

ETFBKMT transfers 3xCH₃ from 3xAdoMet to ETFB

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21/09/2024

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: 89

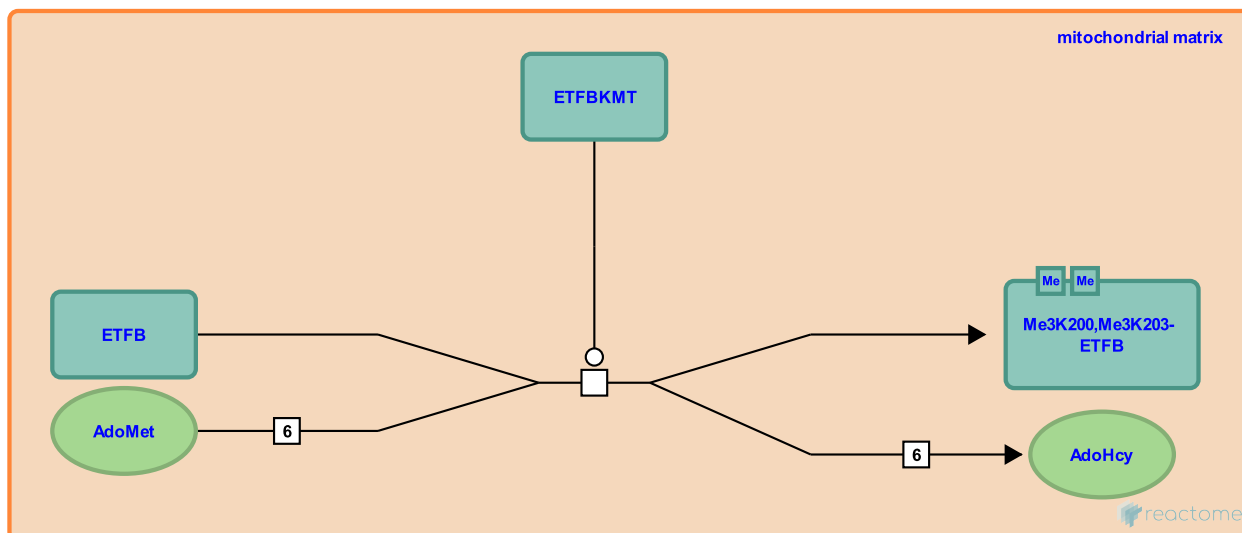
This document contains 1 reaction ([see Table of Contents](#))

ETFBKMT transfers 3xCH₃ from 3xAdoMet to ETFB ↗

Stable identifier: R-HSA-8931858

Type: transition

Compartments: mitochondrial matrix



Electron transfer flavoprotein beta subunit lysine methyltransferase (ETFBKMT, METTL20) specifically methylates Lys-200 and Lys-203 of Electron transfer flavoprotein beta (ETFB) (Rhein et al 2014, Malecki et al. 2015). ETF shuttles electrons between several FAD-containing dehydrogenases present in the mitochondrial matrix and the membrane-bound ETF:quinone oxidoreductase (Ramsay et al. 1987). ETFB is proposed to contain 'recognition loop' at residues 191–200, responsible for interaction with the dehydrogenases (Toogood et al. 2004). Methylation of ETFB impairs its ability to extract electrons from two acyl-CoA dehydrogenases, MCAD and GCDH, suggesting a functional role for ETFBKMT-mediated methylation of ETFB (Malecki et al. 2015).

Literature references

Falnes, PØ., Malecki, J., Moen, A., Dahl, HA., Ho, AY. (2015). Human METTL20 is a mitochondrial lysine methyltransferase that targets the β subunit of electron transfer flavoprotein (ETF β) and modulates its activity. *J. Biol. Chem.*, 290, 423-34. ↗

Editions

2016-06-16	Authored	Jupe, S.
2016-10-10	Reviewed	Falnes, PØ.
2016-10-10	Edited	Jupe, S.