Microprocessor complex cleaves pri-miRNA to pre-miRNA

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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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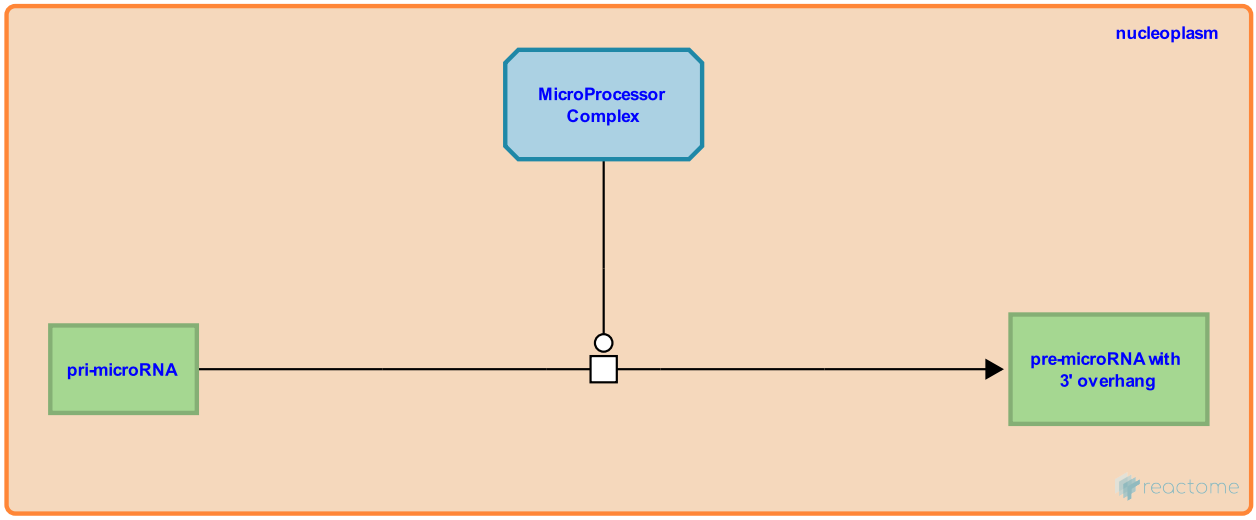
Stable identifier: R-HSA-203893

Type: transition

Compartments: nucleoplasm



Nuclear processing by Drosha Microprocessor complex. The primary-microRNA (pri-miRNA) is recognized by the Microprocessor complex (Drosha:DGCR8) and both strands of the pri-miRNA are cleaved by Drosha near the free 5' and 3' ends of the pri-miRNA, that is, at the ends distal from the internal loop. The product is a double-stranded RNA having 2 nucleotides protruding at the 3' end and having an internal loop.

Literature references

Song, H., Lim, DH., Kwon, YS., Lee, YS., Seong, Y., Kim, A. et al. (2014). Global identification of target recognition and cleavage by the Microprocessor in human ES cells. *Nucleic Acids Res., 42*, 12806-21. ↗

Gregory, RI., Doratotaj, B., Chendrimada, TP., Shiekhattar, R., Amuthan, G., Cooch, N. et al. (2004). The Microprocessor complex mediates the genesis of microRNAs. *Nature, 432*, 235-40. ↗

Kim, YK., Kim, VN., Yeom, KH., Jin, H., Han, J., Lee, Y. (2004). The Drosha-DGCR8 complex in primary microRNA processing. *Genes Dev, 18*, 3016-27. ↗

Kim, S., Provost, P., Ahn, C., Kim, J., Yim, J., Kim, VN. et al. (2003). The nuclear RNase III Drosha initiates microRNA processing. *Nature, 425*, 415-9. ↗

Editions

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