

SOCS1,3:p-4Y-CSF3R:CSF3 dimer:LYN:p-Y- JAK1:p-JAK2:p-SYK:p-HCK:p-TYK2 binds CUL5, ELOB, ELOC, RNF7

May, B., Touw, IP.

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](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

07/05/2024

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](#))

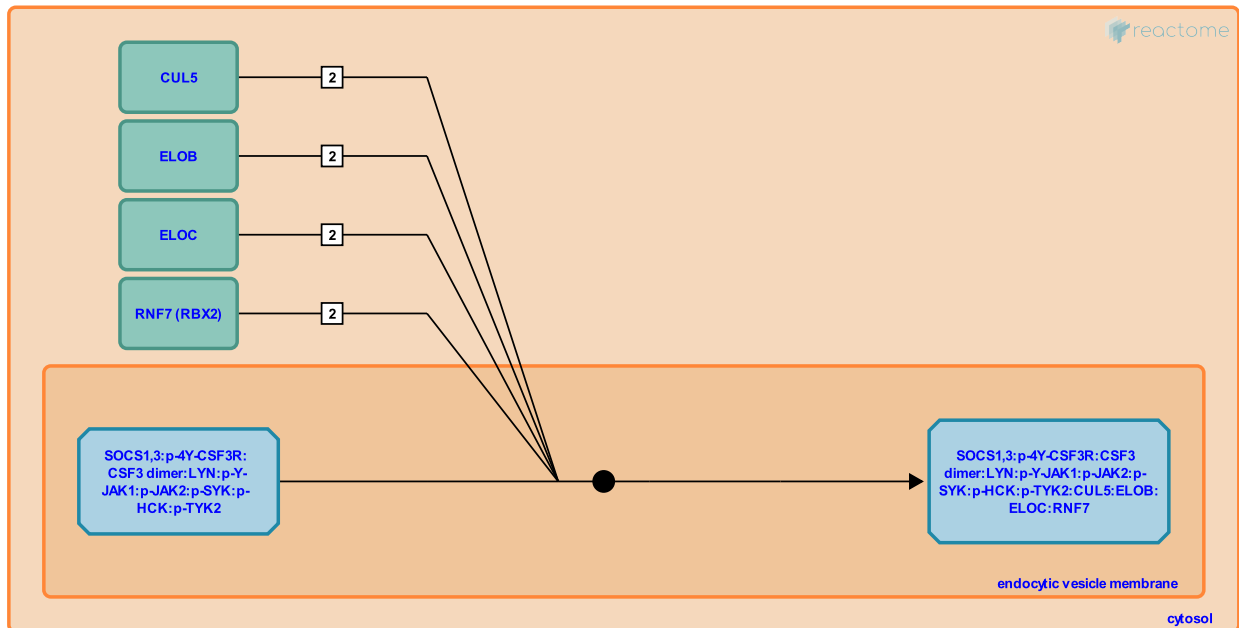
SOCS1,3;p-4Y-CSF3R:CSF3 dimer:LYN:p-Y-JAK1:p-JAK2:p-SYK:p-HCK:p-TYK2 binds CUL5, ELOB, ELOC, RNF7 [↗](#)

Stable identifier: R-HSA-9705729

Type: binding

Compartments: endocytic vesicle membrane

Inferred from: [Socs1,3;p-4Y-Csf3r:Csf3 dimer:Lyn:p-Y-Jak1:p-Jak2:p-Syk:p-Hck:p-Tyk2 binds Cul5, EloB, EloC, and Rnf7 \(Mus musculus\)](#)



SOCS1 and SOCS3 recruit Elongin B (ELOB), Elongin C (ELOC), Cullin5 (CUL5), and RNF7 to CSF3R to form a ubiquitin E3 ligase complex (Kamura et al. 2004 and inferred from mouse homologs). SOCS3 has 100-fold higher affinity for CUL5 than SOCS1 has (inferred from mouse homologs).

Literature references

Kotoshiba, S., Kamura, T., Kohda, D., Maenaka, K., Nakayama, KI., Conaway, JW. et al. (2004). VHL-box and SOCS-box domains determine binding specificity for Cul2-Rbx1 and Cul5-Rbx2 modules of ubiquitin ligases. *Genes Dev*, 18, 3055-65. [↗](#)

Editions

2020-10-24	Authored, Edited	May, B.
2020-12-12	Reviewed	Touw, IP.