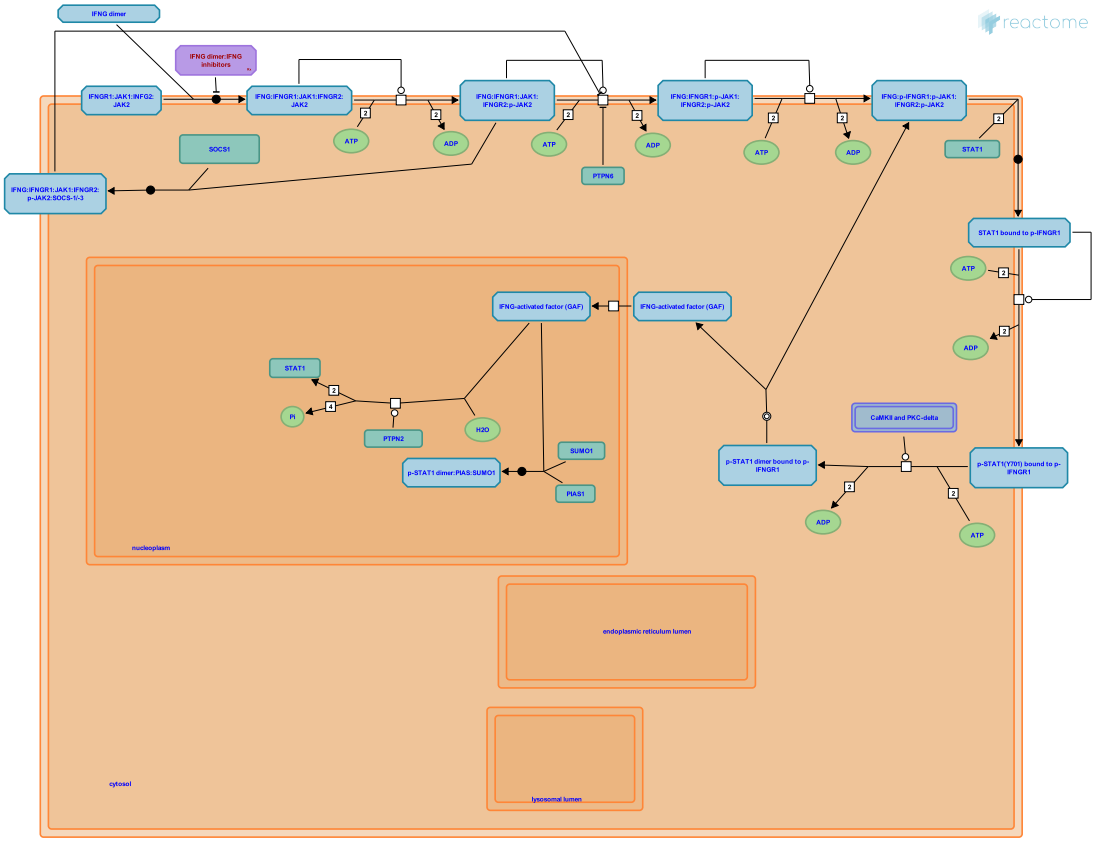
Interferon gamma signaling



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

24/09/2020

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. ↗

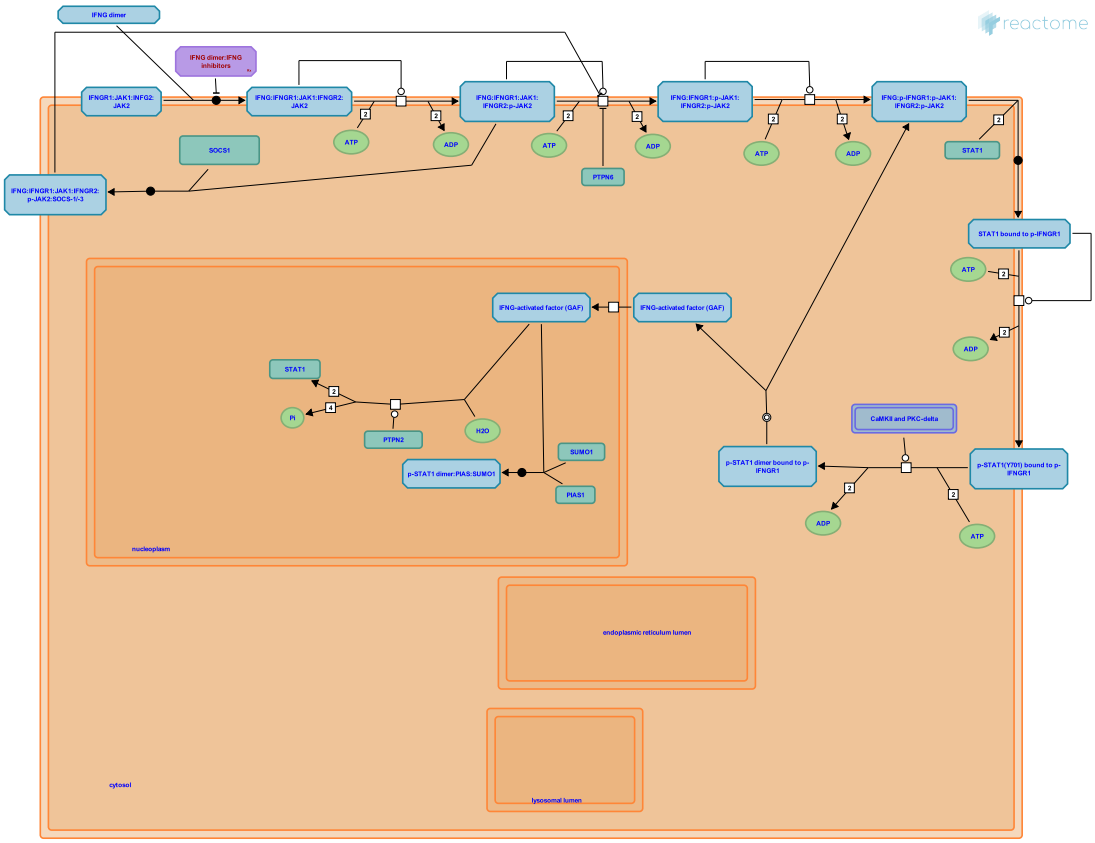
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Interferon gamma signaling ↗

Stable identifier: R-GGA-877300

Inferred from: Interferon gamma signaling (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

IFNG dimer binds IFNGR ↗

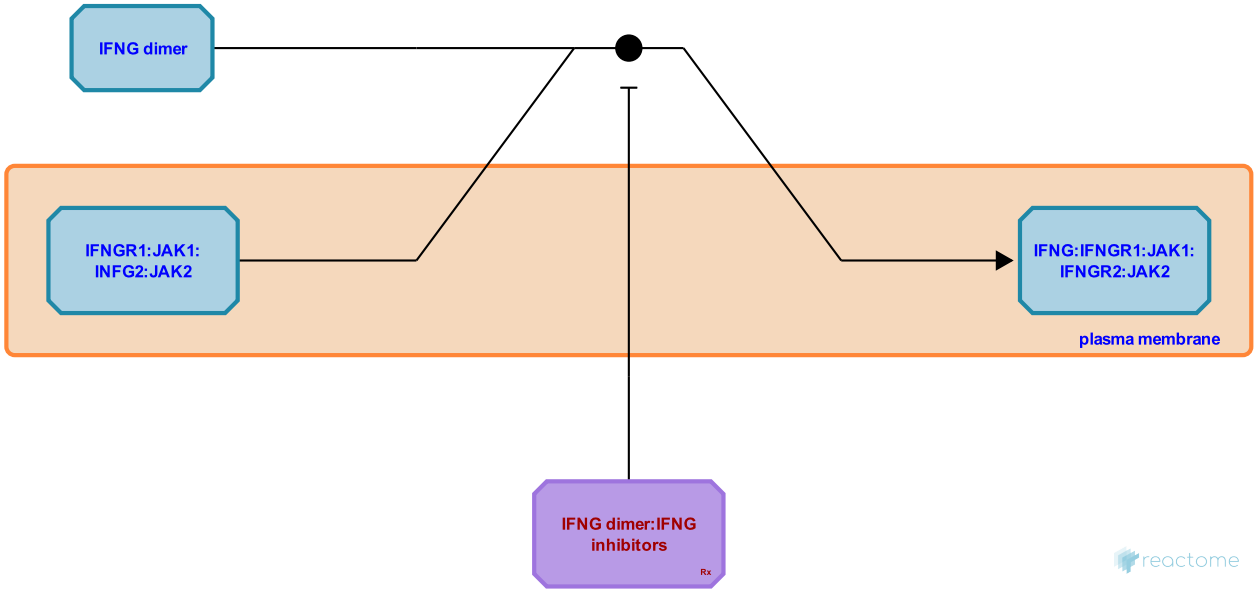
Location: Interferon gamma signaling

Stable identifier: R-GGA-873926

Type: binding

Compartments: extracellular region, plasma membrane

Inferred from: IFNG dimer binds IFNGR (Homo sapiens)



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Followed by: Phosphorylation of JAK2

Phosphorylation of JAK2 ↗

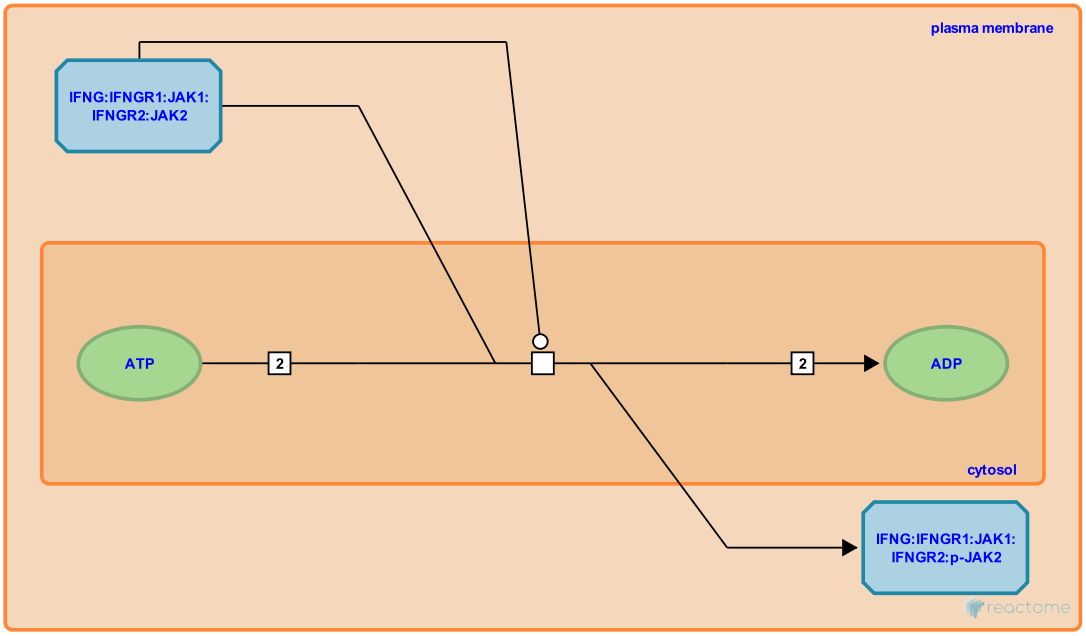
Location: Interferon gamma signaling

Stable identifier: R-GGA-873919

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: Phosphorylation of JAK2 (Homo sapiens)



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Preceded by: IFNG dimer binds IFNGR

Followed by: Transphosphorylation of JAK1

Transphosphorylation of JAK1 ↗

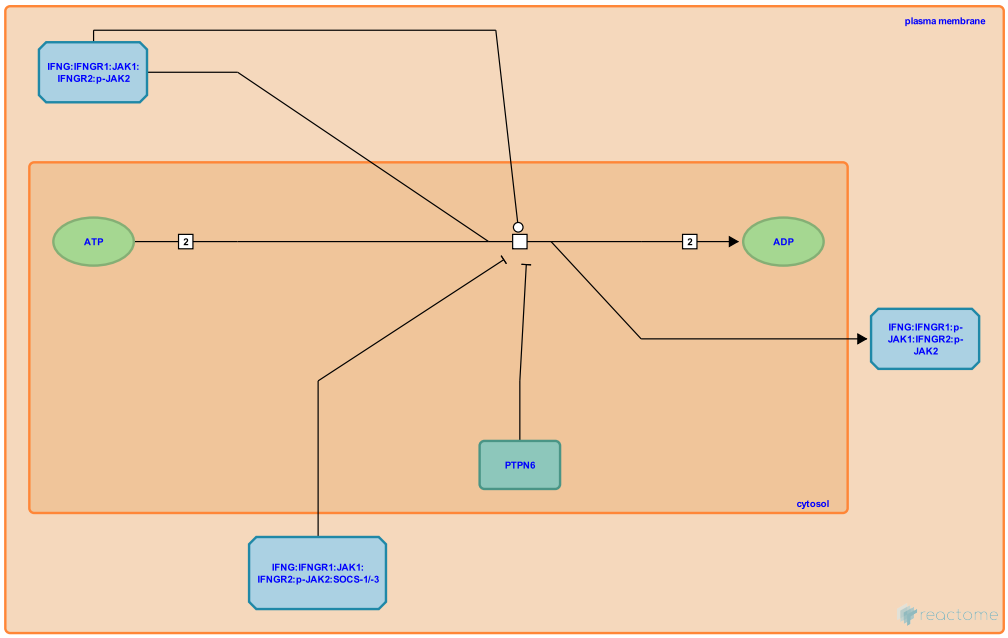
Location: Interferon gamma signaling

Stable identifier: R-GGA-873918

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: Transphosphorylation of JAK1 (Homo sapiens)



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Preceded by: Phosphorylation of JAK2

Followed by: Phosphorylation of IFNGR1 by JAK kinases

Phosphorylation of IFNGR1 by JAK kinases ↗

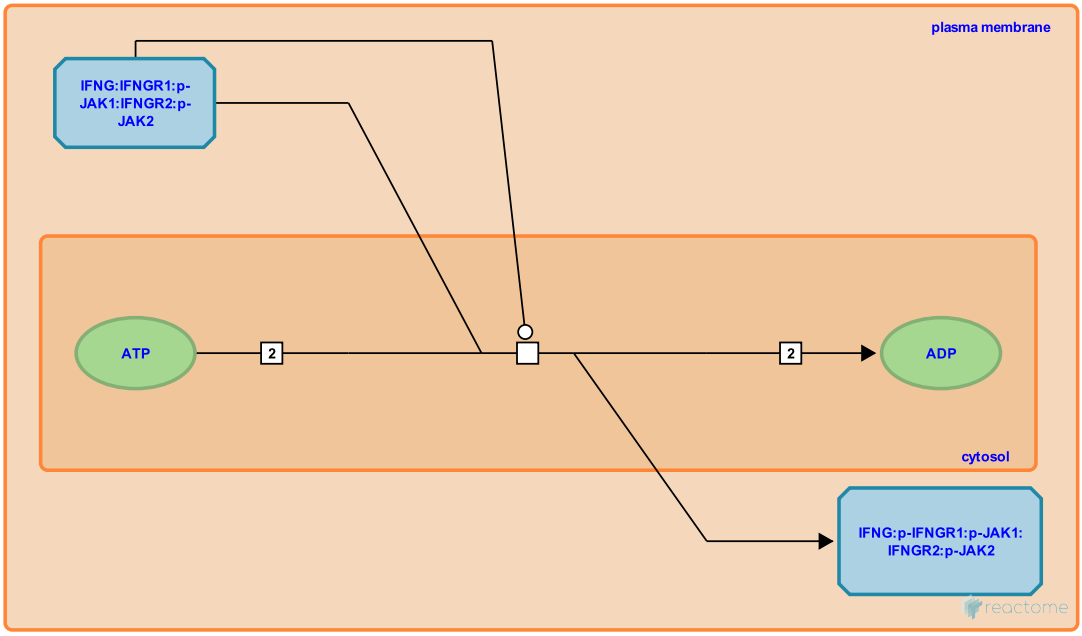
Location: Interferon gamma signaling

Stable identifier: R-GGA-873924

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: Phosphorylation of IFNGR1 by JAK kinases (Homo sapiens)



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Preceded by: Transphosphorylation of JAK1

Followed by: Binding of STAT1 to p-IFNGR1

Binding of STAT1 to p-IFNGR1 ↗

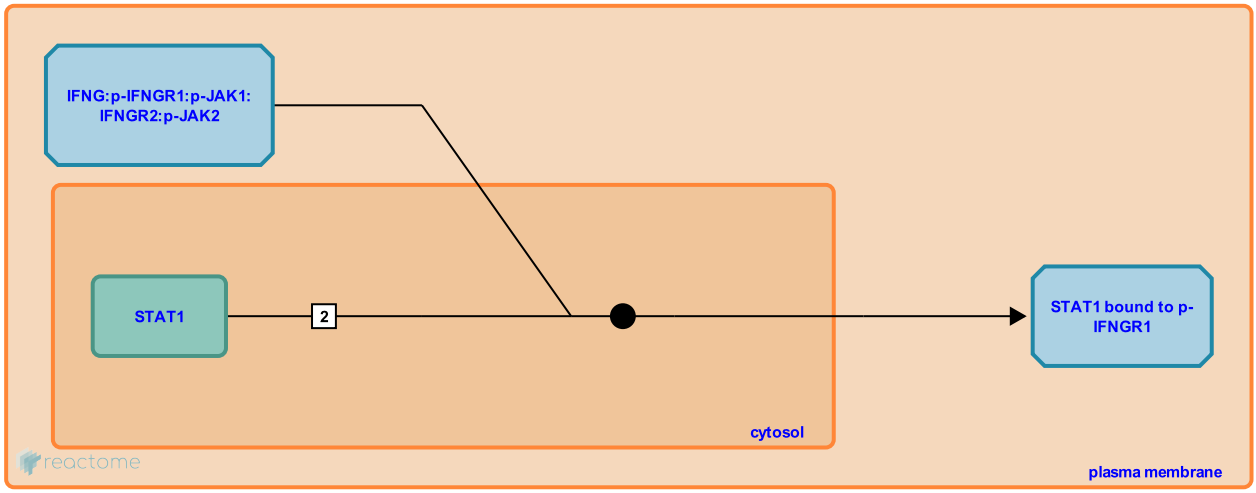
Location: Interferon gamma signaling

Stable identifier: R-GGA-873921

Type: binding

Compartments: cytosol, plasma membrane

Inferred from: Binding of STAT1 to p-IFNGR1 (Homo sapiens)



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Preceded by: Phosphorylation of IFNGR1 by JAK kinases

Followed by: Phosphorylation of STAT1 by JAK kinases

Phosphorylation of STAT1 by JAK kinases ↗

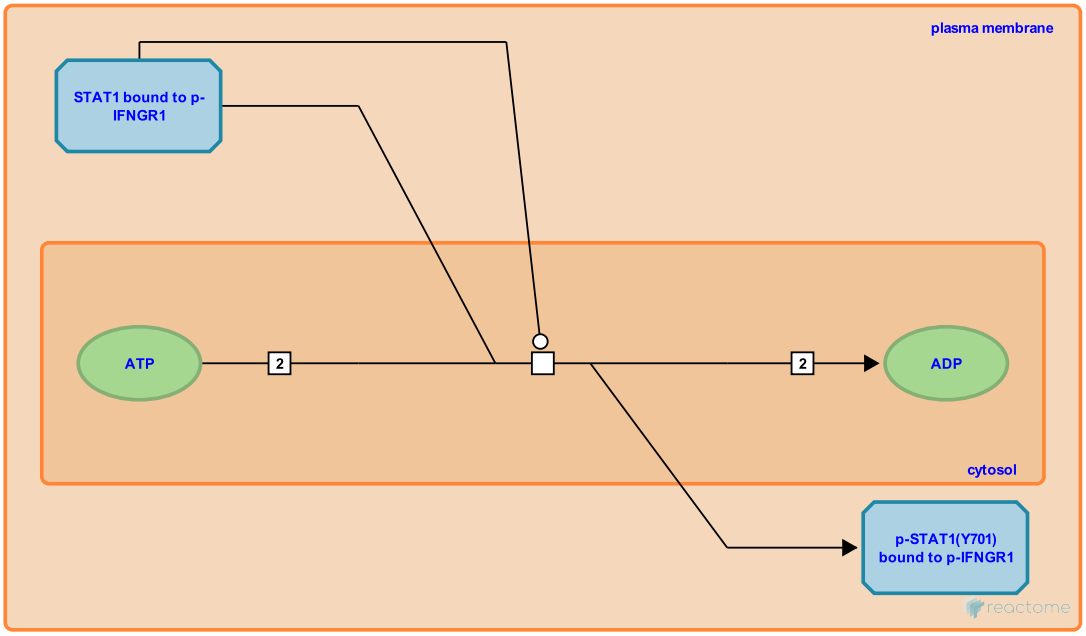
Location: Interferon gamma signaling

Stable identifier: R-GGA-873922

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: Phosphorylation of STAT1 by JAK kinases (Homo sapiens)



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Preceded by: Binding of STAT1 to p-IFNGR1

Followed by: Phosphorylation of STAT1 at Ser727

Phosphorylation of STAT1 at Ser727 ↗

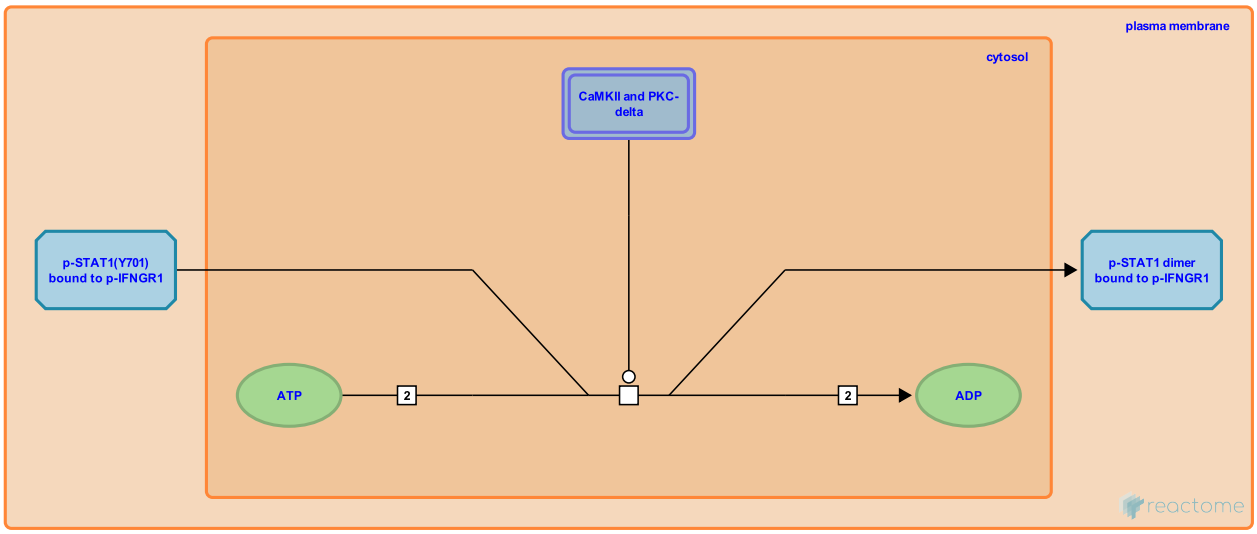
Location: Interferon gamma signaling

Stable identifier: R-GGA-909552

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: Phosphorylation of STAT1 at Ser727 (Homo sapiens)



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Preceded by: Phosphorylation of STAT1 by JAK kinases

Followed by: Release of STAT1 dimer from active receptor unit

Release of STAT1 dimer from active receptor unit ↗

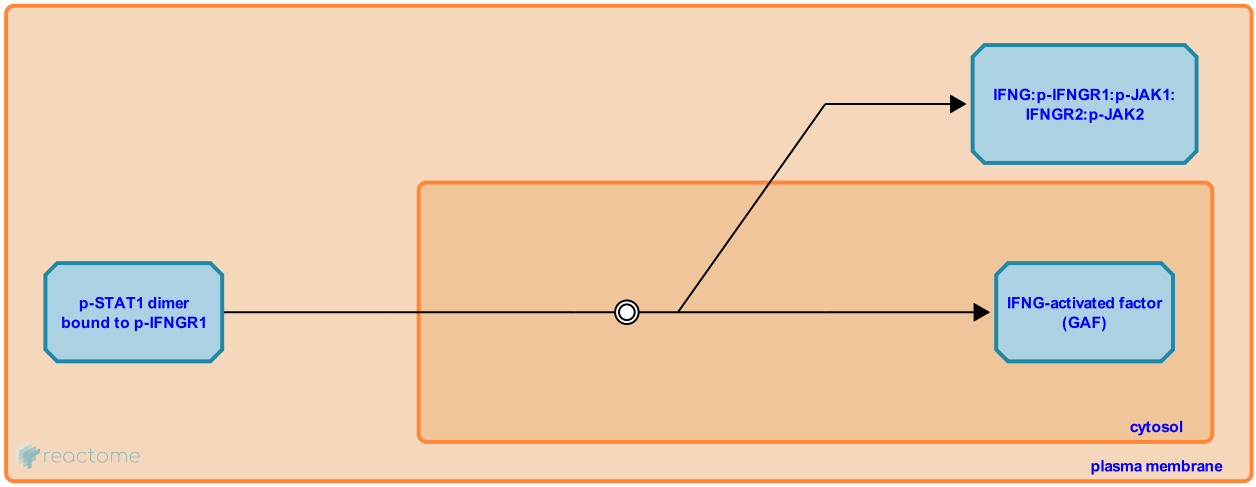
Location: Interferon gamma signaling

Stable identifier: R-GGA-873927

Type: dissociation

Compartments: cytosol, plasma membrane

Inferred from: Release of STAT1 dimer from active receptor unit (Homo sapiens)



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Preceded by: Phosphorylation of STAT1 at Ser727

Followed by: Translocation of STAT1 dimer to nucleus

Translocation of STAT1 dimer to nucleus ↗

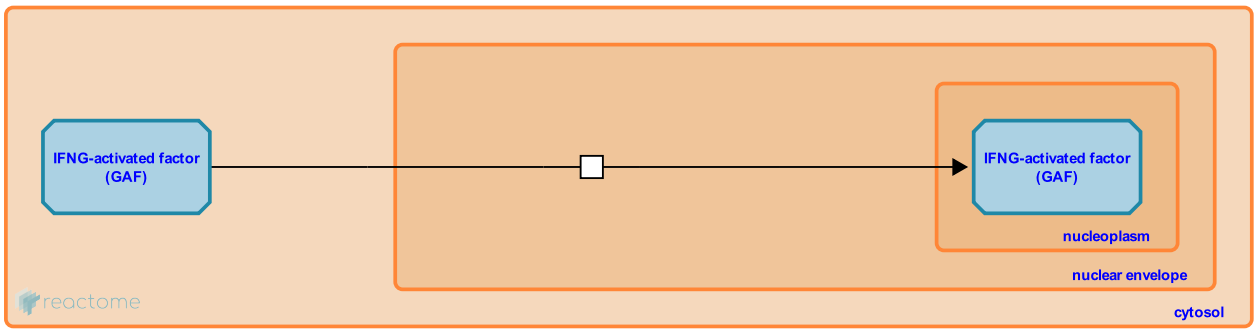
Location: Interferon gamma signaling

Stable identifier: R-GGA-873917

Type: transition

Compartments: nuclear envelope

Inferred from: Translocation of STAT1 dimer to nucleus (Homo sapiens)



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Preceded by: Release of STAT1 dimer from active receptor unit

Regulation of IFNG signaling ↗

Location: Interferon gamma signaling

Stable identifier: R-GGA-877312

Inferred from: Regulation of IFNG signaling (Homo sapiens)

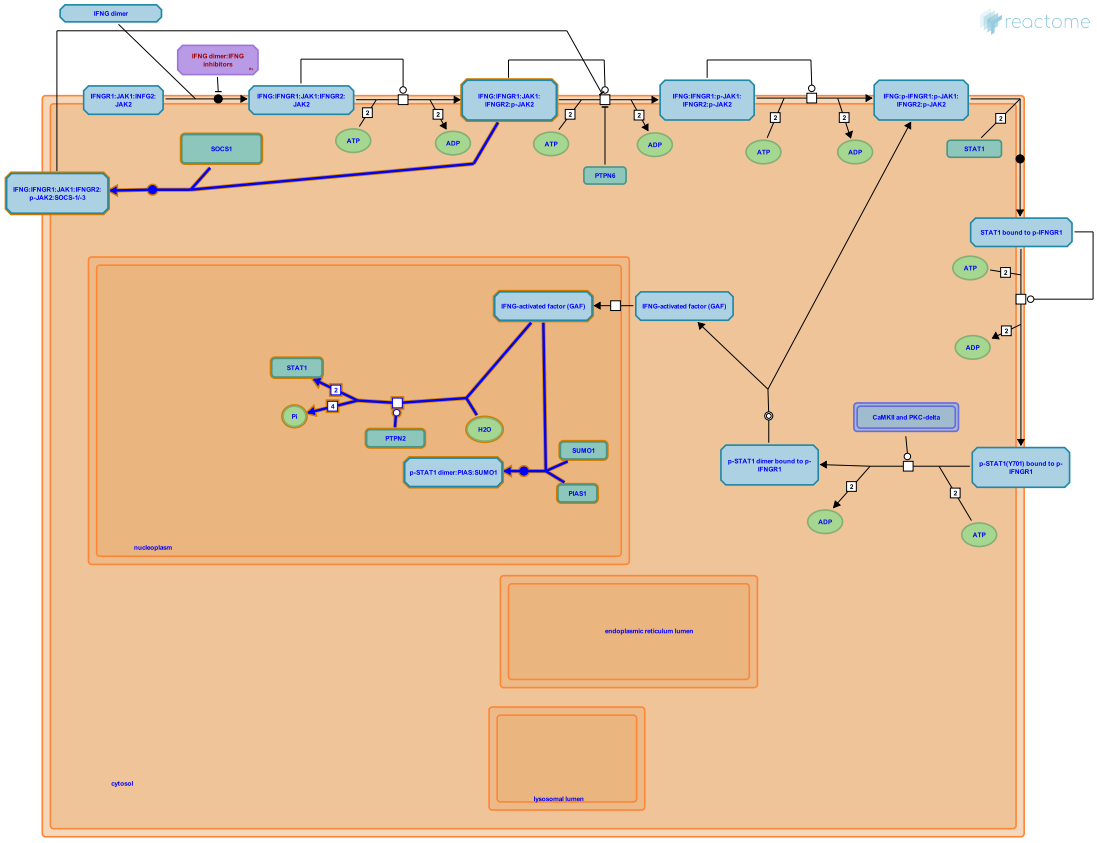

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Table of Contents