

# STAT3 binds TSLP:IL7R:CRLF2

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06/05/2024

## 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](#))

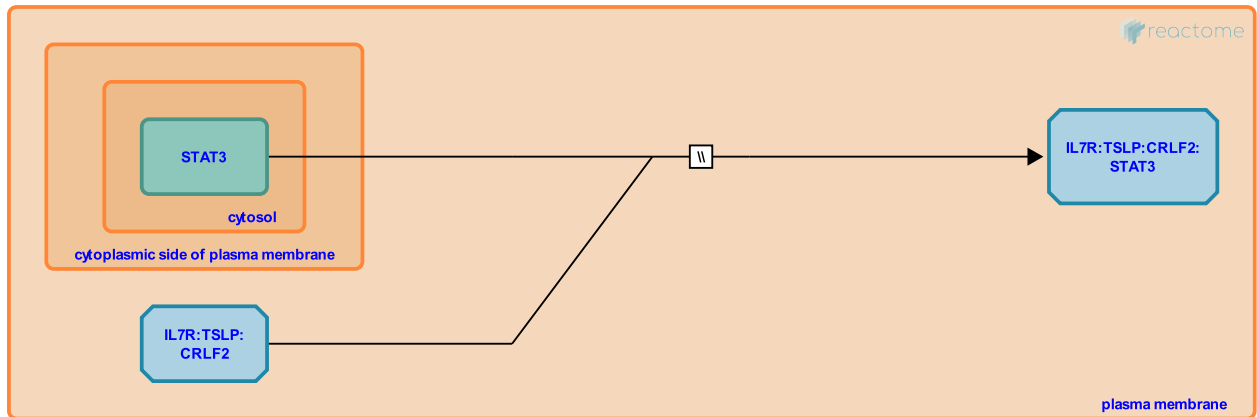
## STAT3 binds TSLP:IL7R:CRLF2 ↗

**Stable identifier:** R-HSA-8983077

**Type:** omitted

**Compartments:** cytosol, extracellular region, plasma membrane

**Inferred from:** [Stat3 binds IL7R:TSLP:CRLF2 \(Mus musculus\)](#)



Inferred from mouse: The receptor for Thymic stromal lymphopoietin (TSLP) consists of Cytokine receptor-like factor 2 (CRLF2, TSLPR) and Interleukin-7 receptor subunit alpha (IL7R). Ba/F3 cells expressing human IL7R or human TSLPR, or both stimulated with TSLP induce phosphorylation of Signal transducer and activator of transcription 3 (STAT3) and Signal transducer and activator of transcription 5A or B (STAT5A, STAT5B or STAT5), only in cells expressing both receptors (Reche et al.2001). This is a black box event since there is no experimental details confirming binding of STAT3 and STAT5 to the receptor complex.

### Editions

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