

# STRUCTURAL BIOLOGY

The structural biology group at ChemPartner is equipped with state-of-the-art technology, such as X-ray crystallography, STD, NMR, SPR, TSA, DLS, and more. This elite team is predominantly made up of scientists with masters degrees and led by Western-trained PhDs with years of biology experience.

## SCIENTIFIC EXPERTISE

### X-RAY CRYSTALLOGRAPHY

- Fragment/Structure-based Drug Design (FBDD/SBDD)
- Antibody structural studies to support IP and/or design
- Lipidic Cubic Phase (LCP) crystallization services
- DNA to structure

### NUCLEAR MAGNETIC RESONANCE (NMR)

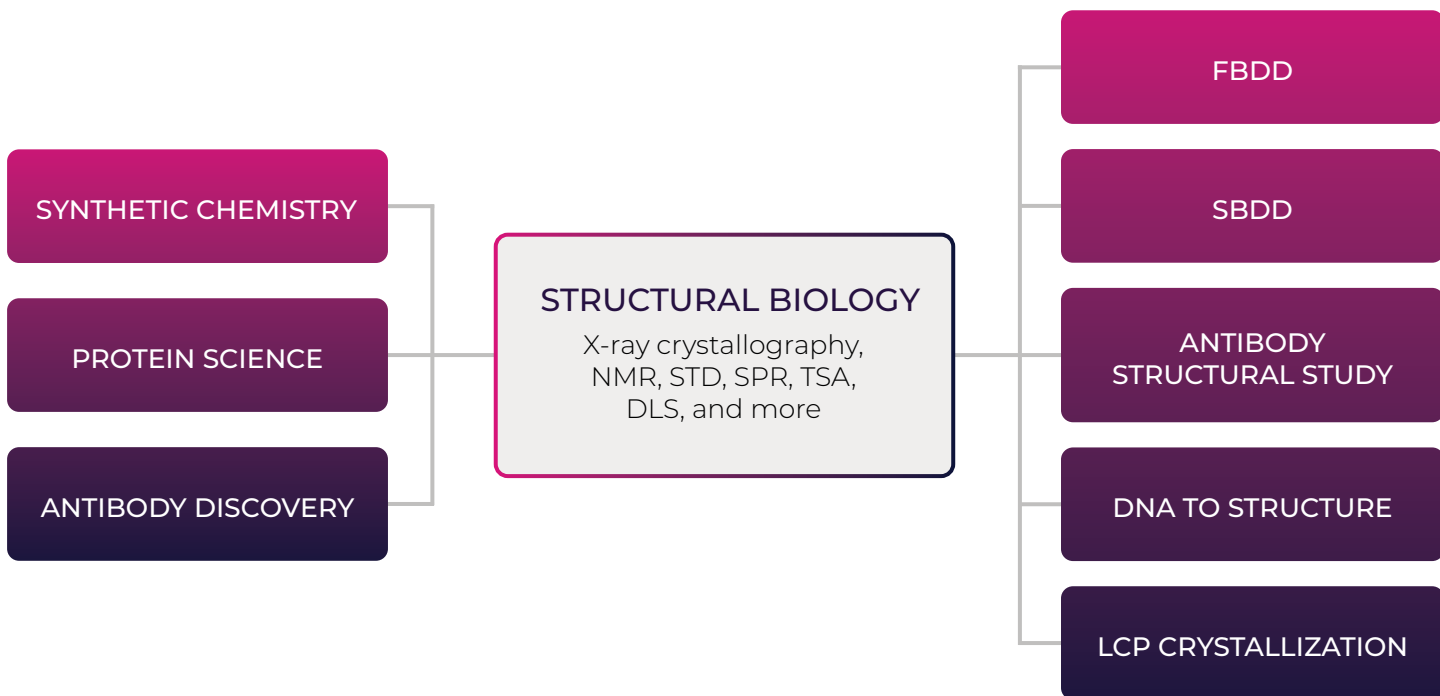
- Fragment / Structure-based Drug Design (FBDD/SBDD)
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### DEDICATED PROTEIN PRODUCTION TEAM

- Membrane protein production to support GPCR drug discovery
- Isotope-labeled protein production to support NMR services

### BIOPHYSICS STUDIES

- Surface Plasmon Resonance (SPR)
- Thermal Shift Assay (TSA)
- Dynamic Light Scattering (DLS)



CASE STUDY:

## FBDD PROJECT

	PROTEIN 1	PROTEIN 2
Fragments Received	140 (17 batches)	18
Crystals Screened	982	78
Datasets Collected	221	19
Structures Delivered	77	15
Turnaround (best batch/overall)	15/30 days	15/15 days
Average Success Rate	55%	93.3%

- Regular and easy access to Shanghai Synchrotron Radiation Facility (SSRF)
- High quality structural data
- Fast and steady turnaround

CASE STUDY:

## AB-ANTIGEN COMPLEX STRUCTURAL STUDY

### CRYSTAL STRUCTURE OF ANTIBODY AND ANTIBODY-ANTIGEN COMPLEX

- In-house developed Ab-specific screening kits
- Structural Modeling

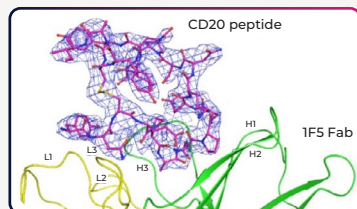
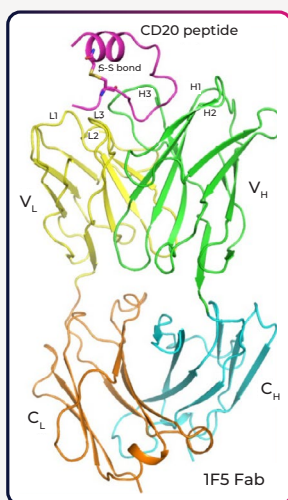
### MODEL BASED HUMANIZATION DESIGN

- Antigen modeling
- Epitope prediction

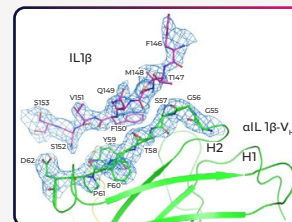
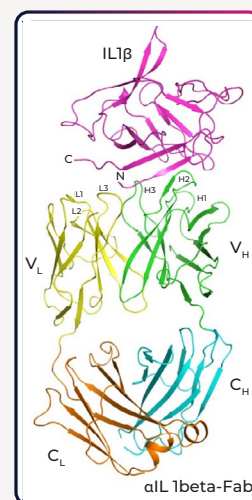
### BIOINFORMATICS PLATFORM

- Stability prediction
- Immunogenicity prediction

DIFFRACTION DATA STATISTICS	
Space group	P2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>
Unit cell (Å)	a=86.76 b=164.06 c=296.38
Resolution (Å)	50.00-2.95 (3.00-2.95)
Completeness (%)	16.3 (41.9)
Rmerge (%)	6.159E-11
I/s<I>	6.0 (1.8)
Redundancy	3.8 (2.4)



DIFFRACTION DATA STATISTICS	
Space group	I 4122
Unit cell (Å)	a=98.632 b=98.632 c=377.541
Resolution (Å)	50.00-2.75 (2.82-2.75)
Completeness (%)	95.7 (80.0)
Rmerge (%)	18.9 (45.7)
I/s<I>	9.6 (1.85)
Redundancy	7.7 (2.6)



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