76th Mosbacher Kolloquium

„AI-driven (r)evolution in structural biology & protein design"

Program

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Legend - Rooms

- Lecture hall
- Darre
- Malzboden
- Schalander
- Tenne
- unspecific

Welcome

Janosch Hennig

Birte Höcker

Ina Koch

Dear Friends and Colleagues,

The traditional spring meeting of the German Society for Biochemistry and Molecular Biology (GBM) is held annually in the picturesque town of Mosbach to promote the exchange of scientific ideas, discuss the latest discoveries and emerging topics and foster the education of young scientists. The topic of the 76th Mosbacher Kolloquium is "AI-based (r)evolution of structural biology and protein design".

Recent AI-driven techniques have become available to explore protein structures, from prediction and analysis to protein design. The availability of a large amount of protein structure data makes the extensive use of ML and AI methods in a wide range possible. The development of AlphaFold and many other tools show the potential but also the challenges in the field not only determined by data handling and storage but also by the integration of data that differ in quality and quantity due to experimental settings. As this multi-disciplinary field is rapidly developing there is a great need for knowledge exchange and discussions bringing together scientists and students from biology, biochemistry, bioinformatics, physics, and computer science.

At the meeting, emerging concepts will be discussed by leading international experts covering the different facets of the field. The topics include theory & tool development, machine learning in structural biology, AI-based structure prediction & integrative modeling, and AI-driven protein design. Critical discussions of state-of-the-art research will allow us to together chart future developments at the interface of basic science and applications, while fruitful scientific exchange of ideas will help inspire young scientists in their future research endeavors in this rapidly developing field.

We warmly welcome you!

Janosch Hennig Birte Höcker Ina Koch

Program

Wed., March 19

Congress center „Alte Mälzerei"

Davide Amendola

Alexander Braun

Britta Lipinski

16:00 **Arrival and registration**

18:00 **Introductory lecture („Primer")**

A short intro to the topic of this year's Mosbacher Kolloquium (delivered by the organizers)

19:00 - 19:30 **Rainer Rudolph Awards**

The Rainer Rudolph Foundation promotes and supports basic and applied research in protein biochemistry and biotechnology. Every year awards are given to young scientists who have made outstanding advances in these fields.

Davide Amendola /Zürich [DE]
The arsenal of a bacterial predator revealed by cryo-electron microscopy

Alexander Braun /Bayreuth [DE]
Designing triosephosphate isomerases using generative language models

Britta Lipinski /Darmstadt [DE]
Engineering of single domain antibody-based bispecifics

20:00 **Welcome reception /Get together**

City hall

The steering committee of the German Society for Biochemistry and Molecular Biology (GBM) and the city of Mosbach invite you to a welcome reception in the town hall of Mosbach (no registration required)

We thank the city of Mosbach for the kind hospitality.

Program

Thu., March 20


David Jones


Lea Brönnimann


Matthias Rarey


Andrea Volkamer


David Medina-Ortiz


Burkhard Rost

08:50 **Opening remarks**
by the scientific organizers

Session 1 (09:00 - 12:00)
Theory and development
(Chair: Clara Schoeder)

09:00 **David Jones** /London [UK]
The encyclopedia of domains and quickly searching for multi-domain protein structures

09:30 **Early career investigator talk 1**
Lea Brönnimann /Bern [CH]
Exploring antibody repertoires using deep language models

09:45 **Matthias Rarey** /Hamburg [DE]
Artificial intelligence or intelligent computing? Examples from computer-aided molecular design

Coffee break (10:15 - 10:45)

10:45 **Andrea Volkamer** /Saarbrücken [DE]
Hybrid AI and open source for drug design

11:15 **Early career investigator talk 2**
David Medina-Ortiz /Halle (Saale) [DE]
Integrating geometric deep learning with explainable artificial intelligence to assist protein engineering

11:30 **Burkhard Rost** /Munich [DE]
Artificial intelligence deciphers the code of life written in proteins?

Lunch break (12:00 - 13:00)

Program

Thu., March 20

12:00 **Meet the Industrial Scientist with Alexander Rives**

(info on page 29)

12:00 **Meet the Prof with Tanja Kortemme**

(info on page 29)

12:15 **Panel discussion „Big Data, Big Challenges - How do we manage research data?“**

Do you want to organize and store your research data efficiently? Do you wonder how to ensure the reproducibility and integrity of your data? Do you ask yourself how to comply with data management policies and best practices?

Join the GBM Young Investigators and explore these questions and more with experts from both academia and industry, and learn how to manage your research data effectively!

13:00 Workshop by Thermo Fisher Scientific: **„Empowering Cryo-EM workflows with AI and CryoFlow“**

13:00 Workshop by Deltablot **„Demonstrating eLabFTW: A free and open-source electronic laboratory notebook“**

13:00 **Poster session I**

(even numbers, info on page 30f)

Program

Thu., March 20


Sergey Ovchinnikov


Noelia Ferruz


Martin Steinegger


Leif Seute

Session 2 (14:30 - 16:45)
Machine Learning in Structural Biology
(Chair: Ora Furman)

14:30 **Sergey Ovchinnikov** /Cambridge [USA]
Inverting protein structure prediction models for protein design

15:00 **Noelia Ferruz** /Barcelona [ES]
Optimizing proteins with reinforcement learning

Coffee break (15:30 - 16:00)

16:00 **Martin Steinegger** /Seoul [KR]
Supercharged protein analysis in the era of accurate structure prediction

16:30 **Early career investigator talk 3**
Leif Seute /Heidelberg [DE]
Learning conformational ensembles of proteins based on backbone geometry

Program

Thu., March 20

Franziska Sendker

Davide Tamborrini

Tanja Kortemme

16:45 **Bayer Pharmaceuticals PhD Award**
(Laudatio: Claus Seidel)

Franziska Sendker /Boston [USA]
Evolution of a protein fractal

17:00 **Karl Lohmann Prize**
(Laudatio: Claus Seidel)

Davide Tamborrini /Basel [CH]
Structural investigation of the relaxed cardiac sarcomere by electron cryo-tomography

17:15 **GBM General Meeting** (17:15 - 19:30)
(for GBM members only)

19:30 **Feodor Lynen Lecture**
(Laudatio: Birte Höcker)

Tanja Kortemme /San Francisco [USA]
De novo protein design: From new structures to programmable molecular and cellular functions

The German Society for Biochemistry and Molecular Biology honors Tanja Kortemme with the distinguished Feodor Lynen medal.

After the prize lecture the GBM invites all participants to join the Lynen Reception.

20:30 **Lynen reception & poster session II**
(even & odd numbers, info on page 30f)

22:00 **Get Together & Networking**

GESELLSCHAFT FÜR BIOCHEMIE
UND MOLEKULARBIOLOGIE E.V.

GBM Compact

Focus on Condensate Biology

Sept 18 - 19, 2025 / Frankfurt am Main

Organization:

Simon Alberti /Dresden
Sara Cuylen-Haering /Heidelberg
Dorothee Dormann /Mainz
Edward A Lemke /Mainz
Julia Mahamid /Heidelberg
Claus Seidel /Düsseldorf
Konstanze Winklhofer /Bochum

77th Mosbacher Kolloquium

More than lipidic barriers - New horizons in membrane biology

March 26 - 28, 2026 / Mosbach (Baden), Germany

Organization

Britta Brügger (Universität Heidelberg) || Robert Ernst (Universität des Saarlandes)
Andre Nader (MPI CBG Dresden) || Christian Ungermann (Universität Osnabrück)

Program

Fri., March 21


Yang Zhang


Arman Simonyan


Jan Kosinski


Possu Huang


Sophie Binder


Bruno Correia

Session 3 (09:00 - 10:15)
AI-based structure prediction & integrative modelling
(Chair: Saacnicteh Toledo Patino)

09:00 **Yang Zhang** /Singapore [SG]
Towards an AI-based solution of protein structure prediction problem

09:30 **Early career investigator talk 4**
Arman Simonyan /Copenhagen [DK]
New machine learning-driven approaches for peptide probe and drug discovery

09:45 **Jan Kosinski** /Hamburg [DE]
AI-based integrative structural modeling

Coffee break (10:15 - 10:45)

Session 4 (10:45 - 12:00)
From protein engineering to AI-based protein design
(Chair: Alena Khmelinskaia)

10:45 **Possu Huang** /Stanford [USA]
SHAPES of protein generative models

11:15 **Early career investigator talk 5**
Sophie Binder /Bonn [DE]
AI-based protein design and validation

11:30 **Bruno Correia** /Lausanne [CH]
Exploring the structural and functional landscape of proteins by computational design

Lunch break (12:00 - 13:00)

Program

Fri., March 21


Alex Rives


Stanislaw Dunin-Horkawicz


Anna Backeberg


Kateryna Maksymenko

12:00 **Meet the prof with Matthias Hentze**
(info on page 29)

12:00 DFG workshop: **Funding opportunities for graduates in life sciences**

12:00 Workshop by Elsevier & Biochemica et Biophysica Acta: **How to publish your research in scholarly journals**

13:00 **Poster session III**
(odd numbers, info on page 30f)

13:45 **Research funding at the Klaus Tschira Foundation**

Junior GBM Session (14:30 - 16:00)
(Chairs: Frederike Knipp, Marcel Zimmeck)

14:30 **Alex Rives** /New York [USA]
Language models at the scale of evolution

15:00 **Stanislaw Dunin-Horkawicz** /Tübingen [DE]
What can we learn from incorrect AlphaFold2 models? (the case of signal transduction)

15:30 **Early career investigator talk 6**
Anna Backeberg /Munich [DE]
De novo design of multiple-geometry forming protein scaffolds

15:45 **Early career investigator talk 7**
Kateryna Maksymenko /Tübingen [DE]
Training-free framework to design protein-based binders

Program

Fri., March 21

Dorothee Kern

Matthias Hentze

Otto Warburg Medal

Coffee break (16:00 - 16:30)

16:30

Eduard Buchner Prize
(Laudatio: Janosch Hennig)

sponsored by Springer

Dorothee Kern /La Jolla [USA]
The protein dance –
from experiments to AI predictions

17:30

Otto Warburg Lecture & Medal
(Laudatio: Volker Haucke)

Matthias Hentze /Heidelberg [DE]
From Otto Warburg to riboregulation: a 100 year journey in metabolism

This year the GBM, Elsevier and Biochimica et Biophysica Acta (BBA) will honor Matthias Hentze from the European Molecular Biology Laboratory (EMBL) in recognition of his fundamental contributions to the understanding of gene regulation by RNA-binding proteins and the identification of RNA-binding proteins with the Otto Warburg Medal.

The highest award in Germany for biochemists and molecular biologists promotes outstanding scientific excellence and encourages groundbreaking achievements in the field of fundamental biochemical and molecular biological research.
Since 1963 the Otto Warburg Medal is intended to commemorate the outstanding achievements of Otto Heinrich Warburg. To emphasize the importance of excellent scientific research and motivate young researchers to achieve outstanding results, the prize is endowed with 25.000 Euro.

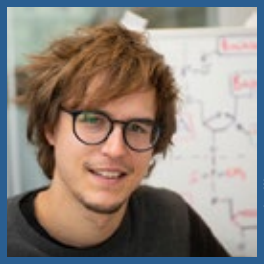
sponsored by BBA ELSEVIER

Program

Sat., March 22


Andrea Thorn


Marharyta Makarova


Maximilian Fürst

Young Investigator Session (09:00 - 10:15)
(Chair: Andrea Hupfeld)

09:00 **Andrea Thorn** /Hamburg [DE]
The potential of AI for experiments in structural biology

09:30 **Early career investigator talk 8**
Marharyta Makarova /Erlangen [DE]
A novel rotamer library for nucleic acids enables the design of protein-nucleic acid complexes with the protein design software MUMBO

09:45 **Maximilian Fürst** /Groningen [NL]
Big data from wet-lab biochemistry and dry-lab biophysics to advance AI protein design

Coffee break (10:15 - 10:45)

Program

Sat., March 22


Judith Zaugg


Salomé Guilbert


Jens Meiler


Gevorg Grigoryan

Session 5 (10:45 - 12:30)
AI application in Life Sciences
(Chair: N.N.)

10:45 **Judith Zaugg** /Heidelberg [DE]
Mining cryo-electron tomography data with self-supervised deep learning models

11:15 **Early career investigator talk 9**
Salomé Guilbert /Lausanne [CH]
In silico design of enzymes to degrade short-chain Per- and Polyfluoroalkyl Substances (PFAS)

11:30 **Jens Meiler** /Leipzig [DE]
How artificial intelligence is reshaping protein structure prediction and therapeutic design – from small molecules to new modalities

12:00 **Gevorg Grigoryan** /Somerville [USA]
Programmable generative protein design: from molecules to medicines

13:00 **Poster prizes & closing remarks**

Tanja Kortemme

Matthias Hentze

Alex Rives

Meet the Prof

This year's guests of the Junior GBM are Tanja Kortemme and Matthias Hentze.
The scientists will give insights into their lives as researchers and their personal careers.
In addition, you can ask questions in an informal atmosphere that may help you with your personal orientation in research and career or that simply interest you.

Thursday, March 20, 12:00 - 13:00
(Room: Darre)
(Chair: Katharina Bachschwöller)
Tanja Kortemme (University of California UCSF)

Friday, March 21, 12:00 - 13:00 (Room: Darre)
(Chair: Philip Müller)
Matthias Hentze (EMBL Heidelberg)

The number of participants is limited. A registration is required.

Meet the industrial scientist

The Junior GBM succeeded in winning Alex Rives from EvolutionaryScale for the „Meet the industrial scientist". Similar to the „Meet the Prof" format, the scientist will talk about his work and career and answer your questions.

Thursday, March 20, 12:00 - 12:45 (Room: Tenne)
(Chair: Jens Martin)
Alex Rives (EvolutionaryScale)

The number of participants is limited. A registration is required.

Poster Sessions

Session Times

Thursday, 13:00 - 14:30 (even numbers)

Thursday, 20:30 - 22:00 (all numbers)

Friday, 13:00 - 14:30 (odd numbers)

During the poster sessions the presenting authors are requested to stay near their posters. Posters should be presented throughout the whole meeting.

Poster Specifications

The posters should be presented in portrait format (DIN A0 resp. ~120 x 85 cm).

Poster Abstracts

All poster abstracts are available as pdf-file for download on the meeting homepage.

A printed abstract booklet is available for viewing purposes at the registration desk.

Poster Numbers

Please see the poster list on page 40 for poster numbers.

Poster Prizes

The best three posters will be awarded at the end of the meeting with a poster prize by GBM and FEBS Open Bio (300 € each). In addition, three further posters will be awarded a book voucher worth €150, sponsored by Wiley-VCH.

The winners will be announced at the end of the meeting on Saturday. To receive the prize, personal attendance is required.

GBM intern

for GBM stakeholders

March 19 — 14:00 - 16:30 (Room: Darre)

Sitzung: Arbeitskreis Studium Molekulare Biowissenschaften

March 19 — 17:00 - 19:00 (Room: Malzboden)

Sitzung: Sprecher der GBM-Studiengruppen und Arbeitskreise

March 20 — 12:30 - 14:00 (Room: Malzboden)

Sitzung: GBM-Kontaktpersonen

March 20 — 15:15 - 16:30 (Room: Schalander)

Meeting of Senior Experts in the GBM

March 20 — 17:15 - 19:30 (Lecture hall)

GBM-Mitgliederversammlung

March 21 — 12:00 - 14:30 (Room: Schalander)

Sitzung: Arbeitskreis „Biochemie in der Medizin“

March 21 — 13:30 - 14:30 (Room: Tenne)

Sitzung: Junior GBM Leaders

March 21 — 19:00 - 21:00 (Room: Darre)

Meeting Postdocs@GBM

March 21 — 19:00 - 21:00 (Lecture hall)

Vollversammlung: Junior GBM

Conference Office

Opening hours are

Wednesday:	16.00 - 19:45
Thursday:	08:00 - 17:00
Friday:	08:30 - 16:00
Saturday:	08:30 - 11:00

Phone: +49 69 6605670

Venue

The Kolloquium takes place in the „Alte Mälzerei“ in Mosbach/Baden (Germany)

Alte Mälzerei
Alte Bergsteige 7
74821 Mosbach/Baden

Internet

There will be a wireless LAN access point in the conference centre.

SSID: GBM
Key: gbm-online

Lunch & Coffee Breaks

Coffee, tea and mineral water will be provided for free during the coffee breaks.
Lunch and Dinner is available at your own expense in the conference center or in one of the restaurants in the city of Mosbach.

Please note

Your name badge and the program booklet are available at the registration desk.

We kindly ask to wear your name badge as an entry ticket during the whole meeting.


Elz
Unterm Haubenstein
Merianweg
Landes-Gartenschau-Park
POLIZEI
Hauptstraße
ii Hotel „Zum Amtsstüble“
Amtsgericht
Landesgericht
Lohrtalweg
Kistnerstraße
Hauptstraße
Am oberen Graben
Gartenweg
Harnisch gasse
Ölgasse
Hospitalgasse
Farbg.
Hauptstr.
Schwanengasse
Carl-Theodor-Straße
Zwingerweg
Alte Bergsteige
DHBW
Bussestraße
Alte Mälzerei
Richtung Würzburg
An der Bachmühle
Tief
B27
TAXI
Kesslergasse
Kroneng.
Kronengasse
Marktplatz
Kirchplatz
Collekturgasse
Alter Schulplatz
Badgasse
Schlossgasse
Zwingerstraße
Oberer Mühlenweg
IHK
Entengasse
Frohnbrunneng.
Löwenbrunneng.
Heissensteingasse
Heugasse
Schmelzweg
Pfalzgraf-Otto-Straße
Renzstraße
Finanzamt
1 Oberer Torturm
2 Haus Kickelhain
3 Altes Hospital
3a Scharfrichter-Haus
4 Palm’sches Haus
5 Rathaus
6 Salzhaus
7 Synagogenplatz
8 Altenzentrum Pfalzgrafenstift
9 Mosbacher Schloss
10 Kandel
11 Kiwwelschisserbrunnen
12 Stiftskirche
i Congress Centre „Alte Mälzerei“
ii Hotel „Zum Amtsstüble“
iii City Hall

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Walter deGruter (Booth 1b)
BMG Labtech (Booth 2)
Nikon (Booth 3)
Xceltis (Booth 4)
Cytiva (Booth 5)
xyna.bio (Booth 6)
CryoCloud (Booth 7)

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List of Posters

sorted by presenting author

O 01
Khadija Aichane-Simon
Enforced phosphatase recruitment as a novel strategy in the treatment of acute myeloid leukemia

E 02
Marius Amann
Engineering Plasmodium falciparum Proteins for Small-Molecule Drug Discovery: Investigating Stability, Structural Dynamics, and Biophysical Effects

O 02
Varvara Apet
Design and optimization of flavoproteins for hyperpolarized EPR methods

E 03
Katharina Bachschwöller
Design of functional proteins by fragment-based chimeragenesis

E 04
Anna Backeberg
De novo design of multiple-geometry forming protein scaffolds

A 01
Julian Beck
Scaffolding a Kemp eliminase activity into an idealized de novo TIM barrel

E 05
Philipp Becker
Past to Protocells: Ancestral Min Proteins and Early Pattern Formation

O 03
Stine Behrmann
Predicting structural features of suppressor tRNAs using MD simulations

P 01
Ramachandra M Bhaskara
Decoding homeostatic pathways: from data Streams to molecular mechanisms

O 04
Patryk Bielski
Bicelles assembled with the G protein-coupled receptor rhodopsin as model lipid-protein system for interaction studies

A 02
Sophie Binder
AI-based protein design and validation

A 03
Andreas Blaha
A conserved fertilization complex predicted by AlphaFold2-Multimer bridges sperm and egg in vertebrates

A 04
Alexander Braun
De novo design of triosephosphate isomerases using generative language models

A 05
Breimann Breimann
Charting γ-Secretase substrates by explainable AI

O 05
Constanze Breithaupt
Multimerization of Grb2 revealed by the Grb2-Gab1(497-528) complex structure

E 07
Adrian Bunzel
AI.zymes: A Modular Platform for Evolutionary Enzyme Design

List of Posters

sorted by presenting author

P 02
Grzegorz Chojnowski
gapTrick – Structural characterisation of protein-protein interactions using AlphaFold with multimeric templates

P 03
Sandrine Coquille
Mapping of allosteric protein landscapes using AI approaches

O 06
Jan A. Dewald
Validation and characterization of a fourth $preQ_1$ riboswitch class

O 07
Karthikeyan Dhamotharan
A core network in SARS-CoV-2 nucleocapsid NTD drives domain stability and RNA recognition.

M 01
Simon Dürr
Predicting interactions of proteins with metals using cofolding methods and AllMetal3D

A 06
Stefan Düsterhöft
MaPIN: A computational pipeline to Map Protein Interaction Networks.

O 08
Christoph Elfmann
Cutting-edge tools for structural biology: bringing AlphaFold and Foldseek to the people

O 09
Mohammad ElGamacy
Design and development of synthetic G-CSFR modulators

A 07
Robert Englmeier
Towards automating cryo-EM data analysis using AI, new algorithms and large scale analysis

M 02
Inken Fender
Predicting Molecular Hotspots for Efficient Drug Discovery using Deep Learning

O 10
Anna Franziska Finke
Coupling of ribosome biogenesis and translation initiation in human mitochondria

O 11
Karlo Franke
Functional analysis of synthetic cytokine receptors and possible heterodimerisation for optimised intracellular signalling

E 01
Emily Freund
Redesigned RNA-binding domains to study their effects on helicases

O 12
Béla Frohn
Protein Design For and With Synthetic Cells

O 13
Andreas Gagsteiger
Expanding the available structure and sequence space of PET degrading enzymes

A 08
Chiara Gasbarri
AI in support of drug off-target effect research: the CavitOmix Copilot

List of Posters

sorted by presenting author

O 14
Florian Gisdon
Graph-Theoretical Analysis of Functional Changes in an Open and Closed Conformation of Complex I

E 37
Anastasia Götz
Reprogramming self-inserting nanopores for differential transport across synthetic membranes

E 08
Salomé Guilbert
In Silico Design of Enzymes to Degrade Short-chain Per- and Polyfluoroalkyl Substances (PFAS)

M 03
Jannik Adrian Gut
Synthetic MSAs identify protein conformations

O 15
Jan Hartmann
Severe discrepancies between the newly determined crystal structure of the RNA aptamer B1m15 in complex with the bacterial repressor DasR and the AlphaFold3-predicted structure.

E 09
Noah Ernst Holzleitner
AI-guided engineering of CRISPR-Cas proteins

E 10
Stefan Hristov
ForceYield2: Validating AI-Assisted Protein Design With In Vivo Selection

A 09
Maxim Janzen
Predicting single residue effects on peptide binding specificities in designed Armadillo repeat proteins

E 11
Michael Adrian Jendrusch
Fast and flexible protein structure generation with sparse all-atom denoising (SALAD)

E 12
Alena Khmelinskaia
Tales of Dynamic Protein Assembly Design

E 13
Hubert Klein
In-silico Design of Foldamer - Protein Interactions

A 10
Sarah Knapp
Predicting PARP15 networks with proximity-ligation based mass spectrometry data and MaPIN (Mapping of Protein Interaction Networks)

E 14
Johanna-Sophie Koch
Evaluation of cobalamin-binding chimeras designed by fold recombination

E 15
Kerlen Korbeld
Enriching Stabilizing Mutations through Analysis of Short Molecular Dynamics Simulations by BoostMut

P 04
Jacqueline Krohn
Assessing AI Driven Protein Structure Prediction Methods with Heparanase 2 Splicing Forms

List of Posters

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E 16
Georg Künze
Computational engineering of a metagenome-derived polyester hydrolase for efficient PET depolymerization

P 05
Pasquale Lamagna
Beating viruses at their own game: exploiting structural homology and protein structure predictions to identify new viral host-virus protein-protein interactions.

O 16
Olive Laprévote
Step by step - Engineer Trp Repressor to Walk in a Tandem Gait

E 17
Horst Lechner
Developing Machine-Learning-Driven Sequence Design Strategies to Stabilize and Produce Challenging Enzymes

T 01
Jennifer Leclaire
BiochemicalAlgorithms.jl -- Rapid application development in Julia

E 18
Bruce Lichtenstein
Functional Ligands: Protein design for electrochemical and structural control of ligand properties

P 06
Katja Luck
Structural annotation of disease-relevant protein interaction interfaces involving disorder

O 17
Marharyta Makarova
A novel rotamer library for nucleic acids enables the design of protein-nucleic acid complexes with the protein design software MUMBO

A 11
Yelyzaveta Makedon
The role of Beta-2 microglobulin tryptophan mutagenesis in detecting MHC class I heavy chain folding in vitro

P 07
Anja Marquardt
Integrating Artificial Intelligence Based and Classical Structural Biology Methods to Understand the Impact of the β-Actin G74S Mutation on Histidine Methylation

E 20
David Medina-Ortiz
Integrating geometric deep learning with explainable artificial intelligence to assist protein engineering

P 08
Pasquale Miglionico
AlphaFold3-based Prediction and Design of GPCR-G protein Coupling

A 12
Johanna Moeller
Computational stabilization and functional characterization of single-chain T cell receptors targeting a cancer epitope

A 13
Felix Moorhoff
SelectZyme: AI-Based Interactive Protein Space Visualization for Enzyme Discovery, Selection, and Mining

List of Posters

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E 21
Lennart Nickel
Engineering Cell Type Specific AAVs by Computational Protein Design

E 22
Martin Pacesa
Accurate binder design using BindCraft

O 18
Marina Parr
Computational analysis of translation elongation factors

O 19
Lars-Oliver Peters
Visual dysfunction caused by mutations in the cGMP-signaling protein complex

A 14
Thorsten Pfirrmann
CiliAI: A Web-Based Machine Learning Platform for Automated Detection, Analysis, and Signal Densitometry of Primary Cilia in Confocal Microscopy Images

O 20
Agata Raczyńska
Enzymes for Polyurethane Degradation: Computational and Experimental Strategies for Design and Discovery

P 10
René Rasche
Pathogenic potential of RalGAP variants explained by combined structural and computational analysis

O 21
Johanna Rathke
Quantitative analysis of Ezrin mutants defective in f-Actin Binding observed with in vitro minimal Actin cortices

E 23
Katharina Rauchenwald-Köchl
Exploring enzymatic active sites using 3D point clouds representing physico-chemical properties of protein cavities

O 22
Johannes Regner
Functional and structural characterization of UbiB

P 11
Bianca Reschke
FRET-assisted structural modeling of dynamic protein ensembles

P 12
Till Rudack
Integration of experiment and theory unveils structure, dynamics, and function of multi-protein complexes

T 02
Jakob Ruickoldt
CryoCrane

P 13
Peter Russ
Challenges for AI driven structure prediction: The peacock's feather keratin

E 24
Marc Scherer
Two-state design enabled the reliable optimisation of dynamic small molecule binding proteins

List of Posters

sorted by presenting author

E 25
Phillip Schlegel
From Genome Mining to Enzyme Engineering: A case study one the Phosphoramidon Biosynthetic Pathway

E 26
Lisa Schmidt
Analysis and design of protein fold switches

T 03
Clara Schoeder
Between sampling and scoring – a fair comparison of self-supervised machine learning methods

M 04
Leif Seute
Learning conformational ensembles of proteins based on backbone geometry

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