

Serum amyloid P binds DNA and chromat-

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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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *对*

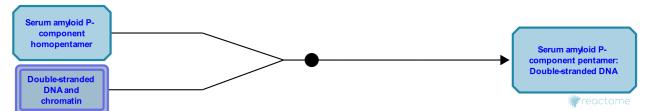
This document contains 1 reaction (see Table of Contents)

Serum amyloid P binds DNA and chromatin 🛪

Stable identifier: R-HSA-977224

Type: binding

Compartments: extracellular region



Serum amyloid P component (SAP) binds DNA and chromatin in a calcium dependent manner in physiological conditions (Pepys et al. 1987). This binding displaces H1-type histones (Butler et al. 1990), solubilizing chromatin which is otherwise insoluble in extracellular fluids. SAP may therefore participate in the in vivo handling of chromatin exposed by cell death. SAP knockout mice spontaneously develop antinuclear autoimmunity and severe glomerulonephritis, a phenotype resembling human systemic lupus erythematosus, a serious autoimmune disease, suggesting that SAP binding may play a role in reducing the immunogenicity of chromatin and preventing autoimmunity (Bickerstaff et al. 1999).

Literature references

- Butler, PJ., Williams, DG., Tennent, GA., Booth, SE., Pepys, MB. (1994). Binding of pentraxins to different nuclear structures: C-reactive protein binds to small nuclear ribonucleoprotein particles, serum amyloid P component binds to chromatin and nucleoli. *Clin Exp Immunol, 97*, 152-7.
- Butler, PJ., Pepys, MB. (1987). Serum amyloid P component is the major calcium-dependent specific DNA binding protein of the serum. *Biochem Biophys Res Commun*, 148, 308-13. ↗

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