CL-LK binds carbohydrates on target cell surface

Jupe, S., Wakamiya, N.

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

30/04/2024

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. ↗

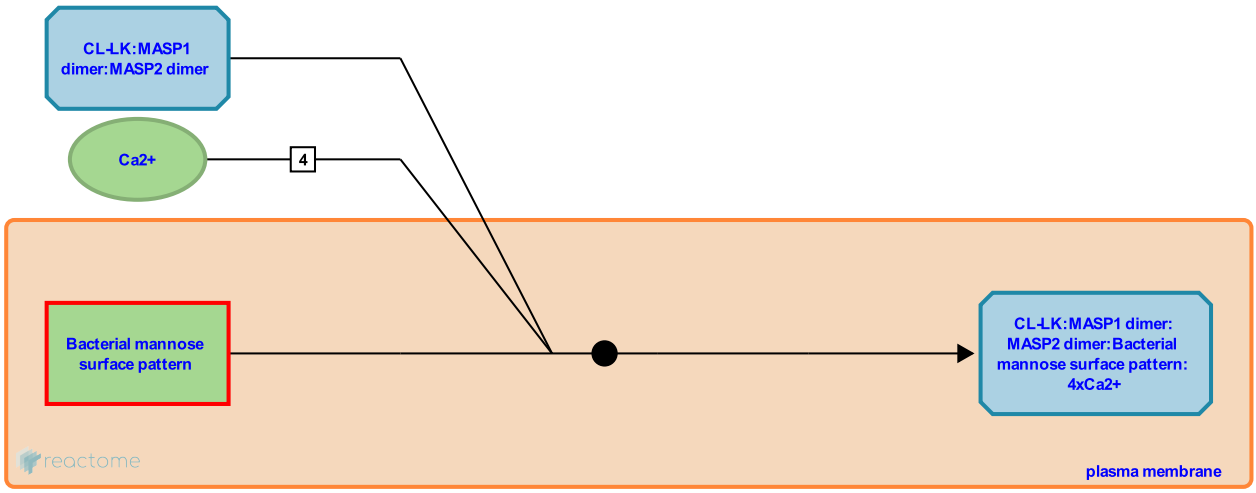
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

CL-LK binds carbohydrates on target cell surface ↗

Stable identifier: R-HSA-8852509

Type: binding

Compartments: extracellular region, plasma membrane



Collectin kidney 1 (CL-K1, CL-11, COLEC11) (Keshi et al. 2006) forms disulfide-bridged stable heteromers with collectin liver 1 (CL-L1, COLEC10) (Otahani et al. 1999), with a ratio of one COLEC10 to two COLEC11 polypeptide chains. The majority of plasma COLEC11 was found in complex with COLEC10 (Henriksen et al. 2013). The resulting COLEC10:2xCOLEC11 heterocomplex, termred CL-LK, contains multiple Ca2+ -dependent carbohydrate-recognition domains (CRDs) and collagen-like regions, which allow high-avidity binding (KD ~10-9 M) to target cell surface carbohydrate patterns (Bajic et al. 2015); COLEC11 recognizes L-fucose and D-mannose and the disaccharide D-mannose(alpha1-2)-D-mannose (Keshi et al. 2006, Hansen et al. 2010, Selman & Hansen 2012,). CL-LK can bind mannose-rich patterns on M. tuberculosis (Troegeler et al. 2015). The CL-LK complex was able to bind mannan-binding lectin-associated serine proteases (MASPs) in vitro with affinities in the nM range, and was associated with MASP1/3 and MASP2 in plasma. Upon binding to mannan or DNA in the presence of MASP2, the COLEC10:COLEC11 complex mediated deposition of C4b (Henriksen et al. 2013). Polymorphisms in the COLEC11 gene cause 3MC syndrome (Rooryck et al. 2011).

Literature references

Rasolofo, V., Nigou, J., Hansen, S., Mercier, I., Duval, C., Troegeler, A. et al. (2015). Collectin CL-LK Is a Novel Soluble Pattern Recognition Receptor for Mycobacterium tuberculosis. *PLoS ONE, 10*, e0132692. ↗

Editions

2016-01-19	Authored	Jupe, S.
2017-02-02	Edited	Jupe, S.
2017-02-07	Reviewed	Wakamiya, N.