pheomelanin formation

Ito, S., Jupe, S., d'Ischia, M.

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

18/05/2024

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. ↗

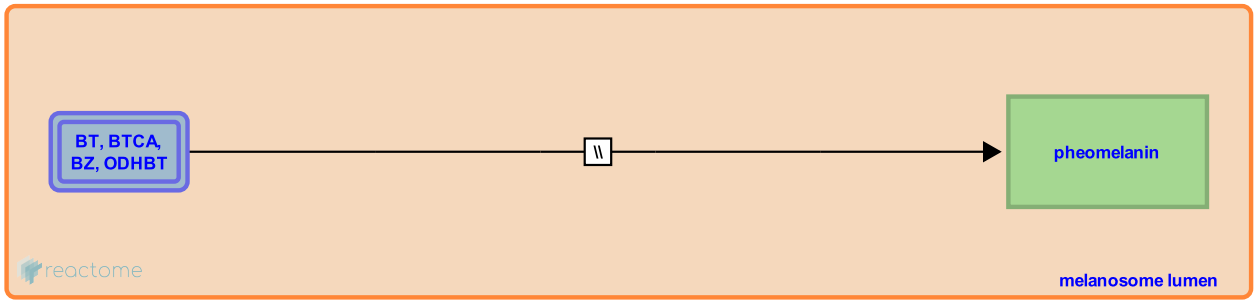
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

pheomelanin formation

Stable identifier: R-HSA-5662891

Type: omitted

Compartments: melanosome lumen



The last stage of pheomelanogenesis is the oxidative polymerization of BT, BTCA, and the products of secondary modifications of the benzothiazine moieties of these to form pheomelanin. Several dimeric and trimeric intermediates have been identified (Napolitano et al. 2001) but it is unclear whether these are major components of natural pheomelanin pigments. Most studies have used powerful chemical oxidants (Di Donato et al. 2002, Napolitano et al. 2008). which may lead to a pheomelanogenesis process that differs from the in vivo process (Wakamatsu et al. 2008).

Literature references

Wakamatsu, K., Ito, S., Ohtara, K. (2009). Chemical analysis of late stages of pheomelanogenesis: conversion of dihydrobenzothiazine to a benzothiazole structure. *Pigment Cell Melanoma Res, 22*, 474-86.

Editions

2015-01-13	Authored	Jupe, S.
2015-02-10	Edited	Jupe, S.
2015-02-13	Reviewed	Ito, S., d'Ischia, M.