Over 20 years of expertise in structure based drug discovery

Trusted partner for global pharma and biotech since 2005

Over 200 targets established for structure-based drug discovery

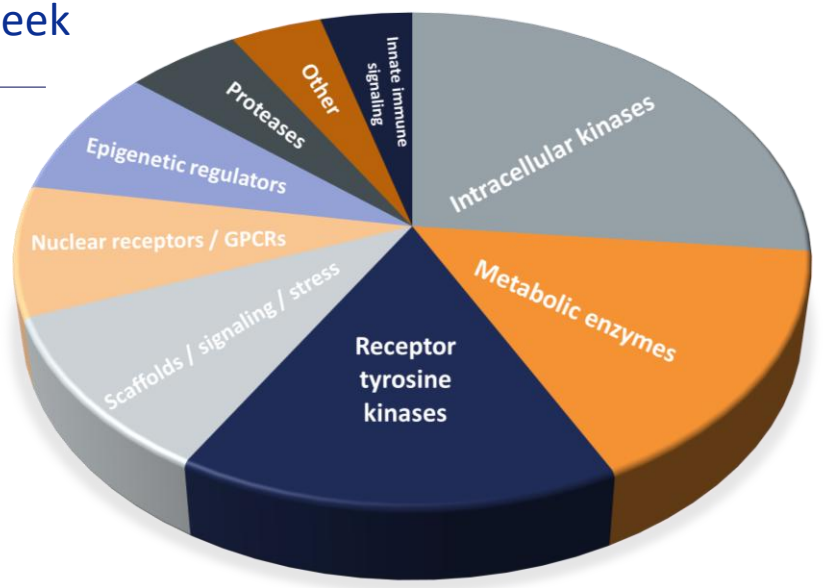
Senior level experts leading and managing projects

Capacity to screen up to 1,000 crystals/week

Over 400 structures determined in 2026

> 250 XPRESS targets

Over 20 off-the-shelf *soakable* targets from a wide range of classes



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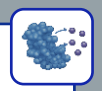
High-Throughput Crystallography for early drug discovery

Hit **Identification**



- Fast and at large-scale
- Confidently includes weak (µM or mM) or fragment binders
- Discovers unexpected biologies
- Reveals allosteric sites, cryptic pockets and alternate binding modes

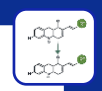
Hit Validation

- Eliminates of false positives
- confirms and contextualizes biophysical signals
- Allows multi-dimensional validation

Hit Prioritization

- Eliminates poor geometries
- Prioritizes productive binding modes
- Differentiates similar affinities & differing structural behaviour

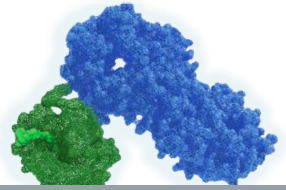
Hit-to-Lead Optimization



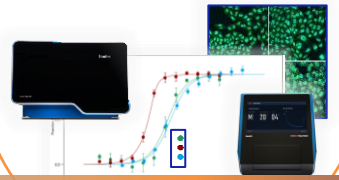
- Identifies vectors for chemical expansion
- Allows more rational optimization of potency
- Creates large training sets for methods development and validation

High-Throuput Crystallography workflows at Crelux

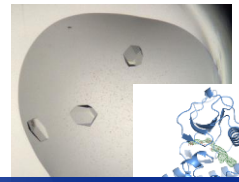
Protein Production



Biophysics & Screening



High-Throughput Crystallography

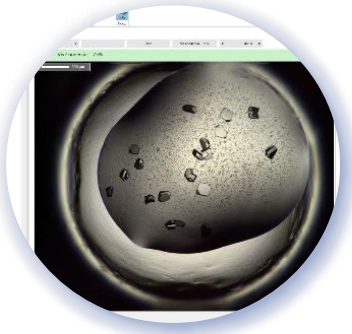


Fully Customized – High-End Support –Comprehensive QC

Broadest Technology Suite for Hit Finding Globally

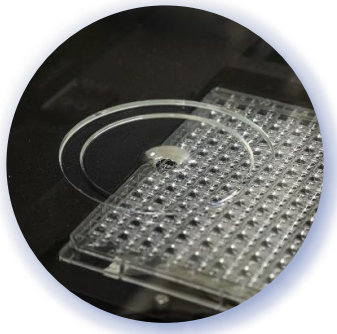
Fast & Scalable Structure Determination

Precise & Reproducible **Crystallisation**



Instant Feedback on **Crystal Growth**

Contact-free **Ligand Transfer**



High-throughput **Crystal Harvesting**

High-resolution, Fully Automated **Data Collection**

Protected & Fast **Data Processing & Structure Determination**

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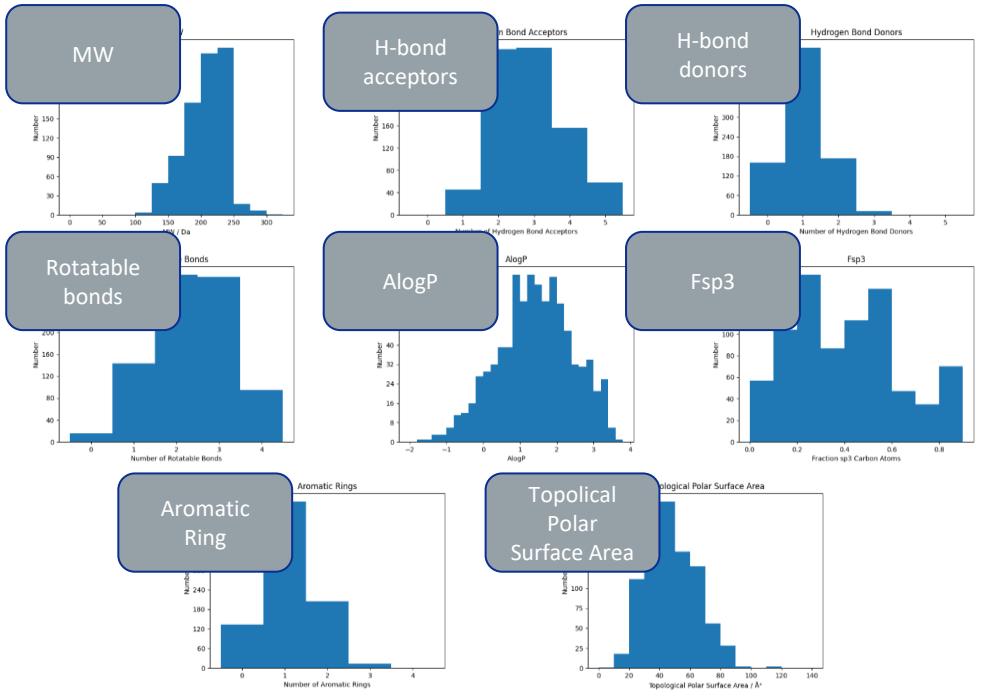
Fragment Libraries for High-Throuput Crystallography

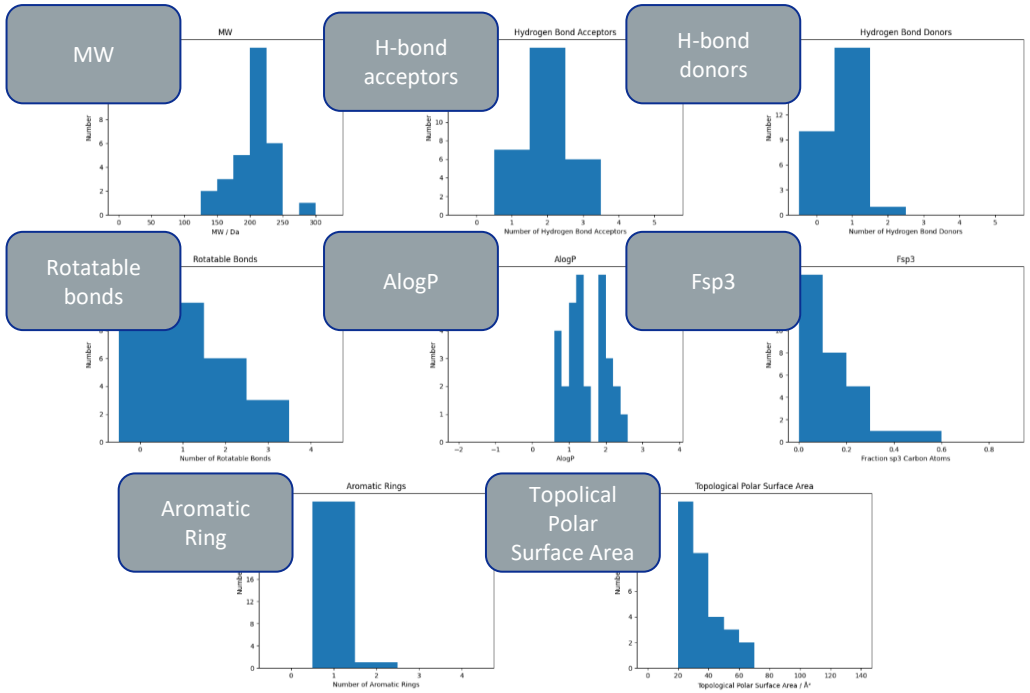
DSI-Posed Library

- Large, optimized for crystallographic fragment screening
- 860 highly diverse fragments for rapid and straightforward hit expansion

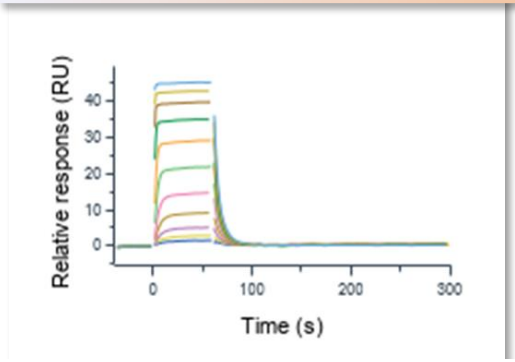
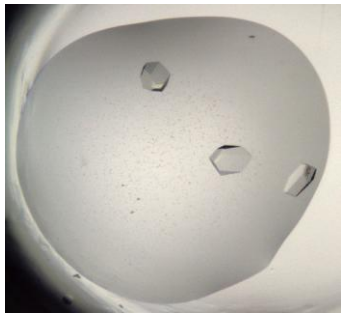
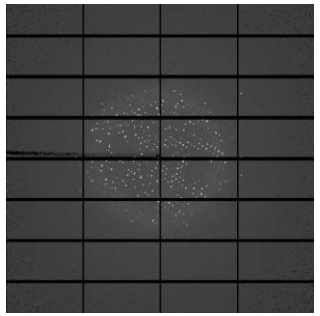
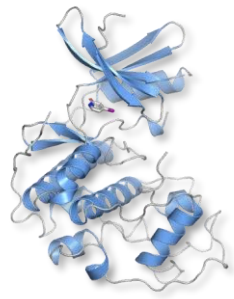


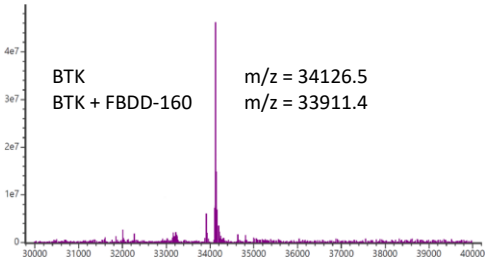
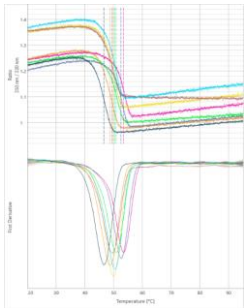
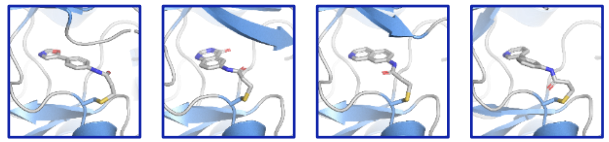
FragLites

- Small , suitable for identification and mapping of potential ligand binding sites
- 31 halogenated fragments with adjacent hydrogen bond acceptors and/or donors



A collaborative track record – Case Studies CDK2 and BTK

SPR Screen	Crystallization	Data Collection	Structure Determination
			
85 SPR hits with KD < 500 µM	HT soaking of 57 fragments	HT data collection	Structure-based identification of **40 fragments bound to CDK2**

Intact Mass Spectrometry	Orthogonal Validation	Structure Determination
		
Intact MS: 62 binders out of 200 covalent fragments	nanoDSF, MST, ADP-Glo assays	HT data collection Confirmation of reaction mechanism for **BTK covalent inhibition**

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