ERCC8 (CSA) binds stalled RNA Pol II

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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

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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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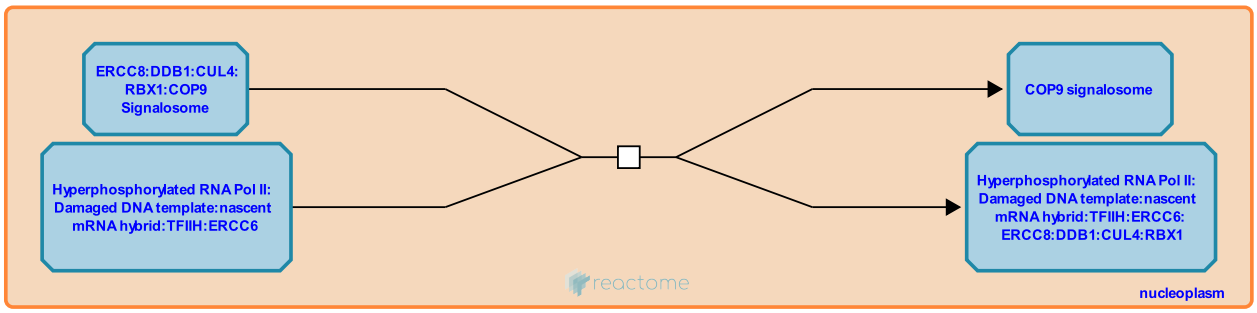
Stable identifier: R-HSA-6781833

Type: transition

Compartments: nucleoplasm



Cockayne syndrome protein A (ERCC8, also known as CSA) is recruited to a stalled RNA polymerase II complex (RNA Pol II) at a site of DNA damage in an ERCC6 (CSB) dependent manner (Kamiuchi et al. 2002; van der Weegen et al. 2020). ERCC8 is part of an ubiquitin ligase complex that, in addition to ERCC8, also contains DDB1, CUL4 (CUL4A or CUL4B) and RBX1 (Groisman et al. 2003). The COP9 signalosome complex prevents the ubiquitin ligase activity of the ERCC8:DDB1:CUL4:RBX1 at the early steps after DNA damage induction (Groisman et al. 2003, Fischer et al. 2011).

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Editions

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