

Phosphorylation and release of IRF3

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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.

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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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *オ*

This document contains 1 reaction (see Table of Contents)

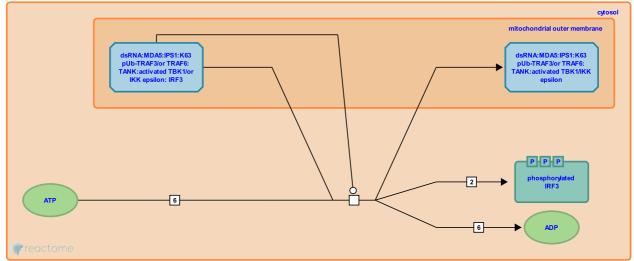
Phosphorylation and release of IRF3 7

Stable identifier: R-GGA-1227881

Type: transition

Compartments: cytosol, mitochondrial outer membrane

Inferred from: Phosphorylation and release of IRF3/IRF7 (Homo sapiens)



IRF-3 is activated by two step phosphorylation. IKK related kinases TBK1 and/or IKKi mediate the phosphorylation of the residues Ser386 and/or Ser385 (site1) and a cluster of serine/threonine residues between Ser396 and Ser405 (site 2) [Panne et al 2007]. Phosphorylation of residues in site 2 alleviates autoinhibition to allow interaction with CBP (CREB-binding protein) and facilitates phosphorylation at site 1. Phosphorylation at site 1 is required for IRF-3 dimerization.

All serine residues mentioned above were empirically defined for human IRF3. Multiple sequence alignment of human, mouse and chicken IRF3 by ClustalW showed similarity in the C-terminal domain and the following chicken residues are predicted to be involved in chicken IRF3 activation:

- Ser463 and/or Ser464 (site 1, corresponding to human Ser385 and Ser386)
- Ser474 and Ser476 (site2, corresponding to human Ser396 and Ser398 from the cluster of Ser396-Ser405)

Literature references

- Maniatis, T., Golenbock, DT., McWhirter, SM., Latz, E., Rowe, DC., Liao, SM. et al. (2003). IKKepsilon and TBK1 are essential components of the IRF3 signaling pathway. *Nat Immunol, 4*, 491-6.
- McWhirter, SM., Maniatis, T., Harrison, SC., Panne, D. (2007). Interferon regulatory factor 3 is regulated by a dual phosphorylation-dependent switch. *J Biol Chem*, 282, 22816-22.
- Hiscott, J., Lin, R., Mamane, Y. (2000). Multiple regulatory domains control IRF-7 activity in response to virus infection. J Biol Chem, 275, 34320-7. 🛪
- Hiscott, J., Paz, S., Lin, R., Romieu-Mourez, R., Goubau, D., Nakhaei, P. et al. (2006). Induction of IRF-3 and IRF-7 phosphorylation following activation of the RIG-I pathway. *Cell Mol Biol (Noisy-le-grand), 52*, 17-28.
- Nishida, E., Fukuda, M., Suhara, W., Fujita, T., Fukuhara, Y., Yoneyama, M. (1998). Direct triggering of the type I interferon system by virus infection: activation of a transcription factor complex containing IRF-3 and CBP/p300. *EMBO J, 17*, 1087-95. *¬*

Editions

2011-01-05	Authored	Shamovsky, V.
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