

C3PO hydrolyzes cleaved passenger strand

Gopinathrao, G., May, B., Tomari, Y.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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. [↗](#)

Reactome database release: 88

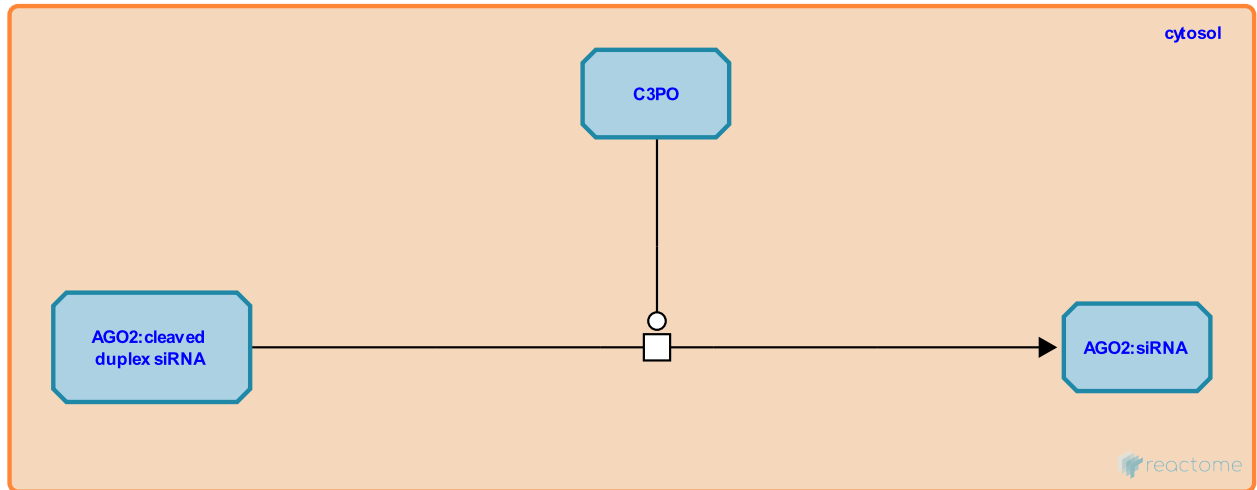
This document contains 1 reaction ([see Table of Contents](#))

C3PO hydrolyzes cleaved passenger strand ↗

Stable identifier: R-HSA-9023909

Type: transition

Compartments: cytosol



C3PO appears to act as a nuclease that hydrolyzes the passenger strand after cleavage by AGO2. C3PO could also be part of a DICER1-independent pathway for loading AGO2. AGO2 of humans may contain either miRNAs or siRNAs.

The mechanism that selects which strand is retained as the guide RNA is not well understood in humans. Overhanging nucleotides and strength of base-pairing at each end of the input duplex are observed to influence strand selection.

Literature references

- Hammond, SM., Marsden, CG., Liu, J., Carmell, MA., Hannon, GJ., Song, JJ. et al. (2004). Argonaute2 is the catalytic engine of mammalian RNAi. *Science*, 305, 1437-41. ↗
- Schwille, P., Mütze, J., Crell, K., Weinmann, L., Staroske, W., Höck, J. et al. (2008). Fluorescence correlation spectroscopy and fluorescence cross-correlation spectroscopy reveal the cytoplasmic origination of loaded nuclear RISC in vivo in human cells. *Nucleic Acids Res*, 36, 6439-49. ↗
- Betancur, JG., Tomari, Y. (2012). Dicer is dispensable for asymmetric RISC loading in mammals. *RNA*, 18, 24-30. ↗
- Rana, TM., Robb, GB. (2007). RNA helicase A interacts with RISC in human cells and functions in RISC loading. *Mol Cell*, 26, 523-37. ↗
- Kawamata, T., Iwasaki, S., Ye, X., Paroo, Z., Tomari, Y., Yoda, M. et al. (2010). ATP-dependent human RISC assembly pathways. *Nat Struct Mol Biol*, 17, 17-23. ↗

Editions

2007-11-19	Authored	Gopinathrao, G., May, B.
2009-06-10	Edited	May, B.
2012-02-11	Reviewed	Tomari, Y.