

HMGCR gene expression

Aletta, J M., Rothfels, K.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

08/05/2024

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. [↗](#)

Reactome database release: 88

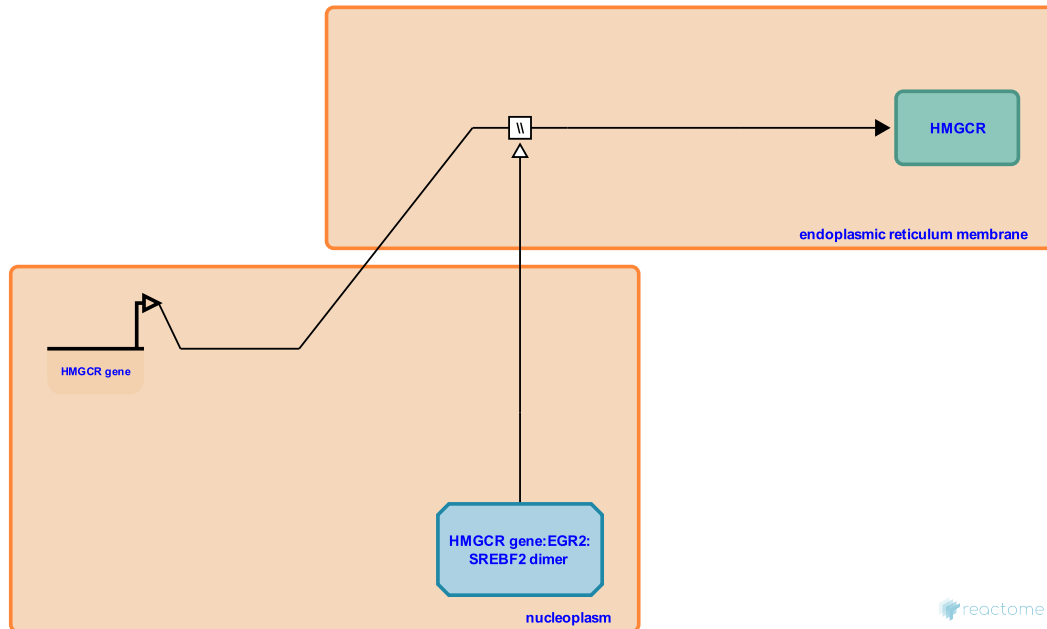
This document contains 1 reaction ([see Table of Contents](#))

HMGR gene expression ↗

Stable identifier: R-HSA-9621410

Type: omitted

Compartments: nucleoplasm, endoplasmic reticulum membrane



Cholesterol is highly enriched in the Schwann cell membrane and it plays an essential role in the maturation of MPZ, a key protein component of the compact myelin sheath (Saher and Simons, 2010). The cholesterol of the myelin sheath is synthesized within the Schwann cells, rather than being absorbed from the blood (Jurevics and Morell, 1994; Jurevics et al, 1998). Consistent with this, a number of genes involved in the cholesterol biosynthesis pathway are upregulated during the myelination program, including HMG synthase and HMG coenzyme-A reductase (HMGR) (Nagarajan et al, 2001; Verheijen et al, 2003; Le Blanc et al, 2005; Jang et al, 2010; Kim et al, 2016; reviewed in Camargo et al, 2009). Myelin-specific expression of HMGR depends on binding of sterol response binding factor 2 (SREBF2) to its cognate SRE site in the HMGR promoter (Vallett et al, 1996; Pai et al, 1998; LeBlanc et al, 2005). SREBF2-dependent expression of HMGR is increased with co-expression of EGR2, suggesting that the transcription factors synergistically activate expression (LeBlanc et al, 2005).

Literature references

- Camargo, N., Verheijen, MH., Smit, AB. (2009). SREBPs: SREBP function in glia-neuron interactions. *FEBS J.*, 276, 628-36. ↗
- Nagarajan, R., Keles, S., Jones, EA., Sun, G., Chang, LW., Svaren, J. et al. (2010). Locus-wide identification of Egr2/Krox20 regulatory targets in myelin genes. *J. Neurochem.*, 115, 1409-20. ↗
- Wrabetz, L., Gillian-Daniel, AL., Mager, GM., Ferri, C., Svaren, J., Leblanc, SE. et al. (2005). Regulation of cholesterol/lipid biosynthetic genes by Egr2/Krox20 during peripheral nerve myelination. *J. Neurochem.*, 93, 737-48. ↗
- Verheijen, MH., Chrast, R., Burrola, P., Lemke, G. (2003). Local regulation of fat metabolism in peripheral nerves. *Genes Dev.*, 17, 2450-64. ↗
- Toews, AD., Morell, P., Bouldin, TW., Jurevics, H. (1998). Regenerating sciatic nerve does not utilize circulating cholesterol. *Neurochem. Res.*, 23, 401-6. ↗

Editions

2019-08-16	Authored	Rothfels, K.
2020-01-17	Reviewed	Aletta, J M.
2020-02-24	Edited	Rothfels, K.