

# BESTs transport cytosolic Cl<sup>-</sup> to extracellular region

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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

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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. [↗](#)

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Reactome database release: 90

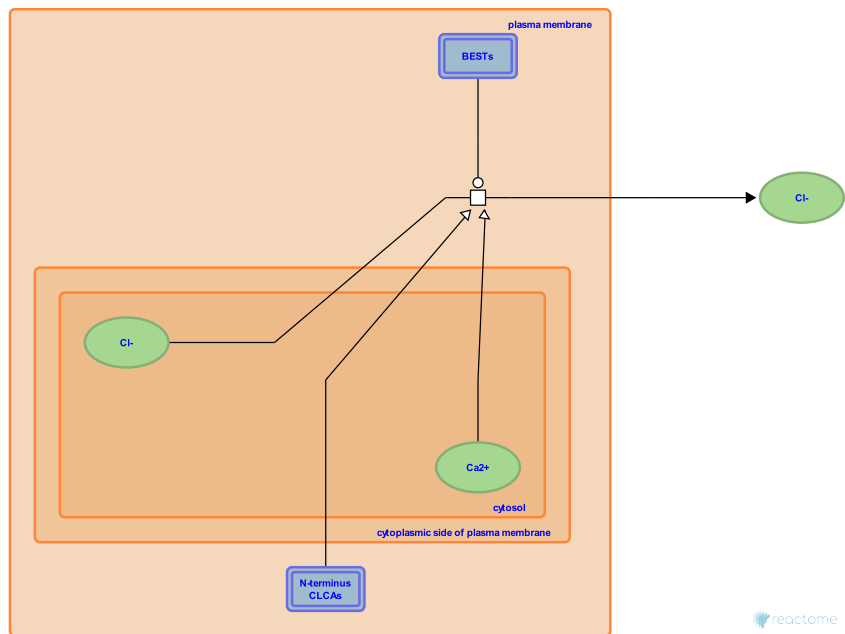
This document contains 1 reaction ([see Table of Contents](#))

**BESTs transport cytosolic Cl<sup>-</sup> to extracellular region** ↗

**Stable identifier:** R-HSA-2744361

**Type:** transition

**Compartments:** cytosol, extracellular region, plasma membrane



Bestrophins 1-4 (BEST1-4, aka vitelliform macular dystrophy proteins) mediate cytosolic Cl<sup>-</sup> efflux across plasma membranes. This transport is sensitive to intracellular Ca<sup>2+</sup> concentrations (Sun et al. 2002, Tsunenari et al. 2003). Mutations in bestrophins that impair their function are implicated in macular degeneration in the eye. Defects in BEST1 cause vitelliform macular dystrophy (BVMD, Best's disease, MIM:153700), an autosomal dominant form of macular degeneration that usually begins in childhood and is characterized lesions due to abnormal accumulation of lipofuscin within and beneath retinal pigment epithelium (RPE) cells (Marquardt et al. 1998, Petrukhin et al. 1998). All CLCAs contain a consensus cleavage motif which is recognised by an internal zincin metalloprotease domain within the N terminus. Self-proteolysis within the secretory pathway yields N- and C-terminal fragments, a step critical for CLCA activation of calcium-activated chloride channels (CaCCs) mediated through the N-terminal fragment (Yurtsever et al. 2012).

**Literature references**

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**Editions**

2012-12-06	Authored, Edited	Jassal, B.
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