Discovery Enablers
Structural Biology

Jubilant has the most experienced Structural Biology team, offering integrated and functional services

Integrated Drug Discovery Support:
- Structure Based Drug Design (SBDD)

Functional Services:
- Gene to Structure, Protein to Structure
- Ligand-bound structures
- Sructure refinement and annotation
- Crystal image annotation
- Low Endotoxin Proteins for Therapeutics
- Cell Line Generation

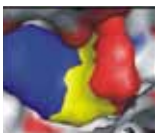
Reagents and Cell Line Generation:
- Kinases, Carboxylases, Ion channels, GPCRs, Decarboxylases, Hydrolases, Transcription factors, NHRs, lipases, Synthetases, Reporter gene constructs, CYPs, etc.

Targets for Crystal Structures:
- Kinases, Phosphatases, Proteases, Carboxylases, NHRs, Hydrolases, Decarboxylases, Apoptotic proteins, Transferases, ß-lactamases, Deaminases, Fab, Fab-antigen complexes, epigenetic targets, Interleukins etc.

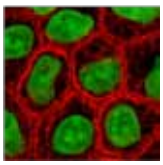
New Initiatives

Antibody Therapeutics

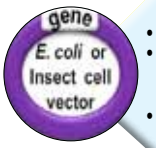
Fragment Based Drug Designing



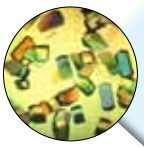
Gram Quantity Production from Mammalian System



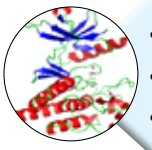
Services



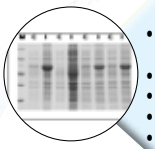
Cloning
- Cloning into various vectors
- Codon optimized or non-codon optimized synthetic genes
- Full length, catalytic domain, chimeras, mutants, etc.



Crystallization
- Various screening kits
- Various seeding techniques
- Soaking /co-crystallization with compounds
- Protein-protein complexes

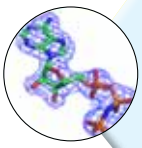


Structure Determination
- 20+ different target proteins in 3+ years
- Both known and novel structures
- Capabilities in experimental phasing (SAD, MAD, etc.)

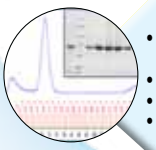


Protein Expression
- E. coli system: Various strains, co-expression
- Insect cell system: Sf9, Sf21, Hi5
- Mammalian expression system
- Co-expression, dual vectors
- BIIC system in place

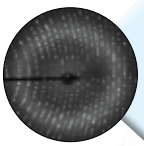
Crystal Image Annotation
- Manual annotation of crystallization images with broad classifications
- Over 40 million images annotated in the past 7 years
- Customized annotation tools
- 99.5% scoring accuracy
- 24 hour turn-around time to support clients based in Europe and USA



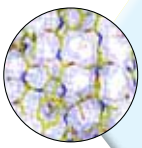
Ligand Fitting
- >150 ligand bound structures delivered for various target proteins
- Accuracy in ligand fitting using automated software
- Quick evaluation of positives in fragment-based screening
- Mode of binding evaluation to support QSAR/scaffold search



Protein Purification
- Various affinity tags: His6, GST, HA, MBP, FLAG, etc.
- Conventional techniques
- Refolding from IBs
- Purification using AKTAs



Data Collection
- X-ray diffraction data collection in house
- Resolution range 1.6 - 2.9Å
- Molecular weight 10kD - 90kD
- ASU containing 1 - 6 molecules



Structure Refinement
- Protein-ligand structure refinement in SBDD projects
- Structure solution using MR for known or similar targets
- Structures thoroughly validated for quality
- Fast turnaround time
- 4000+ structures on 100+ different target proteins refined in 5+ years

bd@jubilantbiosys.com | www.jubilantbiosys.com

bd@jchemsys.com | www.jchemsys.com