

# ALOX12:Fe<sup>2+</sup> dehydrogenates 14(S)-Hp-DPAn-3 to 13,14-epoxy-DPAn-3

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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

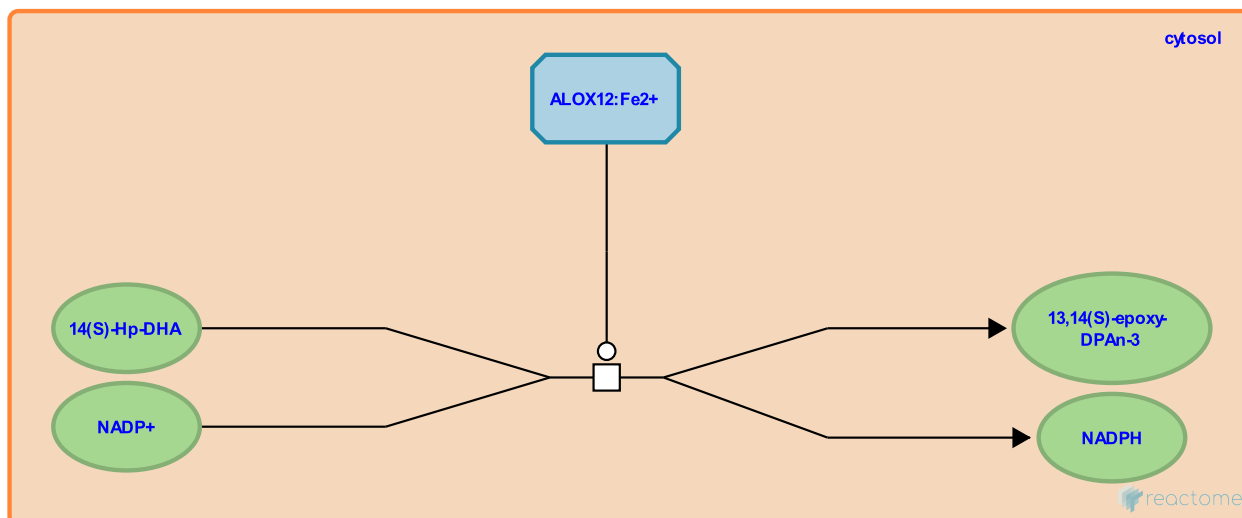
This document contains 1 reaction ([see Table of Contents](#))

## ALOX12:Fe2+ dehydrogenates 14(S)-Hp-DPA<sub>n</sub>-3 to 13,14-epoxy-DPA<sub>n</sub>-3 ↗

**Stable identifier:** R-HSA-9026007

**Type:** transition

**Compartments:** cytosol



In a reaction scheme that could be similar to the one for DHA-derived maresins, a lipoxygenase mediates the abstraction of hydrogen from 14(S)-hydroperoxy-docosapentaenoic acid (14(S)-Hp-DPA<sub>n</sub>-3) to form the epoxy product 13,14(S)-epoxy-docosapentaenoic acid (13,14(S)-epoxy-DPA<sub>n</sub>-3) (Dalli et al. 2013). If, as assumed, DPA metabolism follows the same path as for DHA metabolism, the lipoxygenase could be 12-lipoxygenase (ALOX12).

### Literature references

Serhan, CN., Colas, RA., Dalli, J. (2013). Novel n-3 immunoresolvents: structures and actions. *Sci Rep*, 3, 1940. ↗

### Editions

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