

CHST4 transfers SO₄(²⁻) from PAPS to Core 2 mucins

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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: 70

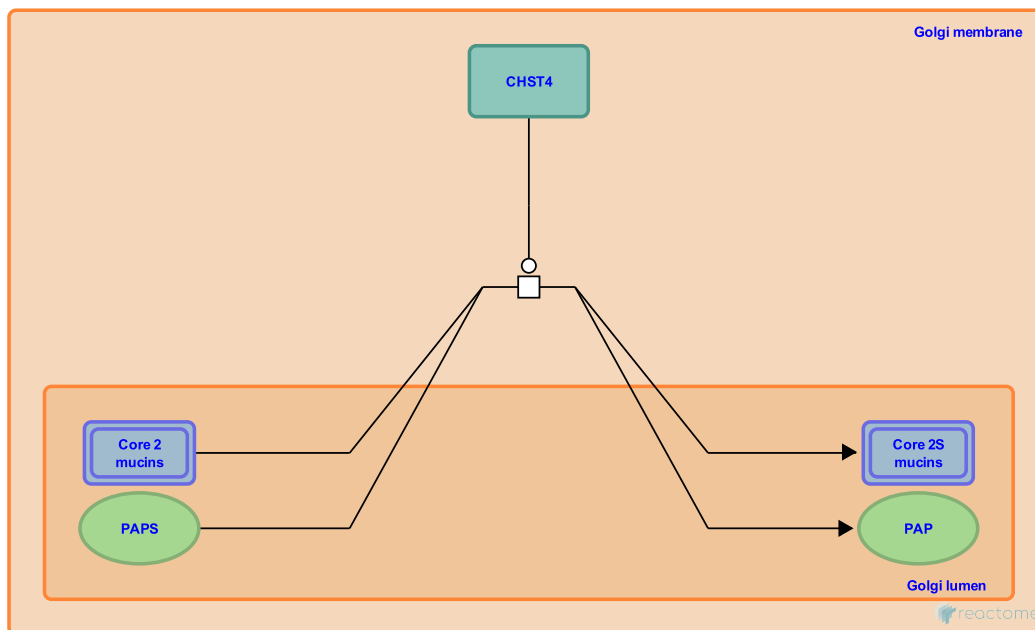
This document contains 1 reaction ([see Table of Contents](#))

CHST4 transfers SO4(2-) from PAPS to Core 2 mucins ↗

Stable identifier: R-HSA-6786012

Type: transition

Compartments: Golgi membrane, Golgi lumen



Carbohydrate sulfotransferase 4 (CHST4) transfers sulfate (SO₄(2-)) from the high energy donor 3'-phospho-5'-adenylyl sulfate (PAPS) to position 6 of non-reducing N-acetylglucosamine (GlcNAc) residues of mucin-associated glycans that ultimately serve as SELL ligands which are present in high endothelial cells (HEVs) and play a central role in lymphocyte homing at sites of inflammation. CHST4 preferentially sulfates Core 2 mucins (Bistrup et al. 1999). CHST4 is localised to the Golgi membrane (de Graffenried & Bertozzi 2004).

Literature references

de Graffenried, CL., Bertozzi, CR. (2003). Golgi localization of carbohydrate sulfotransferases is a determinant of L-selectin ligand biosynthesis. *J. Biol. Chem.*, 278, 40282-95. ↗

Bistrup, A., Bhakta, S., Lee, JK., Belov, YY., Gunn, MD., Zuo, FR. et al. (1999). Sulfotransferases of two specificities function in the reconstitution of high endothelial cell ligands for L-selectin. *J. Cell Biol.*, 145, 899-910. ↗

Editions

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