ACCELERATE
YOUR DRUG DESIGN.

3D STRUCTURE DETERMINATION

ATEM
STRUCTURAL DISCOVERY

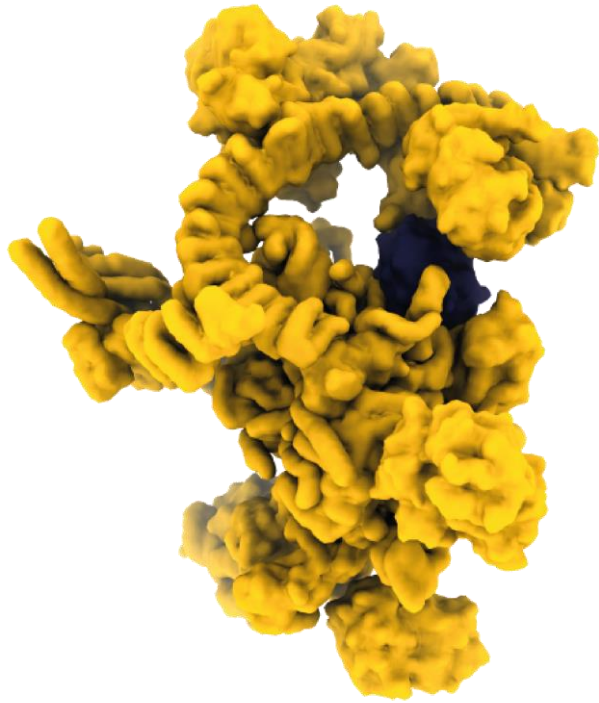
» *At ATEM, we believe industrial cryo-EM is still in its infancy. Using the technology's full potential in drug discovery and R&D, we are building a uniquely integrated platform to meet present and future commercial demands.*

Karl Bertram, PhD / Founder, ATEM Structural Discovery

WE ARE YOUR

CRYO-EM EXPERTS.

ATEM is a technology platform company. We leverage the rapid developments in cryo-electron microscopy (EM) and artificial intelligence (AI) to advance biotech & pharmaceutical companies.



CONTACT

ATEM Structural Discovery GmbH
Birkenweg 5
42781 Haan, Germany

T. +49 (0) 173 / 7 859 627
contact@atem.bio
WWW.ATEM.BIO

CONTENT.

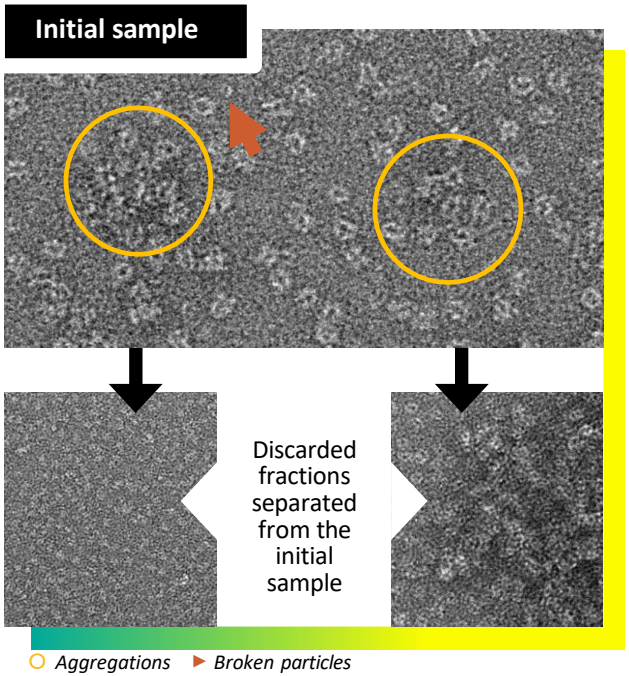
CASE STUDY

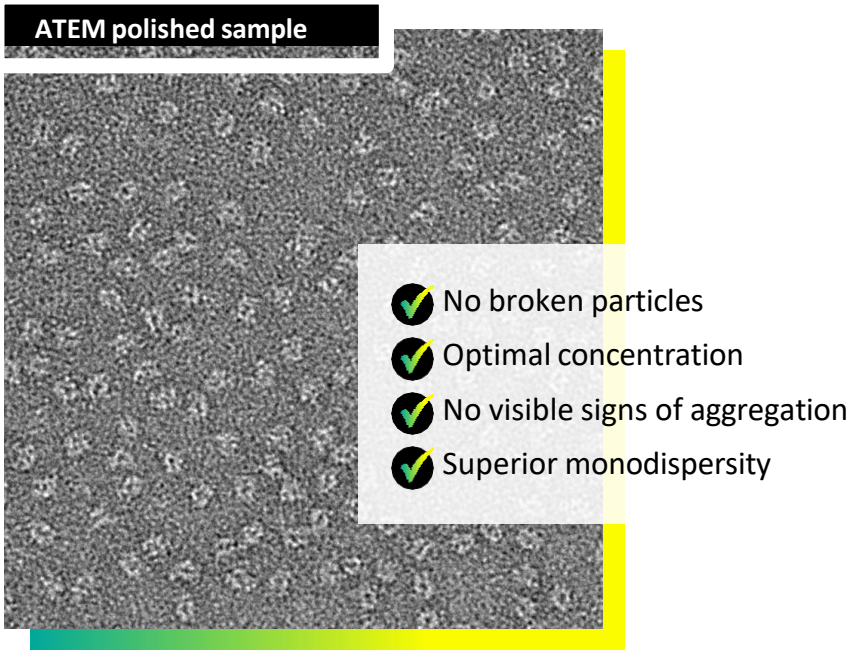
HIGH-RESOLUTION 3D CRYO-EM STRUCTURE.

of Human PRMT5:MEP50

POLISHING WORKFLOW
FOR OUTSTANDING SAMPLE QUALITY

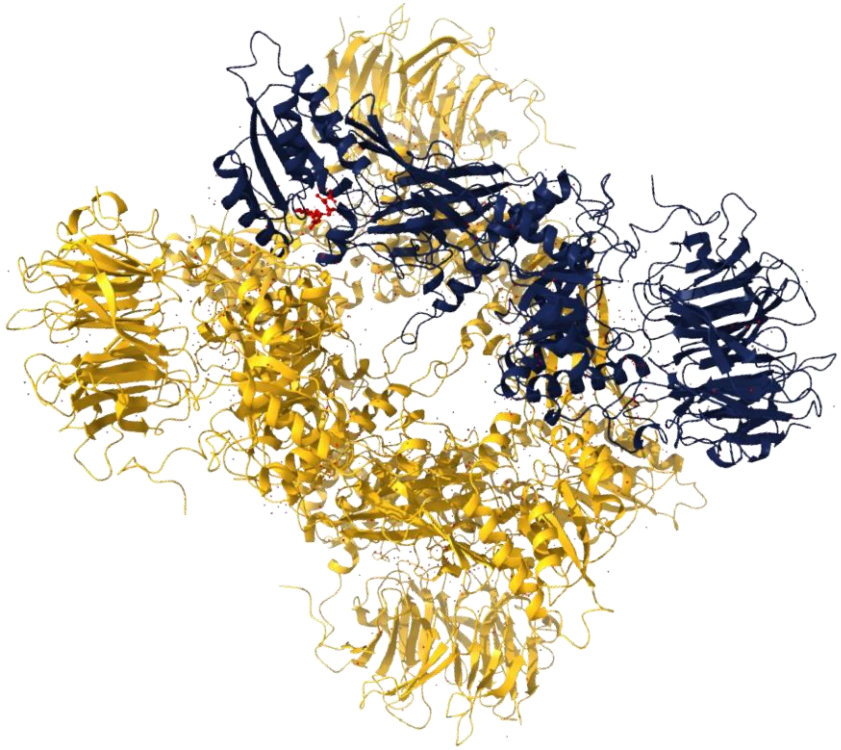
Our experts start by screening new samples and selecting an optimal polishing strategy. This includes chromatographic procedures or gradient density centrifugation, mild sample concentration, or buffer optimization procedures to obtain a sample that is perfectly suited for reliable and high-resolution 3D structure determination. We evaluate samples for improvements in purity, homogeneity, and monodispersity using rapid and reliable negative stain TEM screenings. Ultimately, we select fractions that show the best quality attributes for further cryo-EM preparation & analysis.





RESULT BEST SAM LIGAND BOUND CRYO-EM STRUCTURE TO DATE

The atomic model (ribbon representation) of the human PRMT5:MEP50 holoenzyme forms a complex with its natural cofactor S-Adenosyl methionine (SAM). The SAM ligand was added to the preparation just prior to grid-freezing. One heterodimer of PRMT5:MEP50 (Blue) and SAM (Red) is highlighted.



KEY FEATURES

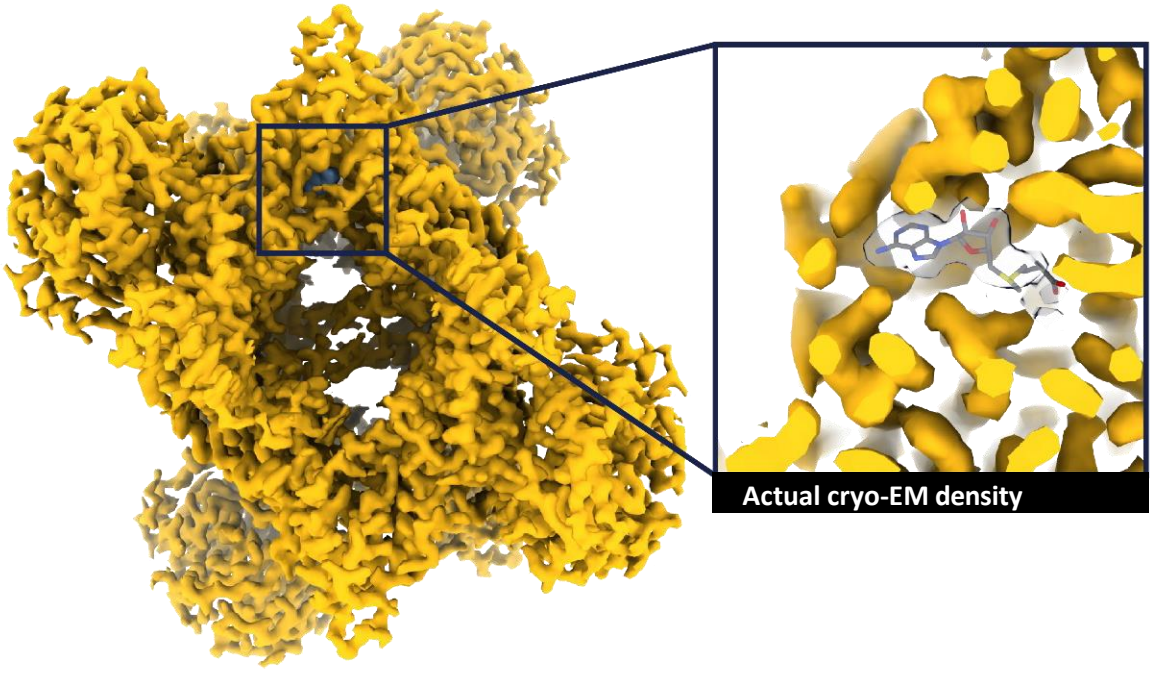
- 3 rounds of ATEM particle polishing were performed to prepare an optimal sample and ideal cryo-EM grids
- High-resolution dataset collected in cryo-EM

  Dataset: ~ 5000 micrographs were collected in one session on a high-end cryo-TEM, resulting in ~$1.0*10^6$ raw particles for data processing. $2.5*10^5$ particles (~25%) were used for the calculations of the final, highest resolution EM-density maps
- Final Resolution:

  2.6 Å Based on the Fourier shell correlation (FSC) 0.143 cut-off criterion
- Unambiguous modeling of the ligand

NEW INSIGHTS
INTO LIGAND CONFORMATION

The model was built and refined based on the 2.6 Å resolution cryo-EM density map. The natural SAM ligand is discerned in the C-terminal catalytic domain of PRMT5.



- Natural ligand clearly discernible (S-Adenosyl methionine, SAM)
- Unambiguous ligand identification in density map
- New insights: differing ligand conformation compared to X-ray crystallography based structures (i.e. PDB 7L1G)

High-resolution screening campaigns for multiple small-molecules or biological ligands possible

MEET OUR FOUNDERS:

Dr. Karl Bertram
T. +49 (0) 177 / 4 174 665
karl.bertram@atem.bio

Daniel Winkler
T. +49 (0) 173 / 7 859 627
daniel.winkler@atem.bio

SCHEDULE A MEETING TODAY

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