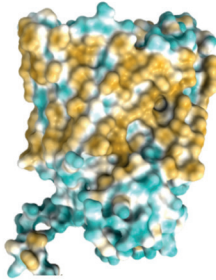


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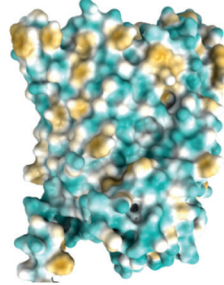
AUSTRIAN
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WEDNESDAY, 10 APRIL 2024
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1010 VIENNA

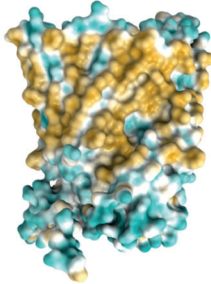
GLUT1^{Crystal}



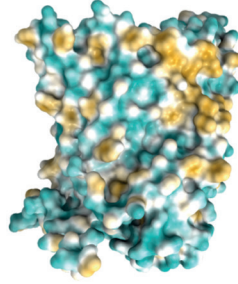
GLUT1^{QTY}



GLUT3^{Crystal}



GLUT3^{QTY}



PUBLIC LECTURE

THE SIMPLE QTY CODE FOR PROTEIN DESIGN

SHUGUANG ZHANG

MIT Media Lab and Austrian Academy of Sciences

WELCOME

Ulrike Diebold | *Vice President of the Austrian Academy of Sciences*

INTRODUCTION

Uwe Sleytr | *University of Natural Resources and Life Sciences, Vienna,
and Austrian Academy of Sciences*



Shuguang Zhang is employed at MIT Media Lab. He received his Ph.D. from University of California, Santa Barbara. In 2006 he won a Guggenheim Fellowship as well as the Wilhelm Exner Medal of Austria. He was elected as member of the Austrian Academy of Sciences in 2010, into the US National Academy of Inventors in 2013, and the European Academy of Science and Arts in 2021. He won the 2020 Emil Thomas Kaiser Award from the Protein Society. He has published over 200 scientific papers cited over 39,000 times with an h-index of 95.

In 2011, Shuguang Zhang conceived the QTY code to design water-soluble membrane proteins. There are approximately 26 % genes in the human genome that encode membrane proteins, which are crucial for both internal and external cellular communications. The QTY code is a simple molecular code: namely, glutamine (Q), Threonine (T) and Tyrosine (Y) systematically replace the hydrophobic amino acids Leucine (L), Valine (V), Isoleucine (I), and Phenylalanine (F) in the transmembrane α -helices of membrane proteins including G protein-coupled receptors (GPCRs). GPCRs function similarly to our mobile phones, communicating and interacting with the external world. The QTY code results suggest that despite 46–56 % transmembrane α -helices changes, water-soluble QTY variants still maintain stable structures and biological function, namely, ligand-binding activities. This simple QTY code is likely to be a useful tool and has a major impact on the design of water-soluble variants of previously water-insoluble glucose transporters, solute carrier transporters, ABC transporters, ion channels, voltage-gated ion channels, and perhaps aggregated proteins including amyloids.



Further information can be found here
www.oeaw.ac.at/veranstaltungen/aktuelle-veranstaltungen

ORGANIZER: Austrian Academy of Sciences

CONTACT:

Natalie Kapfer-Rupp, BA, Austrian Academy of Sciences
T: +43 1 51581-3633 | natalie.kapfer-rupp@oeaw.ac.at

Figure caption: Surface hydrophobic surfaces of crystal structures of native glucose transporters GLUT1 and GLUT3 (left) and AlphaFold2 predicted water-soluble QTY variants (right).

Fotos: © Smorodina E, Tao F, Qing R, Jin D, Yang S, Zhang S. Comparing 2 crystal structures and 12 AlphaFold2-predicted human membrane glucose transporters and their water-soluble glutamine, threonine and tyrosine variants. QRB Discovery. 2022;3:e5. doi:10.1017/qrd.2022.6, © Shuguang Zhang