AIM2 binds dsDNA

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19/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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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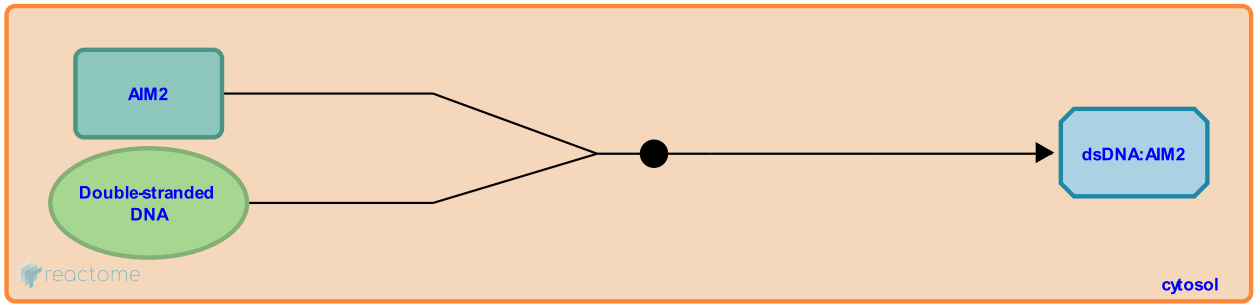
Stable identifier: R-HSA-844619

Type: binding

Compartments: cytosol



AIM2 binds to cytosolic dsDNA via its C-terminal HIN domain. The source of the dsDNA can be can be viral, bacterial or derived from the host (Hornung et al. 2009, Muruve et al. 2008). Multiple AIM2 molecules may bind the same dsDNA (Fernandes-Alnemri et al. 2008).

Literature references

Horvath, G., Fitzgerald, KA., Ablasser, A., Bauernfeind, FG., Latz, E., Hornung, V. et al. (2009). AIM2 recognizes cytosolic dsDNA and forms a caspase-1-activating inflammasome with ASC. *Nature, 458*, 514-8.

Wu, J., Datta, P., Alnemri, ES., Yu, JW., Fernandes-Alnemri, T. (2009). AIM2 activates the inflammasome and cell death in response to cytoplasmic DNA. *Nature, 458*, 509-13.

Burckstummer, T., Colinge, J., Superti-Furga, G., Bilban, M., Dixit, E., Bennett, KL. et al. (2009). An orthogonal proteomic-genomic screen identifies AIM2 as a cytoplasmic DNA sensor for the inflammasome. *Nat Immunol, 10*, 266-72.

Editions

2010-04-22	Authored	Jupe, S.
2011-04-28	Edited	Jupe, S.
2011-04-28	Reviewed	Kufer, TA.
2011-06-06	Reviewed	Rittinger, K., Wong, E.