

SORL1 binds APP(18-770)

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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

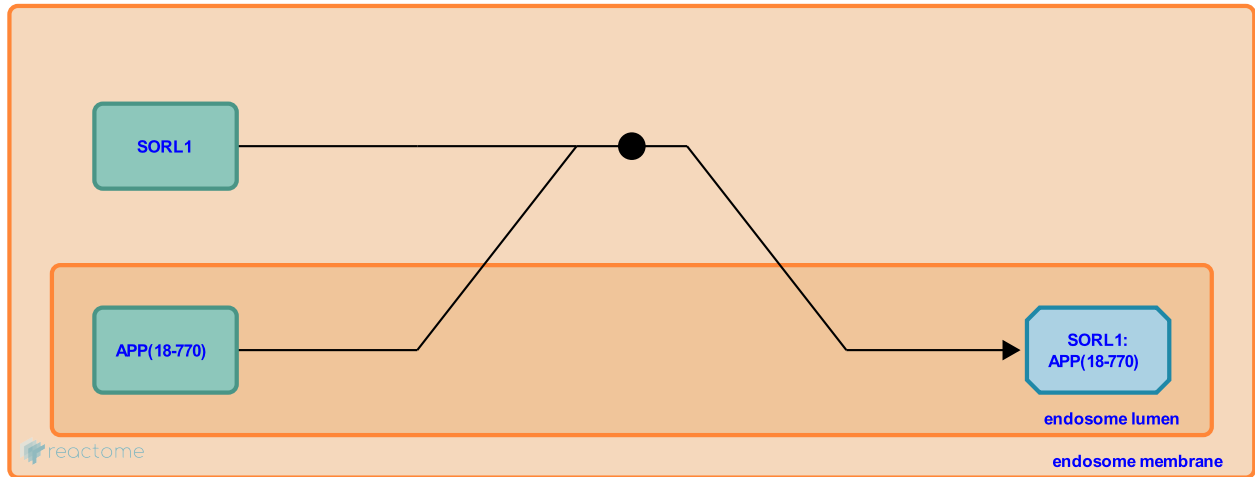
This document contains 1 reaction ([see Table of Contents](#))

SORL1 binds APP(18-770) [↗](#)

Stable identifier: R-HSA-8871494

Type: binding

Compartments: endosome lumen, endosome membrane



The sortilin-related receptor (SORL1) is expressed mainly in brain, where it is most abundant in the cerebellum, cerebral cortex and the occipital pole. It acts as a sorting receptor that mediates anterograde and retrograde movement of APP between the trans-Golgi network and early endosomes, thereby restricting delivery of the APP precursor to endocytic compartments that favour amyloidogenic peptide production (Andersen et al. 2005, Willnow & Andersen 2013, Yin et al. 2015, Hermey 2015). Targeting SORL1 might present novel opportunities for Alzheimer's disease therapy.

Literature references

- Andersen, OM., Willnow, TE. (2013). Sorting receptor SORLA--a trafficking path to avoid Alzheimer disease. *J. Cell. Sci.*, 126, 2751-60. [↗](#)
- Hermey, G. (2015). Intracellular sorting pathways of the amyloid precursor protein provide novel neuroprotective strategies. *Neural Regen Res*, 10, 1727-8. [↗](#)
- Jansen, P., Schmidt, V., Hyman, BT., Reiche, J., Breiderhoff, T., Wu, X. et al. (2005). Neuronal sorting protein-related receptor sorLA/LR11 regulates processing of the amyloid precursor protein. *Proc. Natl. Acad. Sci. U.S.A.*, 102, 13461-6. [↗](#)
- Yin, RH., Tan, L., Yu, JT. (2015). The Role of SORL1 in Alzheimer's Disease. *Mol. Neurobiol.*, 51, 909-18. [↗](#)

Editions

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