

D'Eustachio, P., Hannun, YA., Jassal, B., Luberto, C.

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](#).

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: 70

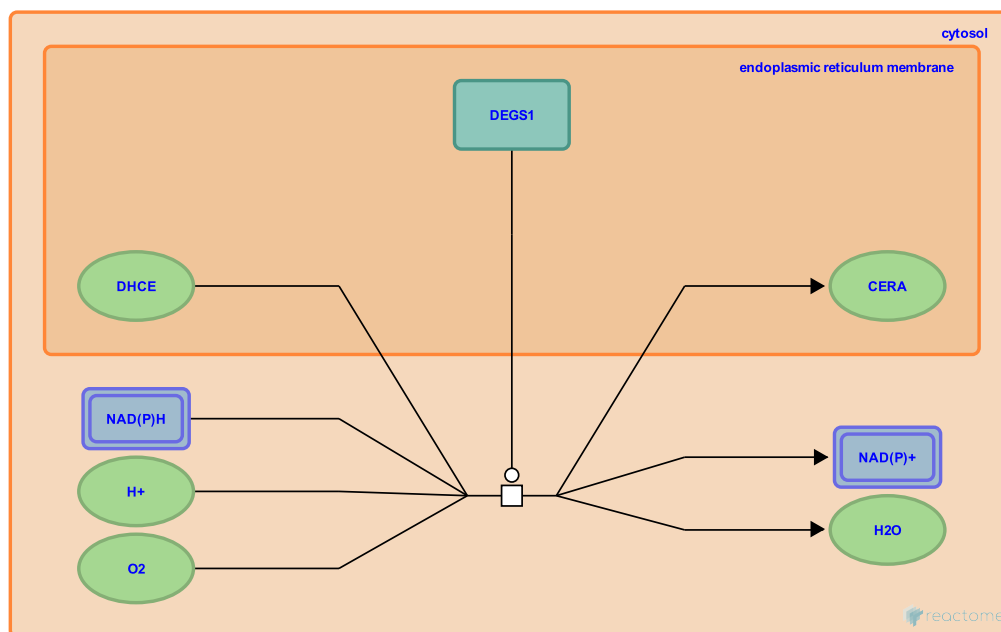
This document contains 1 reaction ([see Table of Contents](#))

dihydroceramide + NAD(P)H + H+ + O2 => ceramide + NAD(P)+ + H2O ↗

Stable identifier: R-HSA-428259

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane



DEGS1 (sphingolipid delta(4)-desaturase 1 / “degenerative spermatocyte homolog 1”) enzyme associated with the cytosolic face of the endoplasmic reticulum catalyzes the desaturation of dihydroceramide to form ceramide (Cadena et al. 1997; Ternes et al. 2002). The stoichiometry and cofactor requirements of the reaction are inferred from those observed in studies of ceramide synthesis in vitro catalyzed by rat liver microsomes (Michel et al. 1997). DEGS1 may also catalyze the 4-hydroxylation of dihydroceramide to form 4-hydroxysphinganine, but with low efficiency.

Literature references

- Cadena, DL., Kurten, RC., Gill, GN. (1997). The product of the MLD gene is a member of the membrane fatty acid desaturase family: overexpression of MLD inhibits EGF receptor biosynthesis. *Biochemistry*, 36, 6960-7. ↗
- Ternes, P., Franke, S., Zahringer, U., Sperling, P., Heinz, E. (2002). Identification and characterization of a sphingolipid delta 4-desaturase family. *J Biol Chem*, 277, 25512-8. ↗
- Michel, C., van Echten-Deckert, G., Rother, J., Sandhoff, K., Wang, E., Merrill AH, Jr. (1997). Characterization of ceramide synthesis. A dihydroceramide desaturase introduces the 4,5-trans-double bond of sphingosine at the level of dihydroceramide. *J Biol Chem*, 272, 22432-7. ↗

Editions

2009-08-20	Authored, Edited	D'Eustachio, P.
2009-08-20	Reviewed	Jassal, B.
2009-11-18	Reviewed	Hannun, YA., Luberto, C.