

A Comprehensive Structural Biology Platform for Structure-Based Drug Discovery

WuXi Biology

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Overview

Experience

>20 years of structural biology experience covering all areas of SBDD

Expertise

Integrated protein production, biochemistry, biophysics and structural biology groups

Reliability

Competitive timelines and prices

Infrastructure

State-of-the-art structural biology laboratory and in-house IT infrastructure

Data Collection

Swiss Light Source beamline partner
Rapid access to Titan Krios microscopes

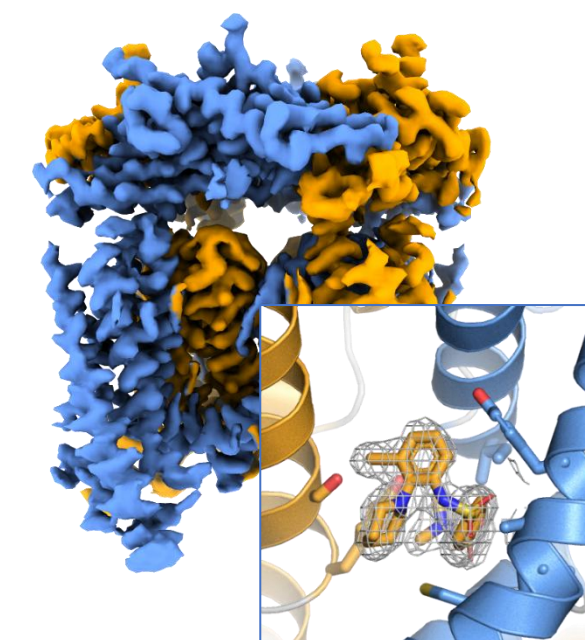
Partnerships

Trusted partner to biotech and pharmaceutical companies

Membrane Proteins

Membrane protein structure determination service

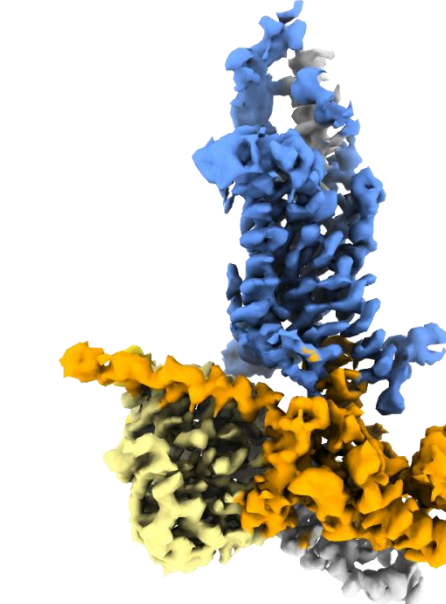
TRPML1



- Protein production in HEK293 cells
- In-house grid preparation with Vitrobot IV
- Data collection with Titan Krios with K3 detector
- Data processing with CryoSPARC

Membrane protein production platform for expression screening and large-scale protein production

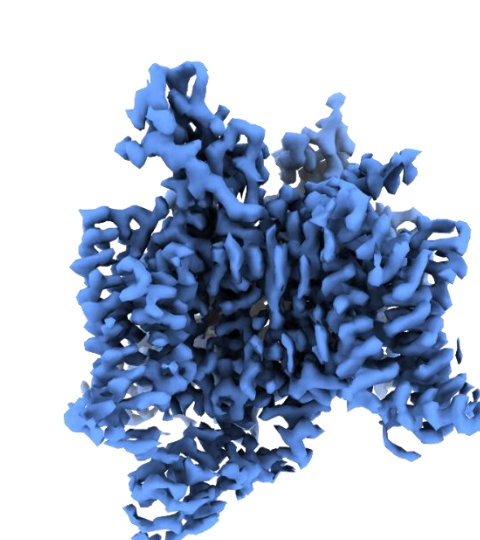
PAC1R-Gα-Gβ-Gγ



- Protein production in insect cells
- Stabilization of complex with antibody
- In-house grid preparation with Vitrobot IV
- Data collection with Titan Krios with Falcon 4i detector
- Data processing with RELION

Biophysical characterization of constructs and protein-ligand interactions by MS, MST, Spectral Shift, nanoDSF and SPR

Voltage-Gated Channel



- Protein production in HEK293 cells
- In-house grid preparation with Vitrobot IV
- Data collection with Titan Krios with Falcon 4i detector
- Data processing with CryoSPARC

Off-the-Shelf Targets

Off-the-shelf service with over 200 targets from broad range of classes

Established protocols for protein production, crystallization and/or grid preparation

Structure determination by X-ray crystallography or cryo-EM

Kinases

AMP kinase, BRAF, BTK, CDC7-DBF4, CDK1-CKS2-CCNB1, CDK2, CDK2-CCNA2, CDK2-CCNE1, CDK4-CCND1, CDK4-CCND3, CDK6, CDK7, CDK7-CCNH-MAT1, CDK9-CCNT1, CDK12-CCNK2, CK1a, CK1d, EGFR, FGFR1, FGFR2, FGFR3, FGFR4, IRAK3, IRAK4, JAK1, JAK2, JNK1, JNK2, JNK3, KIT, LCK, MAP4K1, MKNK2, PIK3Cα, PIK3Cα-PIK3R1, PIK3Cγ, PIP4K2α, PIP4K2β, PIP4K2γ, PKA, PKM2, PKR, RSK1, SIK3, SRC, TYK2, Wee1

Proteases

3C-like protease (SARS-CoV-2 and Norovirus), Cathepsin K, Cathepsin S, MALT1, USP7, USP21

Targeted Protein Degradation

CDK12-CCNK-DDB1 Ternary Complexes, CRBN, DDB1, CRBN-DDB1, CRBN-DDB1 Ternary Complexes, SKP1-SKP2-CKS1, VHL-Elongin B-Elongin C

Histone Modification

BRD4, BRD9, CREBBP, HDAC2, HDAC7, HDAC8, JMJD2C, JMJD2D, MLLT1, NSD1, PRMT5-WDR77, SIRT2

Innate Immunity

cGAS, STING

Nuclear Receptors

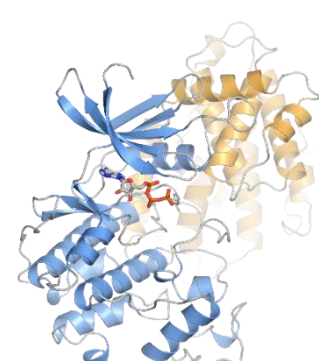
AR, ERα, GR, PXR, RORγ

Nucleic Acid Binding Proteins

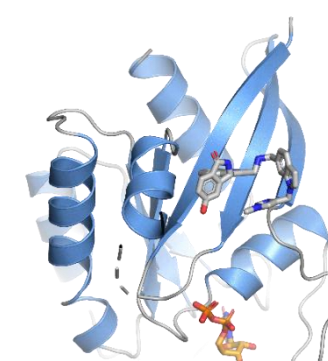
APOBEC3B, cGAS, PARP1, SMARCA2, SND1, STAT1, STAT3, STAT5B, STAT6, WRN



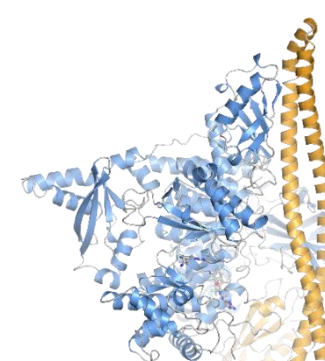
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Cyclin Dependent Kinases



RAS Family



PIK3CA-PIK3R1



WRN

Gene-to-Structure Services

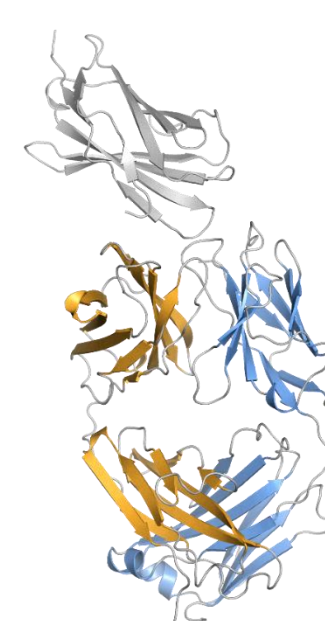
Gene-to-structure service to enable both characterized and uncharacterized targets

Design and production of structural biology constructs

Biophysical characterization of constructs and protein-ligand interactions by MS, MST, nanoDSF and SPR

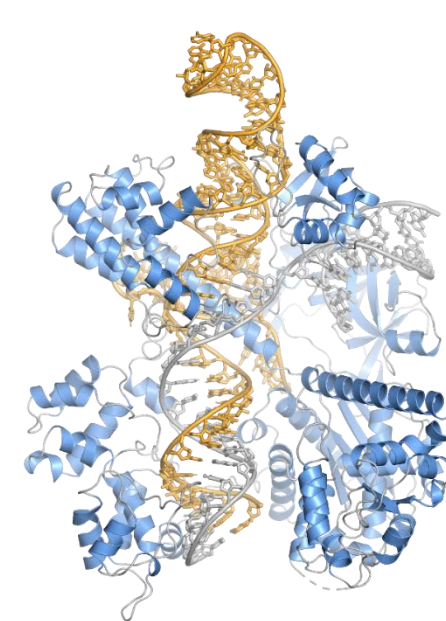
Structure determination by X-ray crystallography or cryo-EM

Biologics



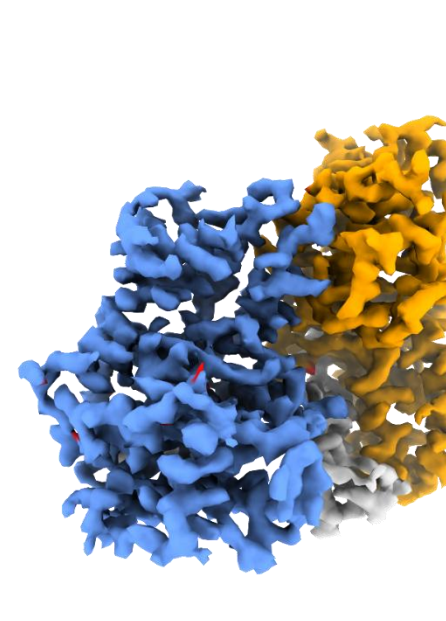
CRBN

CAS9-sgRNA-dsDNA

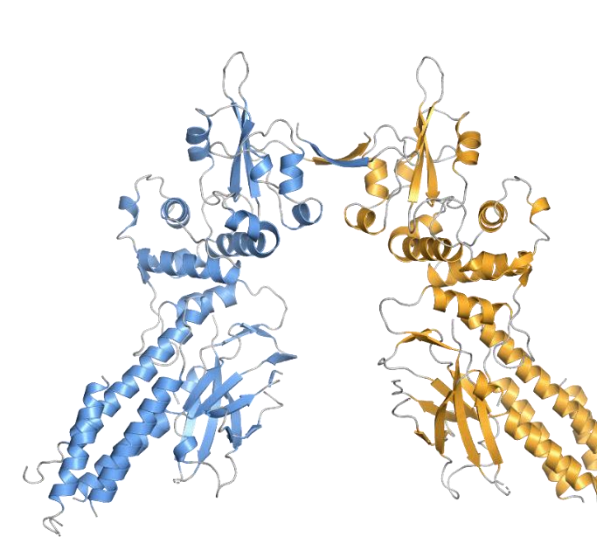
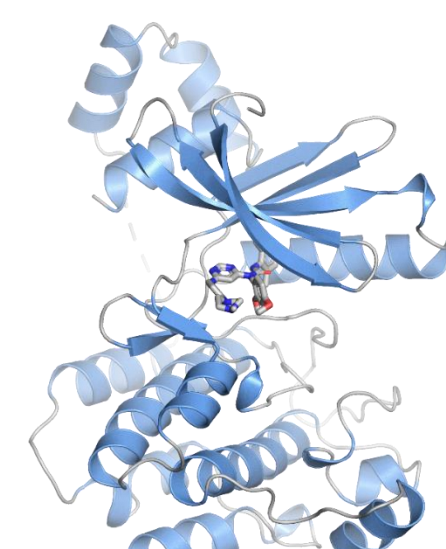
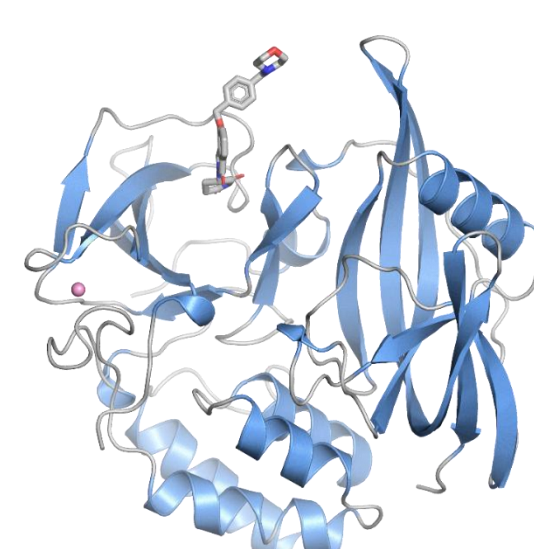


Salt Inducible Kinases

CDK7-CCNH-MAT1



STAT6



High-Throughput Crystallography

High-throughput service for primary and orthogonal screening by X-ray crystallography

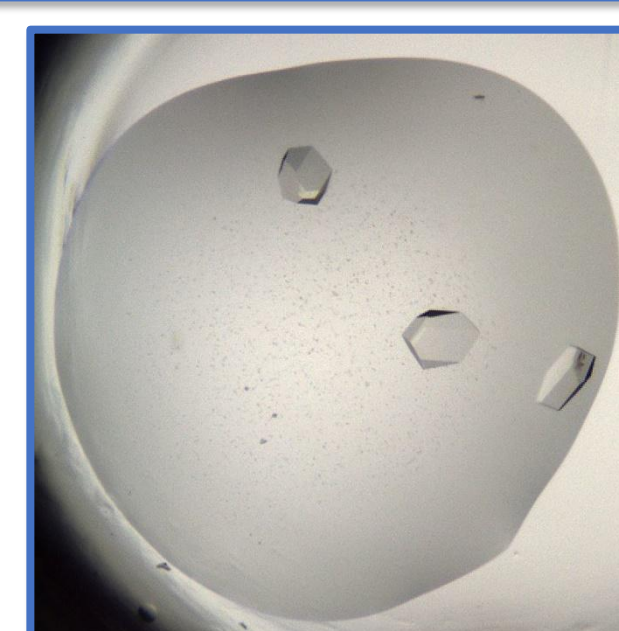
Soaking or co-crystallization of 10s-100s reversible and non-reversible fragments

In-house infrastructure for high-throughput fragment soaking (Labcyte Echo 555) and mounting (OLT Shifter)

High-throughput data collection at Swiss Light Source

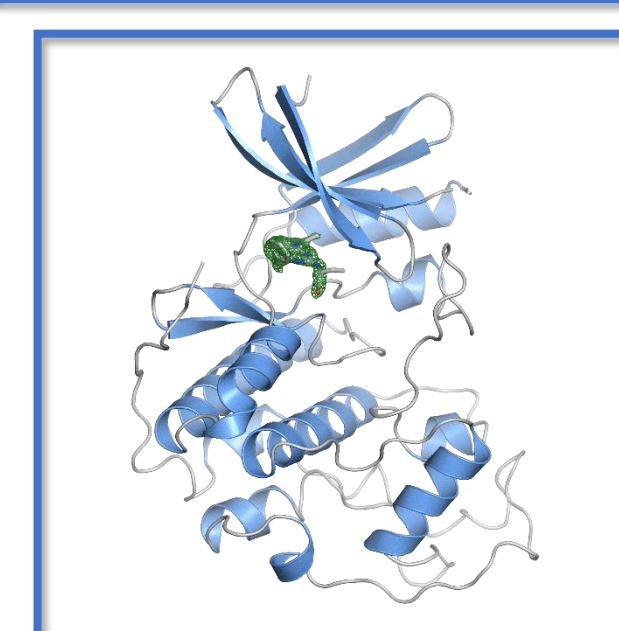
Reversible Interactions

Apo Crystallization



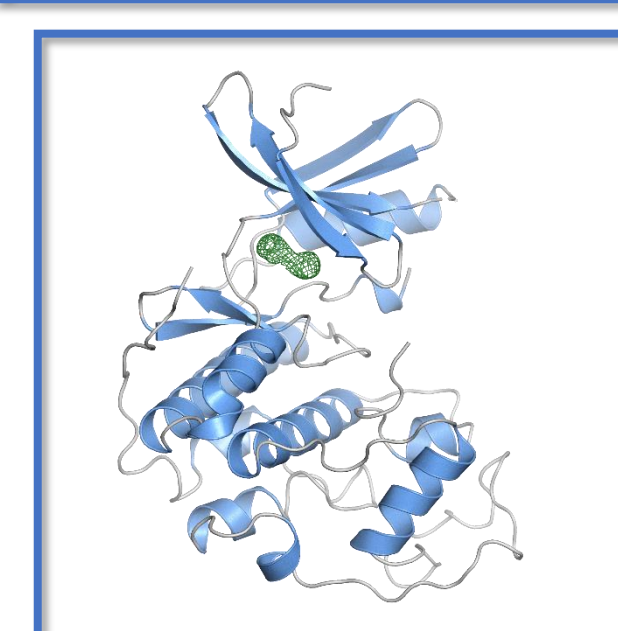
- Initial screening and/or focused screening based on established conditions

Development of Soaking System



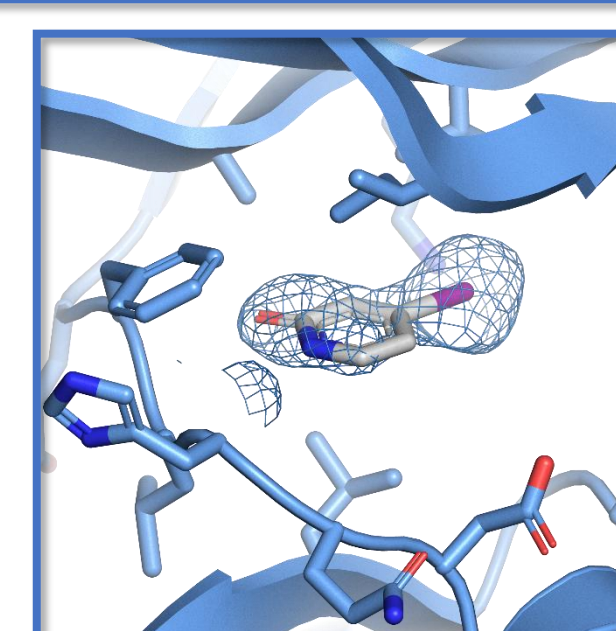
- DMSO tolerance test
- Soaking with tool compounds

Soaking Data Collection



- High-throughput soaking with Echo and data collection on beamline PXII at Swiss Light Source
- Automatic data processing and identification of binders

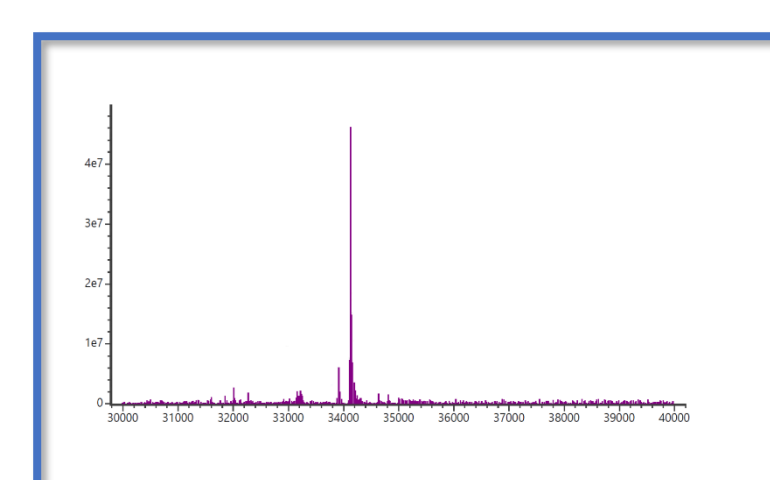
Structure Determination



- Rebuilding and refinement
- Direct observation of binding mode

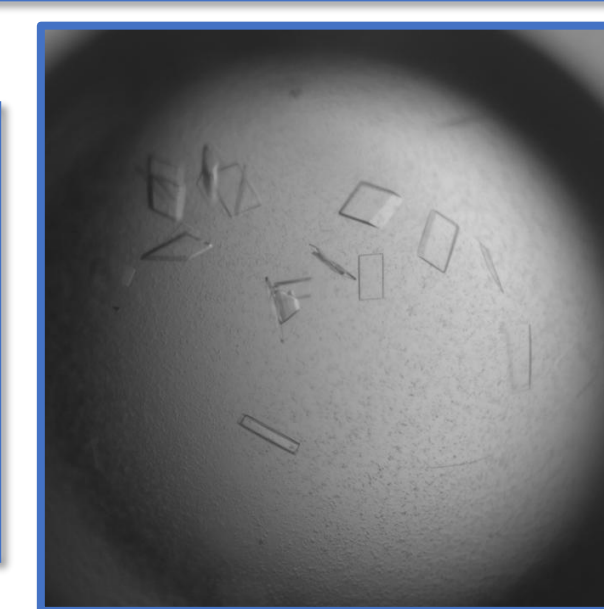
Non-Reversible Interactions

Mass Spectrometry



- Screening of fragments or compounds by MS
- MS-guided optimization of labeling conditions

Crystallization



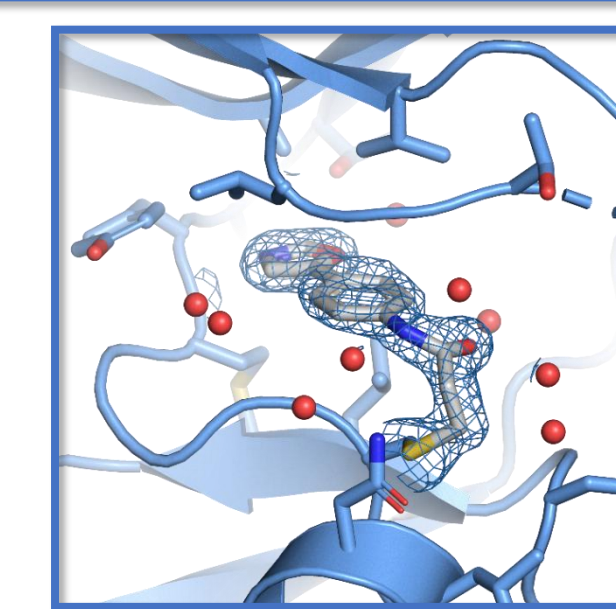
- Initial screening and/or focused screening based on established conditions

Data Collection



- High-throughput data collection on beamline PXII at Swiss Light Source
- Automatic data processing and identification of binders

Structure Determination



- Rebuilding and refinement
- Direct observation of binding mode and labeling chemistry

