

University of Groningen

Structural and functional characterization of tautomerase and aspartase/fumarase superfamily enzymes

Poddar, Harshwardhan

DOI:
[10.33612/diss.126026140](https://doi.org/10.33612/diss.126026140)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2020

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):
Poddar, H. (2020). *Structural and functional characterization of tautomerase and aspartase/fumarase superfamily enzymes*. University of Groningen. <https://doi.org/10.33612/diss.126026140>

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Stellingen

behorende bij het proefschrift

STRUCTURAL AND FUNCTIONAL CHARACTERIZATION OF TAUTOMERASE AND ASPARTASE/FUMARASE SUPERFAMILY ENZYMES

van

Harshwardhan Poddar

1. X-ray crystallography still remains the preferred technique to study enzyme mechanisms at the molecular level. (This thesis)
2. It is very gratifying when the proposed mechanism of an enzymatic reaction is validated with high-resolution crystal structures. (Chapters 2 and 5)
3. For small ligands such as acetaldehyde it is imperative to obtain ultra high-resolution enzyme structures, to be certain of their presence in the active site. (Chapter 2)
4. The rearrangement of the active site of 4-OT, caused by the M45Y/F50A mutations was difficult to predict. The crystal structure of the double mutant highlights the importance of structural information to properly assess the impact of mutations. (Chapter 3)
5. Although unconventional, the mutability landscape method is a powerful way to carry out engineering of an enzyme and presents an effective alternative to the more commonly used structure guided approach. (Chapter 3)
6. The presence of a bound metal in an enzyme does not always mean that it is needed for the enzyme's structural integrity or activity. (Chapter 4)
7. You know you have a winner when you can express, purify, crystallize and solve the structure of an enzyme, all in the same week. (EDDS lyase, Chapter 5)
8. Sometimes in protein crystallography you have to just follow your gut feeling and go ahead with an experiment, no matter how ridiculous it sounds. This helped me to get different ligand-bound structures of EDDS lyase. (Chapter 5)
9. Challenging and difficult projects are the ones that teach you the most in your research career. The same is true for life. Difficult times improve you as a person and although you may still end up making mistakes, it is ultimately how you rise to the challenge that matters.