FA core complex assembles at DNA inter-strand crosslinks (ICLs)

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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. ↗

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. ↗

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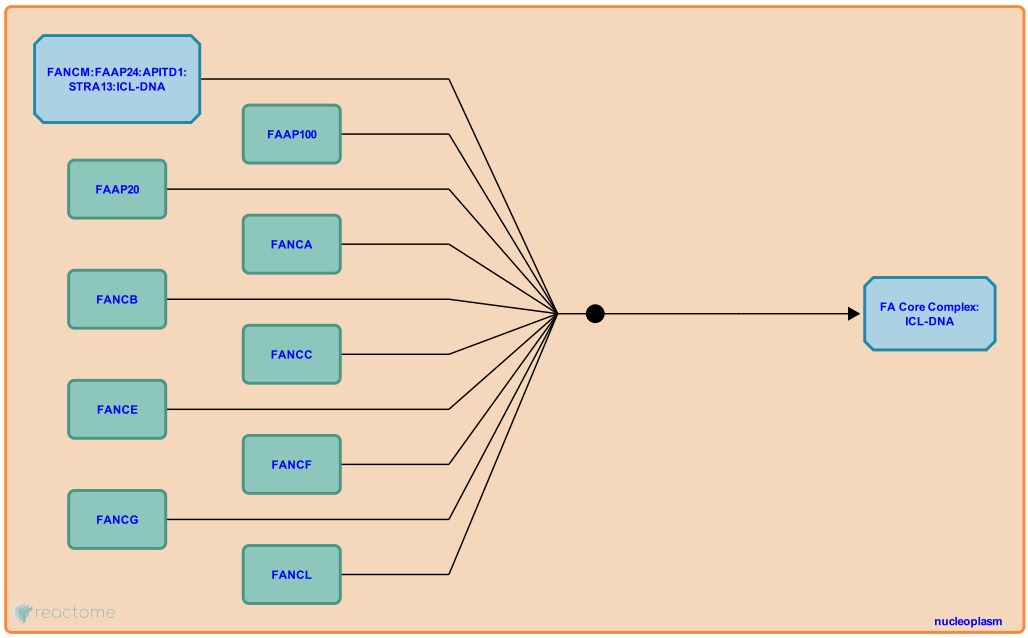
Stable identifier: R-HSA-6785126

Type: binding

Compartments: nucleoplasm



In addition to FANCM, FAAP24, APITD1 (MHF1) and STRA13 (MHF2), the FA core complex also includes FANCA, FANCB, FANCC, FANCE, FANCF, FANCG, FANCL, FAAP20 and FAAP100 (Singh et al. 2010, Yan et al. 2010, Leung et al. 2012). While FANCA, FANCB, FANCC, FANCE, FANCF, FANCG and FANCL, and probably FAAP20 and FAAP100, can assemble a complex in the nucleoplasm, they are unable to load onto DNA in the absence of FANCM and FAAP24 (Kim et al. 2008, Yan et al. 2010, Leung et al. 2012).

Literature references

Singh, TR., Saro, D., Ali, AM., Zheng, XF., Du, CH., Killen, MW. et al. (2010). MHF1-MHF2, a histone-fold-containing protein complex, participates in the Fanconi anemia pathway via FANCM. *Mol. Cell, 37*, 879-86.

Yan, Z., Delannoy, M., Ling, C., Daee, D., Osman, F., Muniandy, PA. et al. (2010). A histone-fold complex and FANCM form a conserved DNA-remodeling complex to maintain genome stability. *Mol. Cell, 37*, 865-78.

Leung, JW., Wang, Y., Fong, KW., Huen, MS., Li, L., Chen, J. (2012). Fanconi anemia (FA) binding protein FAAP20 stabilizes FA complementation group A (FANCA) and participates in interstrand cross-link repair. *Proc. Natl. Acad. Sci. U.S.A., 109*, 4491-6.

Kim, JM., Kee, Y., Gurtan, A., D'Andrea, AD. (2008). Cell cycle-dependent chromatin loading of the Fanconi anemia core complex by FANCM/FAAP24. *Blood, 111*, 5215-22.

Editions

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