

EGR2 and SREBF2 dimer bind SCD5 gene

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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

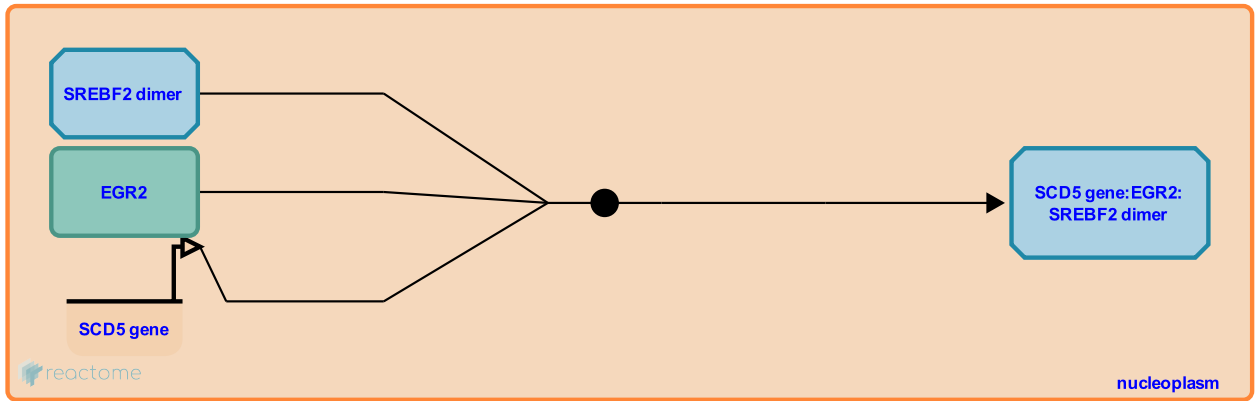
This document contains 1 reaction ([see Table of Contents](#))

EGR2 and SREBF2 dimer bind SCD5 gene ↗

Stable identifier: R-HSA-9621400

Type: binding

Compartments: nucleoplasm



SCD5 expression is upregulated during Schwann cell myelination in an EGR2- and SREBF2 dependent manner (LeBlanc et al, 2005; Jang et al, 2010). SCD5 encodes a stearyl-CoA desaturase involved in long chain fatty acid biosynthesis (Wang et al, 2005; Zhang et al, 2005).

Literature references

Shi, Y., Yang, Y., Zhang, S. (2005). Characterization of human SCD2, an oligomeric desaturase with improved stability and enzyme activity by cross-linking in intact cells. *Biochem. J.*, 388, 135-42. ↗

Cao, G., Wang, J., Su, C., Yu, L., Huang, X., Schmidt, RE. et al. (2005). Characterization of HSCD5, a novel human stearyl-CoA desaturase unique to primates. *Biochem. Biophys. Res. Commun.*, 332, 735-42. ↗

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. ↗

Editions

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