Tet1,2,3 oxidizes 5-hydroxymethylcytosine to 5-formylcytosine

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13/05/2024

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

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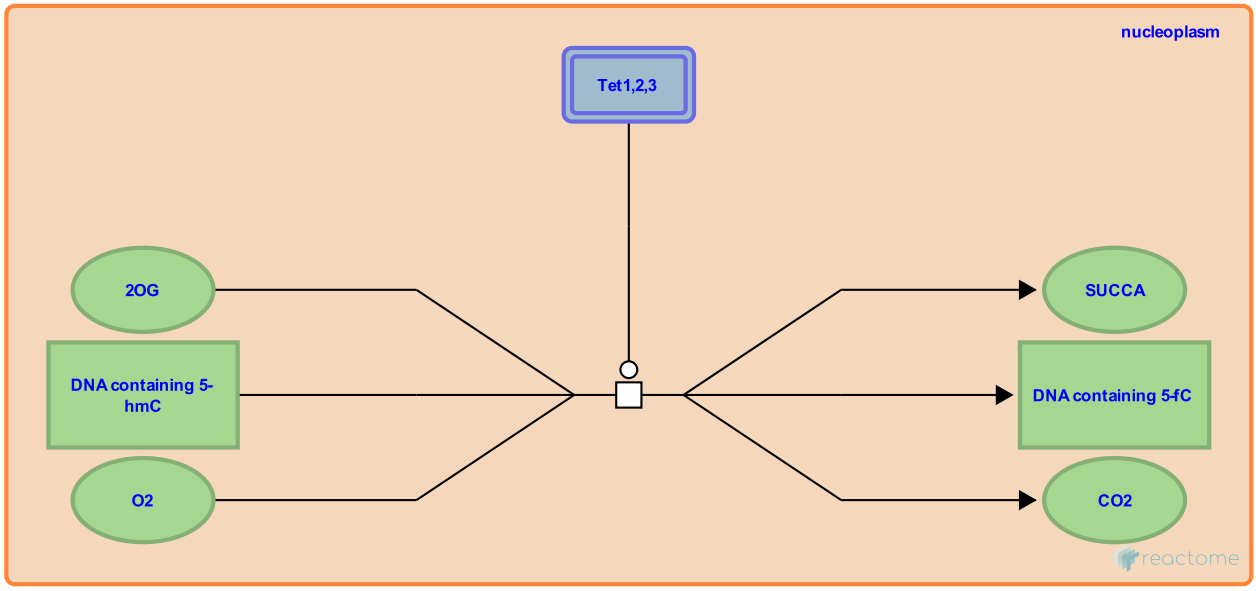
Stable identifier: R-MMU-5220931

Type: transition

Compartments: nucleoplasm



Tet1, Tet2, and Tet3 each catalyze the oxidation of 5-hydroxymethylcytosine (5-hmC) in DNA using molecular oxygen and 2-oxoglutarate to yield 5-formylcytosine (5-fC), carbon dioxide, and succinate (He et al. 2011, Ito et al. 2011, Crawford et al. 2016). 5-fC is present at lower levels than 5-hmC in the genome and is concentrated at CpG islands of transcriptionally active genes (Raiber et al.2012), transcriptionally poised enhancers (Song et al. 2013) and major satellite repeats (Shen et al. 2013). 5-fC is generated in zygotes and its persistence indicates it may be passively removed by dilution during DNA replication (Inoue et al. 2011).

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Editions

2013-12-29	Authored, Edited	May, B.
2014-01-29	Reviewed	Pfeifer, GP.
2014-02-21	Reviewed	Mukherji, M.