DNMT3B:DNMT3L binds chromatin

Beekman, R., Martín-Subero, JI., May, B.

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

26/08/2021

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: 77
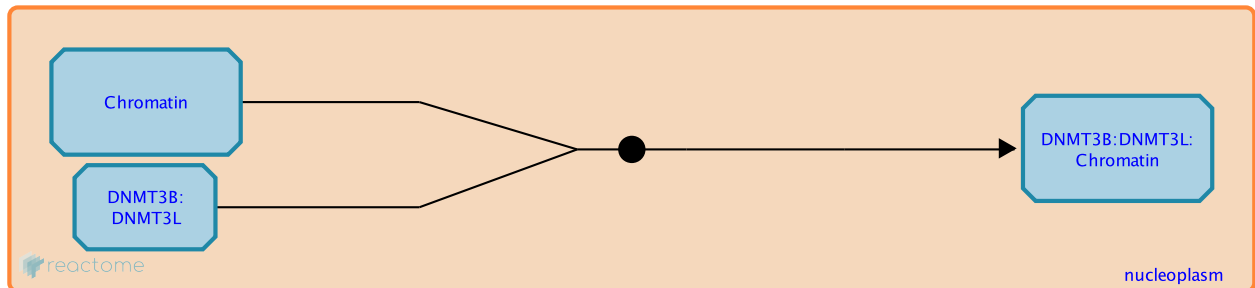
This document contains 1 reaction (see Table of Contents)

DNMT3B:DNMT3L binds chromatin ↗

Stable identifier: R-HSA-5334164

Type: binding

Compartments: nucleoplasm

Inferred from: Dnmt3b:Dnmt3l binds chromatin (Mus musculus)

The C-terminal region of DNMT3L associates with C-terminal regions of DNMT3B-isoform1 and DN-MT3B-isoform2 (Chen et al. 2005, Van Emburgh and Robertson 2011, human DNMT3L with mouse Dnmt3b in Suetake et al. 2004). DNMT3L binds the unmethylated N-terminus of histone H3 (Ooi et al. 2007), leading DNMT3L to target DNMT3B to chromatin (Wienholz et al. 2010). As inferred from mouse homologs, DNMT3B also binds the unmodified N-terminus of histone H3.

Literature references

Van Emburgh, BO., Robertson, KD. (2011). Modulation of Dnmt3b function in vitro by interactions with Dnmt3L, Dnmt3a and Dnmt3b splice variants. *Nucleic Acids Res., 39*, 4984-5002. ↗

Ooi, SK., Qiu, C., Bernstein, E., Li, K., Jia, D., Yang, Z. et al. (2007). DNMT3L connects unmethylated lysine 4 of histone H3 to de novo methylation of DNA. *Nature, 448*, 714-7. ↗

Suetake, I., Shinozaki, F., Miyagawa, J., Takeshima, H., Tajima, S. (2004). DNMT3L stimulates the DNA methylation activity of Dnmt3a and Dnmt3b through a direct interaction. *J. Biol. Chem., 279*, 27816-23. ↗

Wienholz, BL., Kareta, MS., Moarefi, AH., Gordon, CA., Ginno, PA., Chédin, F. (2010). DNMT3L modulates significant and distinct flanking sequence preference for DNA methylation by DNMT3A and DNMT3B in vivo. *PLoS Genet., 6*, e1001106. ↗

Chen, ZX., Mann, JR., Hsieh, CL., Riggs, AD., Chédin, F. (2005). Physical and functional interactions between the human DNMT3L protein and members of the de novo methyltransferase family. *J. Cell. Biochem., 95*, 902-17. ↗

Editions

2014-02-21	Authored, Edited	May, B.
2014-07-24	Reviewed	Beekman, R., Martín-Subero, JI.