

TXLNA (IL14) binds syntaxin1A

Jupe, S., Meldal, BH.

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](#).

26/11/2020

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: 74

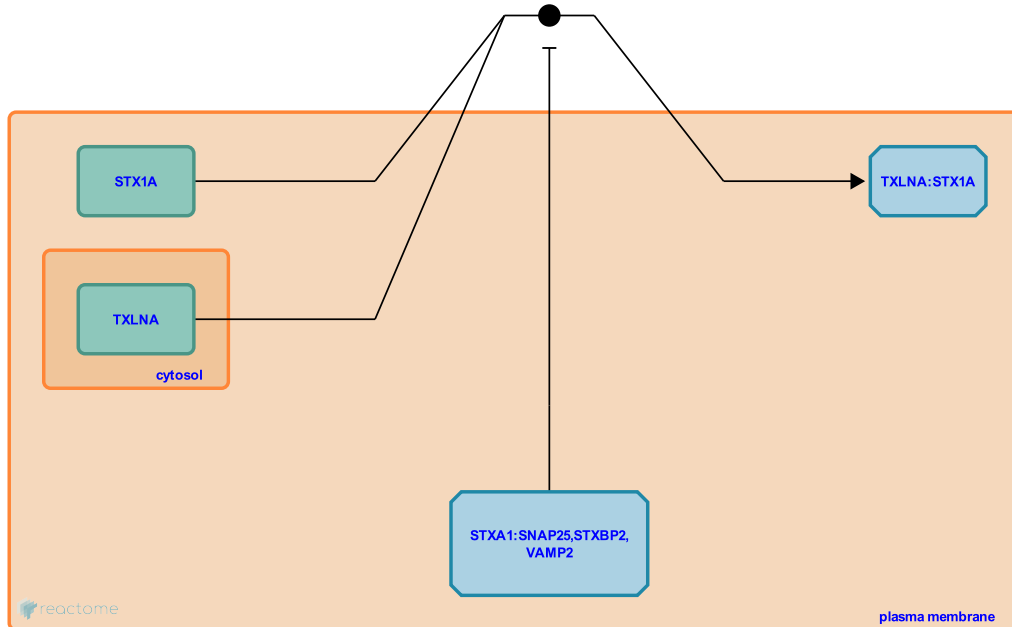
This document contains 1 reaction ([see Table of Contents](#))

TXLNA (IL14) binds syntaxin1A ↗

Stable identifier: R-HSA-449117

Type: binding

Compartments: extracellular region, plasma membrane



Interleukin-14, renamed alpha-taxilin (TXLNA) was originally described as High molecular weight B-cell growth factor (Ambrus et al. 1994). TXLNA binds several forms of syntaxin (Nogami et al. 2003), but not when they are complexed with SNAP25, VAMP2 or STXBP1, suggesting that TXLNA interacts with syntaxins outside the SNARE complex. This observation and a predicted role in intracellular vesicle trafficking led to renaming of the gene. Txl^{na} transgenic mice show a phenotype similar to systemic lupus erythematosus and Sjogren's syndrome (Shen et al. 2006).

Literature references

Nogami, S., Satoh, S., Nakano, M., Shimizu, H., Fukushima, H., Maruyama, A. et al. (2003). Taxilin; a novel syntaxin-binding protein that is involved in Ca²⁺-dependent exocytosis in neuroendocrine cells. *Genes Cells*, 8, 17-28. ↗

Editions

2014-06-04	Authored	Jupe, S.
2016-01-28	Edited	Jupe, S.
2016-01-28	Reviewed	Meldal, BH.