ISGylation of viral protein NS1

Garapati, P V., Zhang, DE.

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

26/02/2021

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.

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

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. ↗

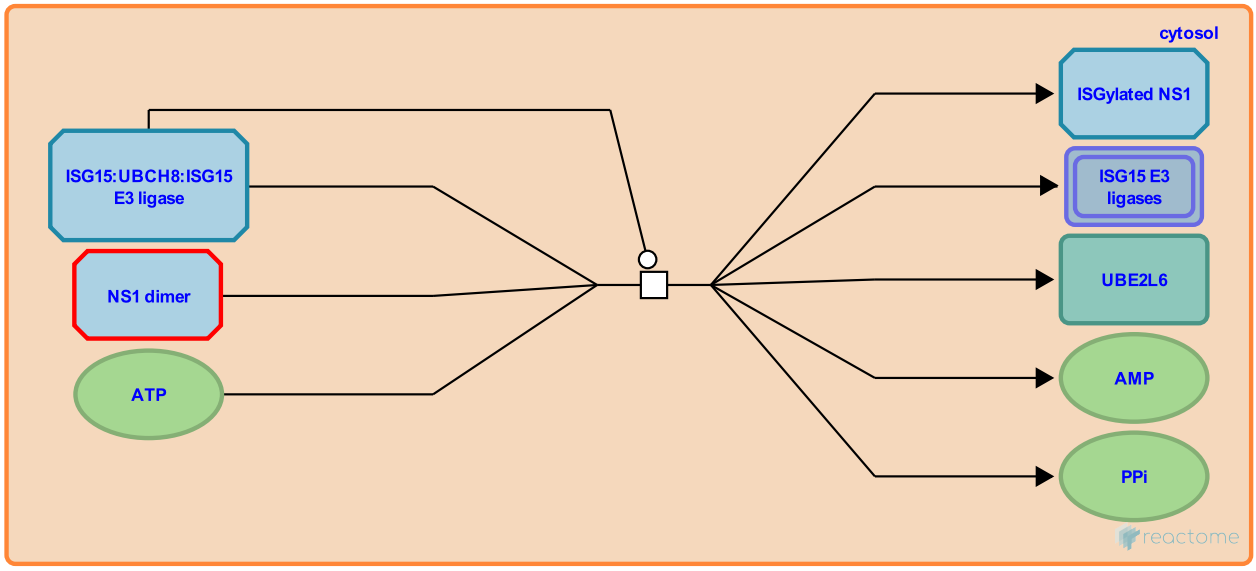
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

ISGylation of viral protein NS1

Stable identifier: R-HSA-1169395

Type: transition

Compartments: cytosol



Some viral proteins are also targeted for ISGylation. The well studied viral protein ISGylation is the modification of the influenza A viral protein NS1, which functions as an IFN antagonist during viral infection. Studies identified seven lysine residues in NS1 as potential ISGylation sites among which K41 (Zhao et al. 2010), K126 and K217 (Tang et al. 2010) were found to be critical. ISGylation at these sites disrupts NS1 association with importin-alpha, a protein required for the nuclear import of NS1.

Literature references

Zhao, C., Hsiang, TY., Kuo, RL., Krug, RM. (2010). ISG15 conjugation system targets the viral NS1 protein in influenza A virus-infected cells. *Proc Natl Acad Sci U S A, 107*, 2253-8.

Tang, Y., Zhong, G., Zhu, L., Liu, X., Shan, Y., Feng, H. et al. (2010). Herc5 attenuates influenza A virus by catalyzing ISGylation of viral NS1 protein. *J Immunol, 184*, 5777-90.

Versteeg, GA., Hale, BG., van Boheemen, S., Wolff, T., Lenschow, DJ., Garcia-Sastre, A. (2010). Species-specific antagonism of host ISGylation by the influenza B virus NS1 protein. *J Virol, 84*, 5423-30.

Editions

2011-01-18	Authored, Edited	Garapati, P V.
2011-02-11	Reviewed	Zhang, DE.