5' incision of damaged DNA strand by ERCC1:ERCC4 in TC-NER

Fousteri, M., Hoeijmakers, JH., Orlic-Milacic, M.

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

05/05/2024

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

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. ↗

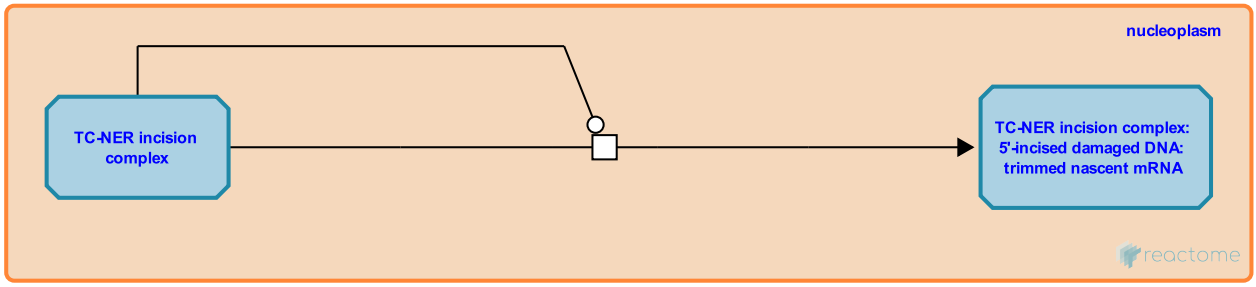
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

5' incision of damaged DNA strand by ERCC1:ERCC4 in TC-NER

Stable identifier: R-HSA-6782204

Type: transition

Compartments: nucleoplasm



In transcription-coupled nucleotide excision repair (TC-NER), just like in global genome nucleotide excision repair (GG-NER), the cleavage of the damaged strand of DNA 5' to the site of damage occurs at the junction of single-stranded DNA and double-stranded DNA that is formed when the DNA duplex is unwound. The 5' incision is carried out by ERCC1:XPF (ERCC1:ERCC4) complex and precedes the 3' incision by ERCC5 (XPG) (Staresincic et al. 2009).

Literature references

Wijgers, N., Staresincic, L., Schärer, OD., Gourdin, AM., Fagbemi, AF., Enzlin, JH. et al. (2009). Coordination of dual incision and repair synthesis in human nucleotide excision repair. *EMBO J., 28*, 1111-20.

Editions

2004-01-29	Authored	Hoeijmakers, JH.
2015-06-16	Authored, Edited	Orlic-Milacic, M.
2015-08-03	Reviewed	Fousteri, M.