

Formation of hydroxylysino-5-ketonorleucine cross-links

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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

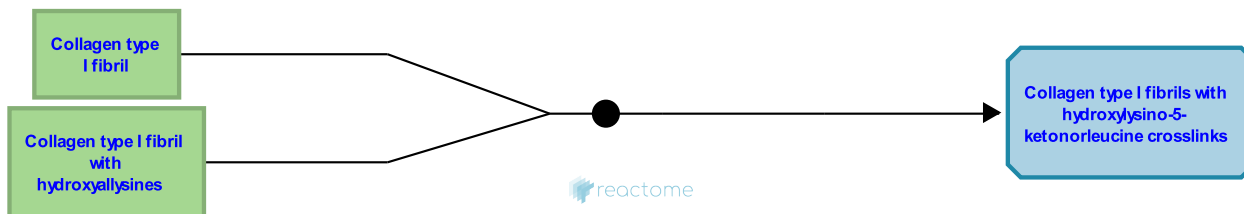
This document contains 1 reaction ([see Table of Contents](#))

Formation of hydroxylysino-5-ketonorleucine cross-links [↗](#)

Stable identifier: R-HSA-2395302

Type: binding

Compartments: extracellular region



Hydroxyallysine and hydroxylysine can react forming the Schiff base, which spontaneously undergoes an Amadori rearrangement resulting in the ketoimine cross-link hydroxylysino-5-ketonorleucine (HLKNL). This is much more stable than the aldimine crosslinks (Bailey et al. 1998).

Literature references

Reiser, K., McCormick, RJ., Rucker, RB. (1992). Enzymatic and nonenzymatic cross-linking of collagen and elastin. *FASEB J.*, 6, 2439-49. [↗](#)

Bailey, AJ., Lehto, M., Sims, TJ. (1985). Skeletal muscle injury--molecular changes in the collagen during healing. *Res Exp Med (Berl)*, 185, 95-106. [↗](#)

Editions

2012-04-30	Authored	Jupe, S.
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