

TFIIH binds GG-NER site to form a verification complex

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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.

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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. [↗](#)

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Reactome database release: 88

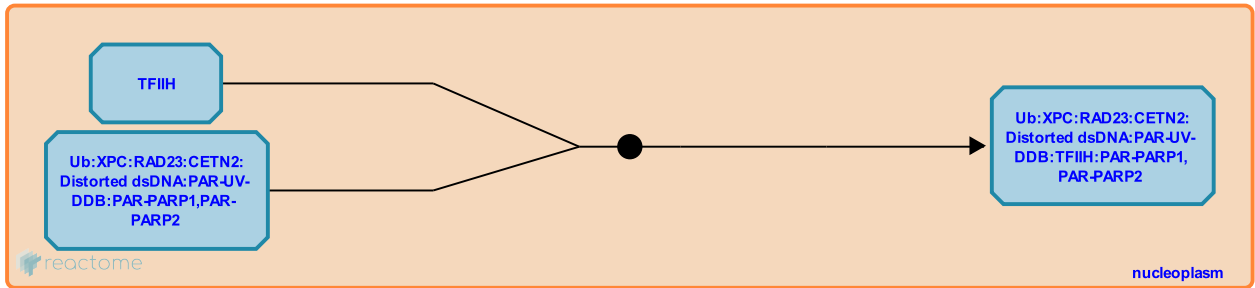
This document contains 1 reaction ([see Table of Contents](#))

TFIIH binds GG-NER site to form a verification complex

Stable identifier: R-HSA-5691000

Type: binding

Compartments: nucleoplasm



Transcription factor II H (TFIIH) complex is recruited to DNA damage sites after the damage is recognized by the XPC:RAD23:CETN2 complex and the UV-DDB complex (DDB1:DDB2) (Volker et al. 2001, Araujo and Wood 1999).

TFIIH consists of ten subunits organized into a ring-like structure (Schultz et al. 2000). The TFIIH core, also forming a ring-like structure, includes a DNA helicase ERCC3 (XPB), GTF2H1 (BTF2-p62), GTF2H2 (BTF2-p44), GTF2H3 (BTF2-p34) and GTF2H4 (BTF2-p52). GTF2H4 directly interacts with ERCC3 and anchors it to the TFIIH complex (Jawhari et al. 2002). Another DNA helicase, ERCC2 (XPD) is anchored to the TFIIH complex by binding to the GTF2H2 subunit (Coin et al. 1998). The CDK-activating kinase (CAK) complex, consisting of CCNH (cyclin H), CDK7 and MNAT1 (MAT1) is included in the TFIIH complex through an interaction with ERCC2 (Reardon et al. 1996, Rossignol et al. 1997). The tenth subunit, GTF2H5 (TTDA, TFB5, BTF2-p5) is important for the stability of the TFIIH complex (Giglia-Mari et al. 2004). The TFIIH complex binds the DNA damage site after XPC:RAD23:CETN2 complex recognizes the damage (Volker et al. 2001, Riedl et al. 2003), and the ERCC3 and GTF2H1 subunits of TFIIH directly interact with XPC (Yokoi et al. 2003).

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Editions

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