

Library Indian Institute of Science Education and Research Mohali



DSpace@IISERMohali (/jspui/)

- / Publications of IISER Mohali (/jspui/handle/123456789/4)
- / Research Articles (/jspui/handle/123456789/9)

Please use this identifier to cite or link to this item: http://hdl.handle.net/123456789/2706

Title: ChaC2, an enzyme for slow turnover of cytosolic glutathione

Authors: Kaur, Amandeep (/jspui/browse?type=author&value=Kaur%2C+Amandeep)

Bachhawat, A.K. (/jspui/browse?type=author&value=Bachhawat%2C+A.K.)

Keywords: Crystal structure

Michaelis-Menten Protein expression

Issue Date: 2017

Publisher: American Society for Biochemistry and Molecular Biology Inc.

Citation: Journal of Biological Chemistry, 292(2).

Abstract:

Glutathione degradation plays an important role in glutathione and redox homeostasis, and thus it is imperative to understand the enzymes and the mechanisms involved in glutathione degradation in detail. We describe here ChaC2, a member of the ChaC family of γ-glutamylcyclotransferases, as an enzyme that degrades glutathione in the cytosol of mammalian cells. ChaC2 is distinct from the previously described ChaC1, to which ChaC2 shows ~50% sequence identity. Human and mouse ChaC2 proteins purified in vitro show 10-20-fold lower catalytic efficiency than ChaC1, although they showed comparable Km values (Km of 3.7 \pm 0.4 mm and kcat of 15.9 \pm 1.0 min-1 toward glutathione for human ChaC2; Km of 2.2 \pm 0.4 mm and kcat of 225.2 \pm 15 min-1 toward glutathione for human ChaC1). The ChaC1 and ChaC2 proteins also shared the same specificity for reduced glutathione, with no activity against either γ -glutamyl amino acids or oxidized glutathione. The ChaC2 proteins were found to be expressed constitutively in cells, unlike the tightly regulated ChaC1. Moreover, lower eukaryotes have a single member of the ChaC family that appears to be orthologous to ChaC2. In addition, we determined the crystal structure of yeast ChaC2 homologue, GCG1, at 1.34 Å resolution, which represents the first structure of the ChaC family of proteins. The catalytic site is defined by a fortuitous benzoic acid molecule bound to the crystal structure. The mechanism for binding and catalytic activity of this new enzyme of glutathione degradation, which is involved in continuous but basal turnover of cytosolic glutathione, is proposed.

Description: Only IISERM authors are available in the record.

URI: https://www.sciencedirect.com/science/article/pii/S0021925820401942?via%3Dihub (https://www.sciencedirect.com/science/article/pii/S0021925820401942?via%3Dihub)

http://hdl.handle.net/123456789/2706 (http://hdl.handle.net/123456789/2706)

Appears in Research Articles (/jspui/handle/123456789/9) Collections:

Files in This Item

THOO IIT THIS ROTH.				
File	Description	Size	Format	
Need to add pdf.odt (/jspui/bitstream/123456789/2706/1/Need%20to%20add%20pdf.odt)		8.63 kB	OpenDocument Text	View/Open (/jspui/bitstream/12345

Show full item record (/jspui/handle/123456789/2706?mode=full)

■ (/jspui/handle/123456789/2706/statistics)

Items in DSpace are protected by copyright, with all rights reserved, unless otherwise indicated.