Autocleavage of ESPL1 (Separase)

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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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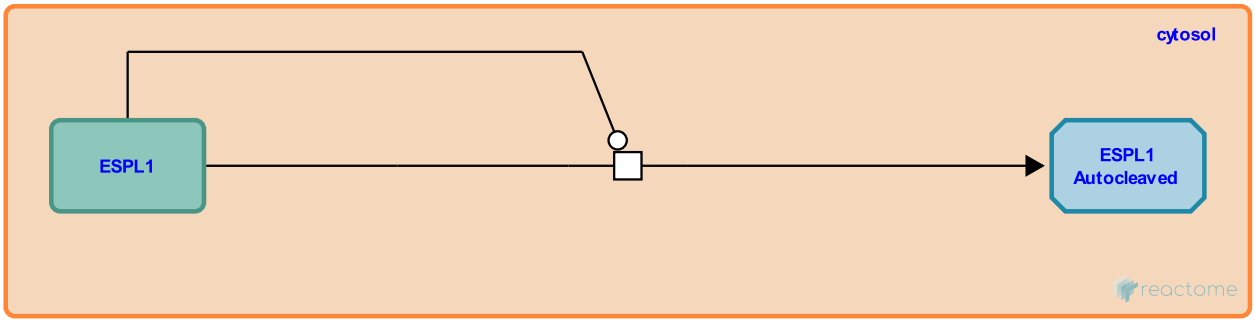
Stable identifier: R-HSA-2467775

Type: transition

Compartments: cytosol



After APC/C-mediated degradation of PTTG1 (securin), ESPL1 (separin i.e. separase) is rapidly autocatalytically cleaved after arginine residues at positions 1506 and 1535. The N-terminal and C-terminal fragments remain bound to each other after cleavage. It has not been examined what happens with the short middle fragment of ESPL1, so it is annotated as a part of the autocleaved ESPL1 complex. The autocatalytic cleavage of ESPL1 is not a prerequisite for the subsequent cleavage of the cohesin subunit RAD21 (Waizenegger et al. 2002).

Literature references

Peters, JM., Waizenegger, I., Wernic, D., Giménez-Abián, JF. (2002). Regulation of human separase by securin binding and autocleavage. *Curr. Biol., 12,* 1368-78.

Editions

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