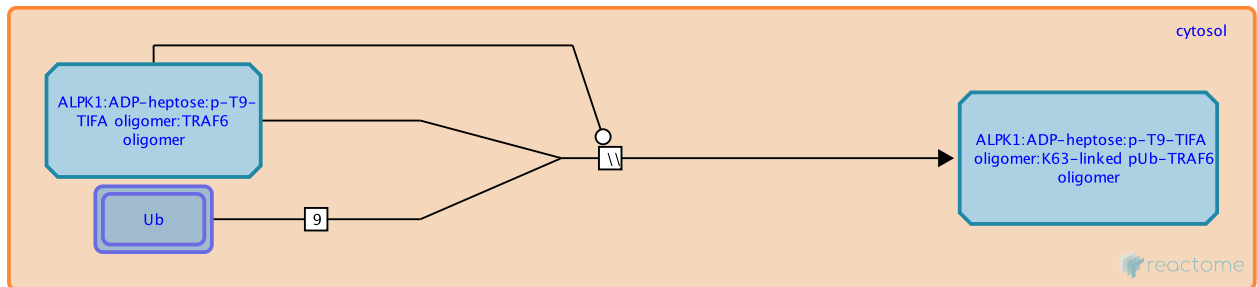## Auto ubiquitination of TRAF6 bound to ALPK1:ADP-heptose:TIFA oligomer ↗

Location: Alpha-protein kinase 1 signaling pathway

Stable identifier: R-CFA-9645414

Type: omitted

Compartments: cytosol

Inferred from: Auto ubiquitination of TRAF6 bound to ALPK1:ADP-heptose:TIFA oligomer (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: TRAF6 oligomerizes within the ALPK1:ADP-heptose:TIFA oligomer complex

Followed by: Activated TRAF6 synthesizes unanchored polyubiquitin chains upon ALPK1:ADP-heptose stimulation

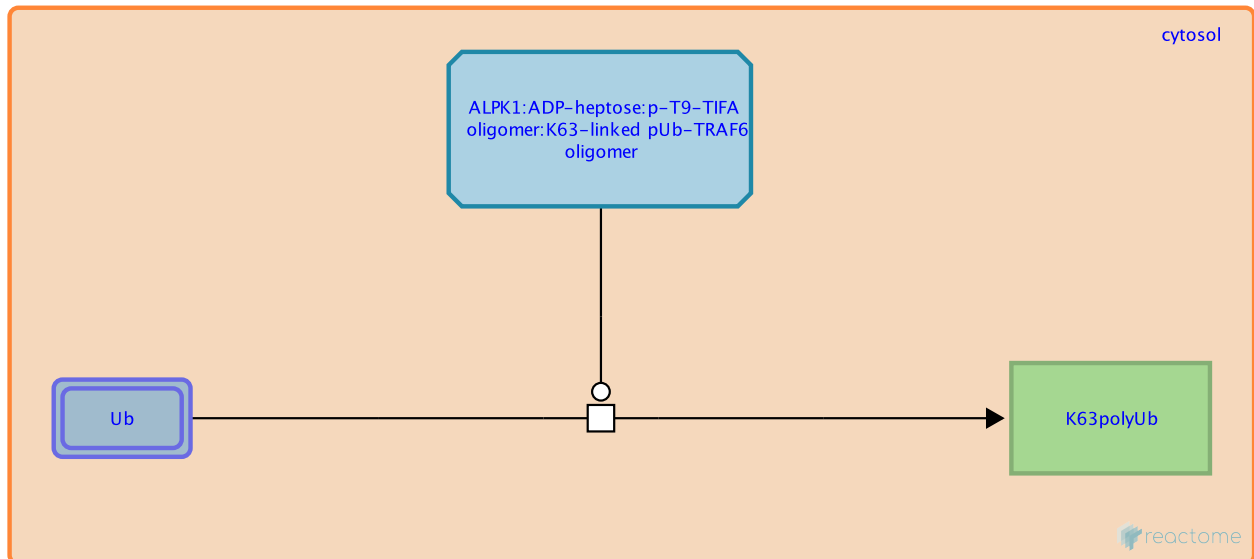## Activated TRAF6 synthesizes unanchored polyubiquitin chains upon ALPK1:ADP-heptose stimulation ↗

Location: Alpha-protein kinase 1 signaling pathway

Stable identifier: R-CFA-9645394

Type: transition

Compartments: cytosol

Inferred from: Activated TRAF6 synthesizes unanchored polyubiquitin chains upon ALPK1:ADP-heptose stimulation (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: Auto ubiquitination of TRAF6 bound to ALPK1:ADP-heptose:TIFA oligomer

Followed by: ALPK1:ADP-heptose:p-T9-TIFA oligomer:K63pUb-TRAF6 oligomer recruits MAP3K7 (TAK1)

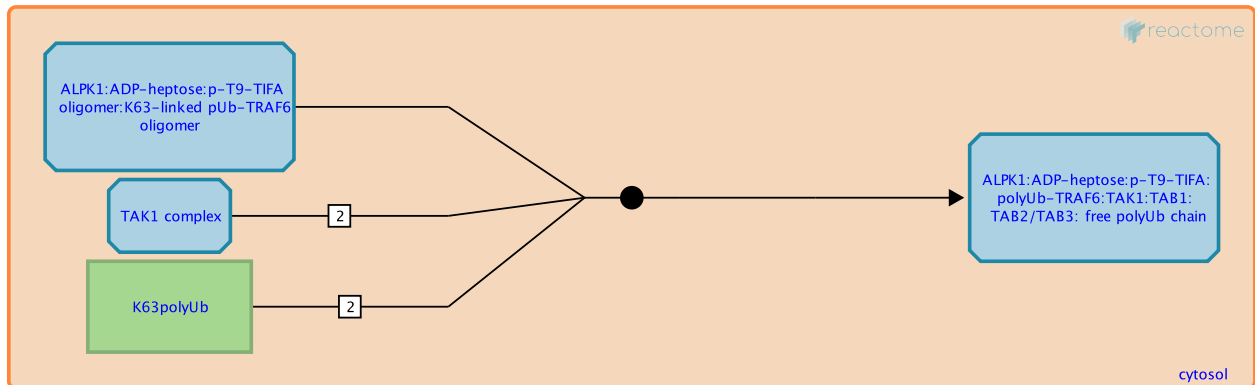## ALPK1:ADP-heptose:p-T9-TIFA oligomer:K63pUb-TRAF6 oligomer recruits MAP3K7 (TAK1) ↗

Location: Alpha-protein kinase 1 signaling pathway

Stable identifier: R-CFA-9645406

Type: binding

Compartments: cytosol

Inferred from: ALPK1:ADP-heptose:p-T9-TIFA oligomer:K63pUb-TRAF6 oligomer recruits MAP3K7 (TAK1) (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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Preceded by: Activated TRAF6 synthesizes unanchored polyubiquitin chains upon ALPK1:ADP-heptose stimulation

Followed by: Auto phosphorylation of TAK1 within the ALPK1:ADP-heptose:p-T9-TIFA:pUb-TRAF6: free K63 pUb:TAB1:TAB2/TAB3 :MAP3K7 complex

Auto phosphorylation of TAK1 within the ALPK1:ADP-heptose:p-T9-TIFA:pUb-TRAF6: free K63 pUb:TAB1:TAB2/TAB3 :MAP3K7 complex ↗

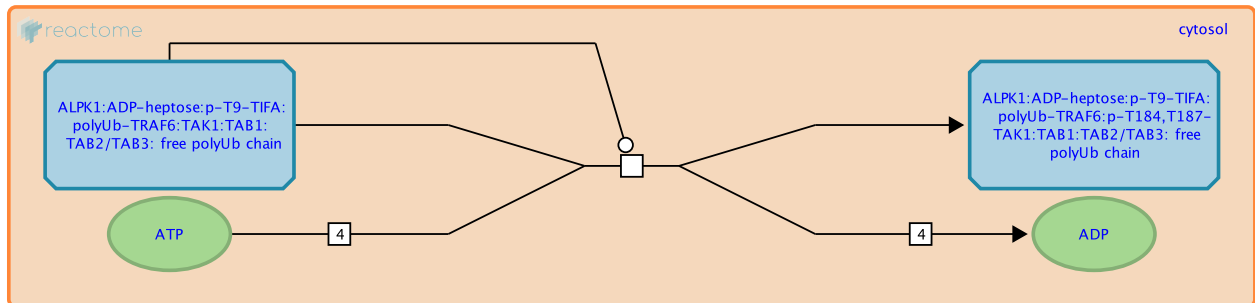**Location:** Alpha-protein kinase 1 signaling pathway

Stable identifier: R-CFA-9645442

Type: transition

Compartments: cytosol

Inferred from: Auto phosphorylation of TAK1 within the ALPK1:ADP-heptose:p-T9-TIFA:pUb-TRAF6: free K63 pUb:TAB1:TAB2/TAB3 :MAP3K7 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.

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Preceded by: ALPK1:ADP-heptose:p-T9-TIFA oligomer:K63pUb-TRAF6 oligomer recruits MAP3K7 (TAK1)

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