

Expression of STAT5 upregulated genes

Duenas, C., Kumar, U.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

19/05/2024

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

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: 88

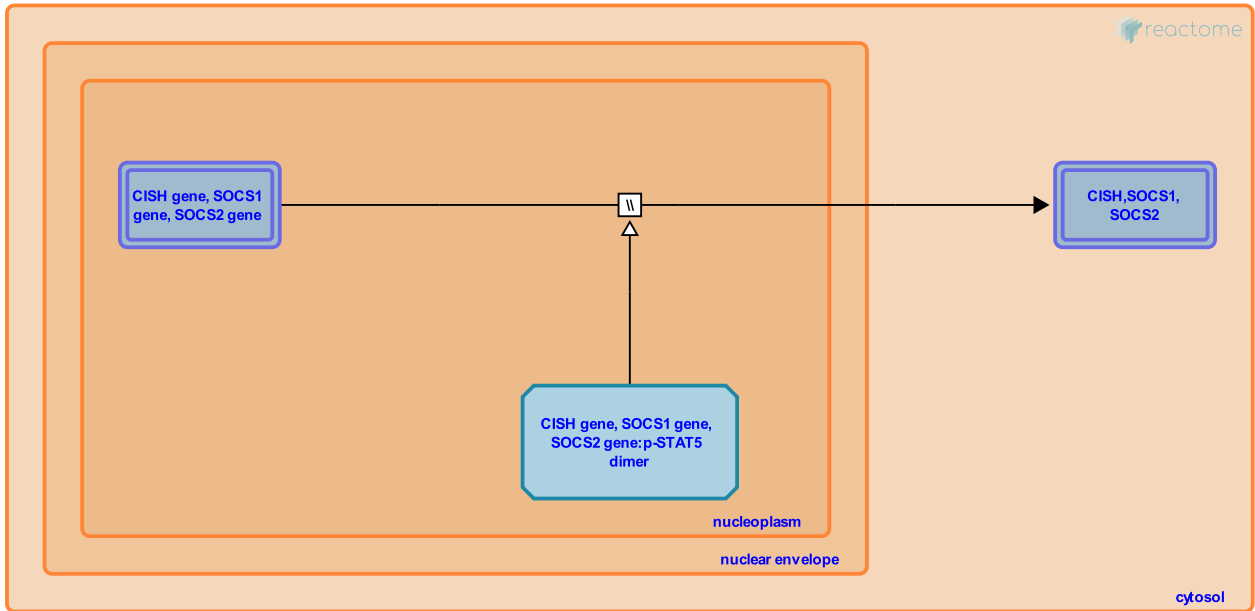
This document contains 1 reaction ([see Table of Contents](#))

Expression of STAT5 upregulated genes ↗

Stable identifier: R-HSA-8983011

Type: omitted

Compartments: cytosol, nucleoplasm



Interleukin-7 (IL7) stimulation upregulates expression of the transcripts and proteins encoding Cytokine-inducible SH2-containing protein (CISH), Suppressor of cytokine signaling 1 (SOCS1) and Suppressor of cytokine signaling 2 (SOCS2) in CD8+ T cells (Ghazawi et al. 2016).

This is a black-box event since details of the mechanism of transcription and translation are omitted.

Literature references

MacPherson, PA., Faller, EM., El-Salfiti, A., Ghazawi, FM., Parmar, P. (2016). Suppressor of cytokine signaling (SOCS) proteins are induced by IL-7 and target surface CD127 protein for degradation in human CD8 T cells. *Cell. Immunol.*, 306, 41-52. ↗

Editions

2017-07-20	Authored	Duenas, C.
2017-07-26	Edited	Duenas, C.
2017-07-26	Reviewed	Kumar, U.