

Mechanistic modeling of *Mycobacterium tuberculosis* β -carbonic anhydrase inhibitors using integrated systems biology and the QSAR approach

Ratul Bhowmik¹, Ajay Manaithiya¹, Jenny Parkkinen¹, Sunil Kumar², Bijo Mathew², Mataleena Parikka¹,
Fabrizio Carta³, Claudiu T. Supuran³, Seppo Parkkila^{1,4}, and Ashok Aspatwar^{1*}

¹Faculty of Medicine and Health Technology, Tampere University, Tampere, Finland

ratul.bhowmik@tuni.fi, ajay.manaithiya@tuni.fi, jenny.parkkinen@tuni.fi, mataleena.parikka@tuni.fi,
seppo.parkkila@tuni.fi

²Department of Pharmaceutical Chemistry, Amrita School of Pharmacy, Amrita Vishwa Vidyapeetham,
AIMS Health Sciences Campus, Kochi, India Sunilkumar@pharmacy.aims.amrita.edu,
Bijomathew@aims.amrita.edu,

³Department of NEUROFARBA, Section of Pharmaceutical and Nutraceutical Sciences, University of
Florence, Firenze, Italy, fabrizio.carta@unifi.it, claudiu.supuran@unifi.it

⁴ ABSTRACT Fimlab Ltd., Tampere University Hospital, Tampere, Finland

The authors have withdrawn their manuscript owing to the inability to complete the revisions or follow up on the manuscript at this time, due to personal circumstances. Therefore, the authors do not wish this work to be cited as reference for the project. If you have any questions, please contact the corresponding author.