Mathematisch-Naturwissenschaftliche Fakultät
Institut für Pharmazeutische und Medizinische Chemie

HEINRICH HEINE
UNIVERSITÄT DÜSSELDORF

Heinrich-Heine-Universität Düsseldorf ✉ 40204 Düsseldorf

An alle Interessierten

Professur für Pharmazeutische und Medizinische Chemie

Univ.-Prof. Dr. Holger Gohlke

Telefon +49-211-81-13662
Telefax +49-211-81-13847
gohlke@uni-duesseldorf.de

cpclab.uni-duesseldorf.de

Düsseldorf, 10.3.2014

Heinrich-Heine-Universität Düsseldorf
Universitätsstraße 1
40225 Düsseldorf
Gebäude 26.23
Ebene 02 Raum 32

www.uni-duesseldorf.de

Einladung zum Vortrag

Dr. Marco Bocola

Gruppenleiter, Lehrstuhl für Biotechnologie, RWTH Aachen

Computer Aided Enzyme Engineering, from sequence to function via homology modeling, docking and QM/MM simulations

In the application of engineered enzymes for stereoselective synthesis, the main question is the sequence-function relationship. Sequence comparisons by alignments with known enzymes can give hints towards more selective enzymes in a protein family of interest. By using computational structure prediction, the active site of enzymes can be analyzed and substrate acceptance can be checked by docking and binding simulations. Enhanced biocatalysts can be identified and predicted using computational methods, thus enlarging the toolbox for biocatalysis.

Carbonyl reductase preparations from Candida parapsilosis (CPCR; EC 1.1.1.1) are described as a suitable catalyst for the asymmetric reduction of various carbonyl compounds, such as aliphatic and aromatic ketones and diketones, keto acids, esters and amides. Two preparations are currently commercially available, they are isolated either from the native production strain C. parapsilosis (Codexis, USA), or from Escherichia coli as recombinant host organism (X-zyme, Germany). However, the preparations reveal clear differences in their biochemical features [1] and do not exactly coincide with the data defining the original target enzyme. Due to this limitation the application of CPCR in research or industrial production is limited.

In our work we describe the elucidation of the molecular identity of CPCR isoenzymes by using methods from computational chemistry. It involves a stepwise identification of two possible enzyme candidates with their amino acid sequences, the establishment of active-site molecular models with catalytic Zinc and bound NADH with subsequent application to the prediction of binding patterns of selected indica-

tor substrates and the reaction pathway calculations using mixed quantum/molecular mechanics calculations.

Ort: Hörsaal 6E
Zeit: Donnerstag, 20. März 2014, 17:00 Uhr c.t.
Gäste sind herzlich willkommen.