

Institute of Bioanalytical Chemistry

Structural Biochemistry: Molecular recognition in extracellular signaling, drug development and biocatalysis

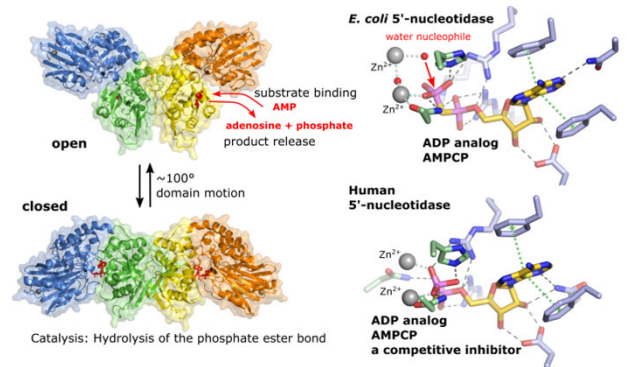
Prof. Dr. Norbert Sträter

Research Interests

Our research is focused on molecular recognition in biocatalysis, enzyme inhibition and cellular signal transduction. We study the interaction of ligands and proteins via X-ray crystallography, binding assays, kinetics as well as biophysical and spectroscopic techniques. A main aim is to characterize the molecular principles of interaction leading to specificity, catalysis as well as conformational changes such as domain motions. This information is used to understand the mode of action of enzymes, receptors and other proteins and also to apply it to structure-based rational design of novel biocatalysts and pharmacologically relevant protein inhibitors. In addition to experimental methods, computational tools are a key method to rationalize structure-function relationships as well as for enzyme or inhibitor design.

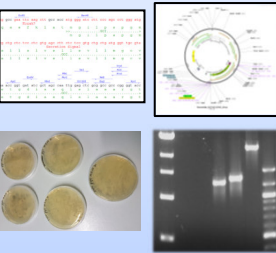
From Protein Sequence to 3-D Structure

Despite recent advances in *in silico* protein fold prediction, experimental methods remain invaluable for the accurate determination of novel protein structures, especially to elucidate protein complexes and protein-ligand binding. Our group is specialized on X-ray crystallography as the method of choice for structure analysis at atomic resolution. This method requires milligram amounts of target protein at high purity.



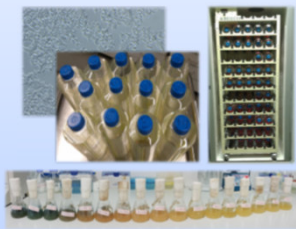
CD73 (human ecto-5'-nucleotidase): A drug target in cancer immunotherapy. We study the domain movement and substrate binding in catalysis and the interaction with synthetic inhibitors.

Molecular Cloning



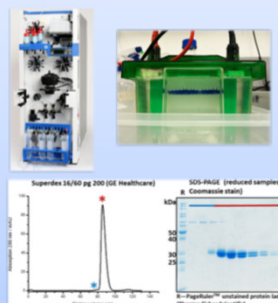
First, the DNA sequence of the protein of interest is inserted into an expression vector which is incorporated into expression host cells.

Recombinant Protein Expression



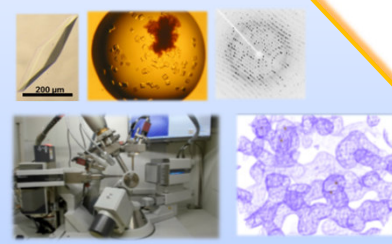
The choice of a suitable expression host depends on the complexity of the protein of interest. We employ *E. coli* as a simple prokaryotic expression system as well as mammalian and insect cell culture for more complex proteins.

Protein Purification and Characterization

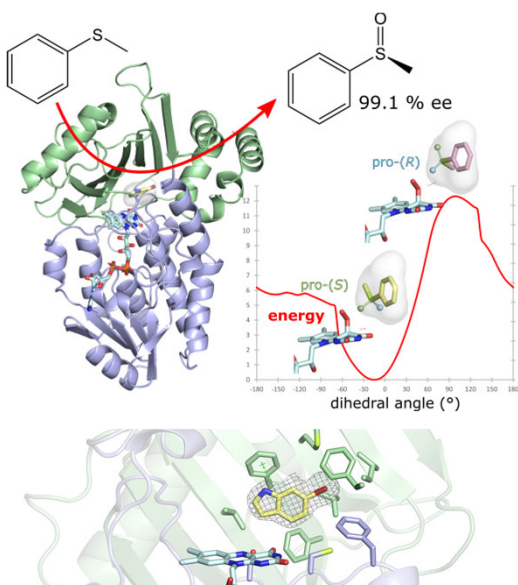


The protein of interest is isolated and purified via several chromatographic steps. Next, it is characterized by gel-based and biophysical methods.

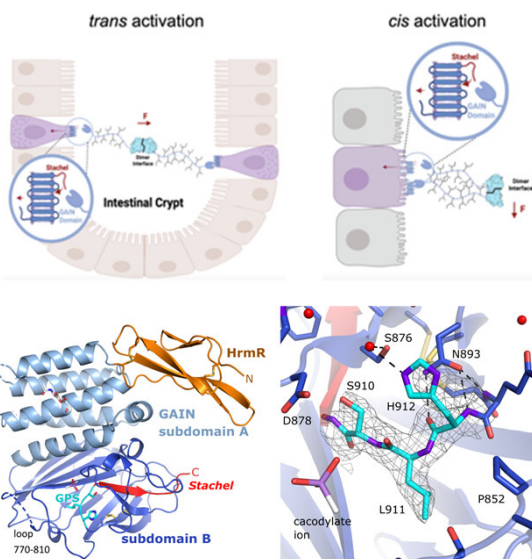
Structure Elucidation



Protein crystals are grown by robot-assisted high-throughput screenings. X-ray diffraction datasets are collected and allow the calculation of electron densities for building a 3-D protein model.



Flavin-dependent monooxygenases. We use structure-based enzyme design to generate new biocatalysts for stereospecific transformations in organic synthesis of fine chemicals.



Structure and function of adhesion GPCR. Adhesion GPCR contain large extracellular domains that have mechanosensing functions at the cell surface.



Dr. Renato Weißer

If you are...

- Interested in protein biochemistry and bioanalytics
- Willing to learn a wide set of interdisciplinary methods
- Looking for lecture or a practical courses, topics for bachelor or master thesis

... please have a look at our webpage for further details or get in contact.

Contact

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