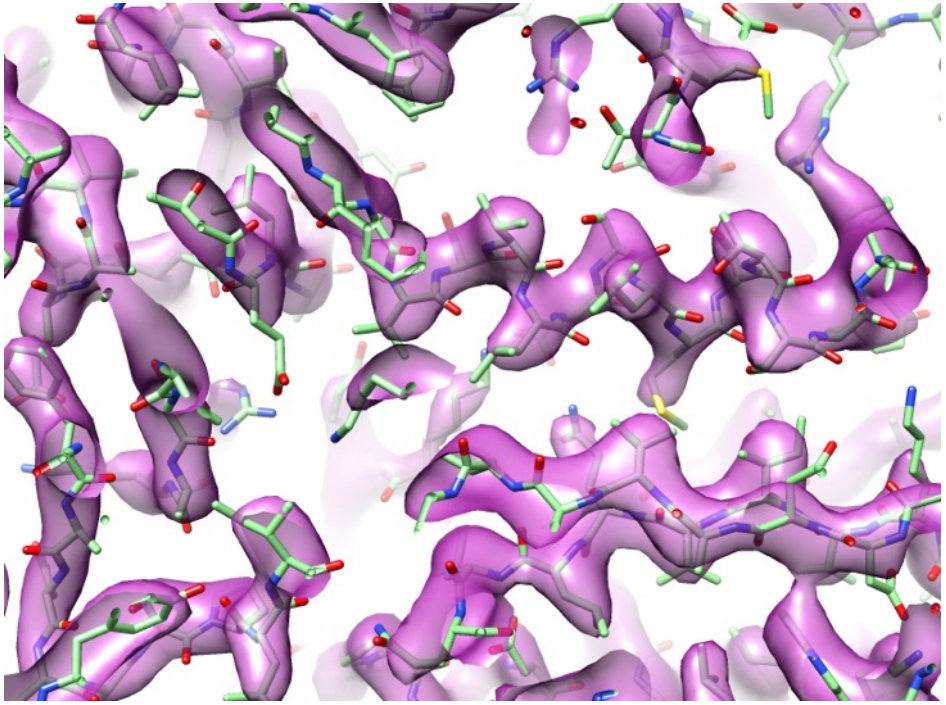
Phenix

Phenix Tools for Cryo-EM



Phenix workshop

Sept. 17, 2018, Cambridge

Tom Terwilliger

Los Alamos National Laboratory

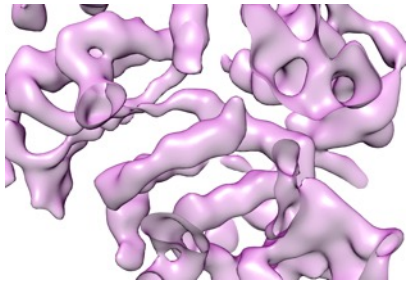
New Mexico Consortium

Los Alamos NATIONAL LABORATORY

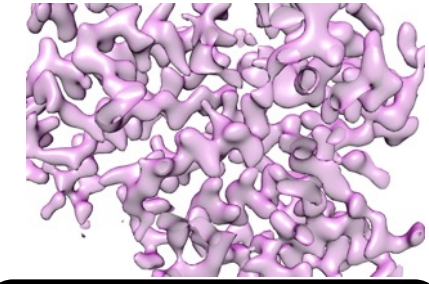
BERKELEY LAB

UNIVERSITY OF CAMBRIDGE

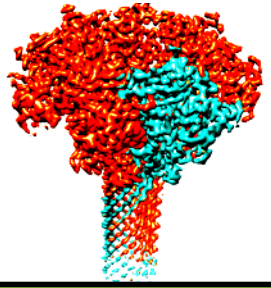
Complete set of cryo-EM tools in Phenix



Starting map

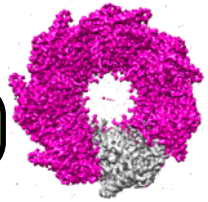


Map improvement

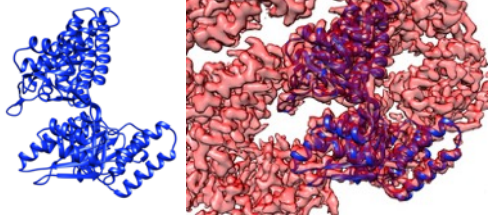


Segmentation

Map manipulation

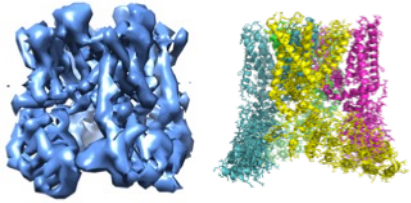


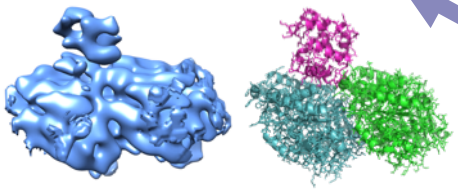
Map symmetry



Docking, model-building

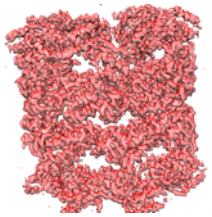
Refinement



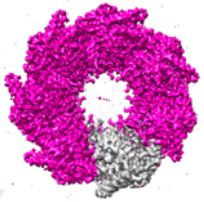


Validation

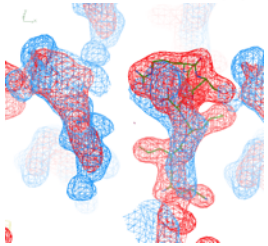
New Phenix cryo-EM tools



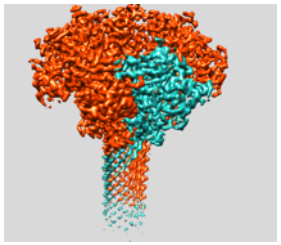
Display map properties → Show-map-info



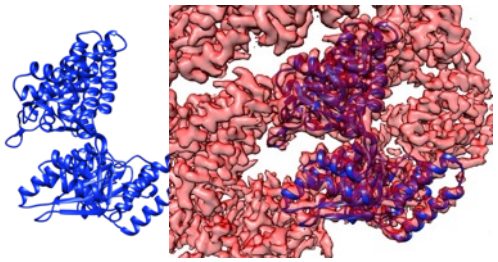
Find symmetry → Map-symmetry



Combine maps → Combine-focused-maps

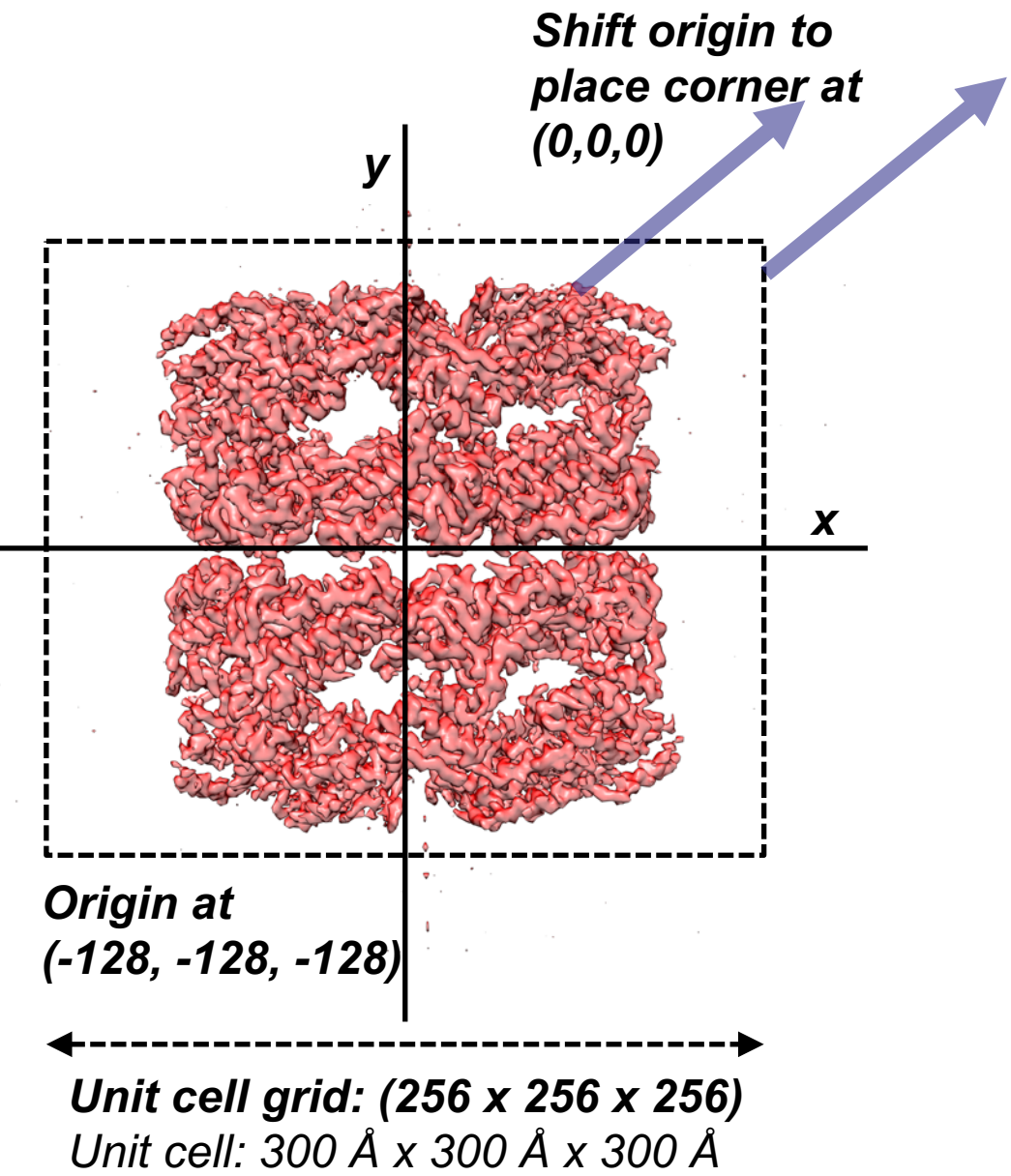


Unique part of map → Map-box (extract-unique)



Docking → Dock-in-map

Displaying map properties with show_map_info



Typical cryo-EM map:

Center: (0,0,0)

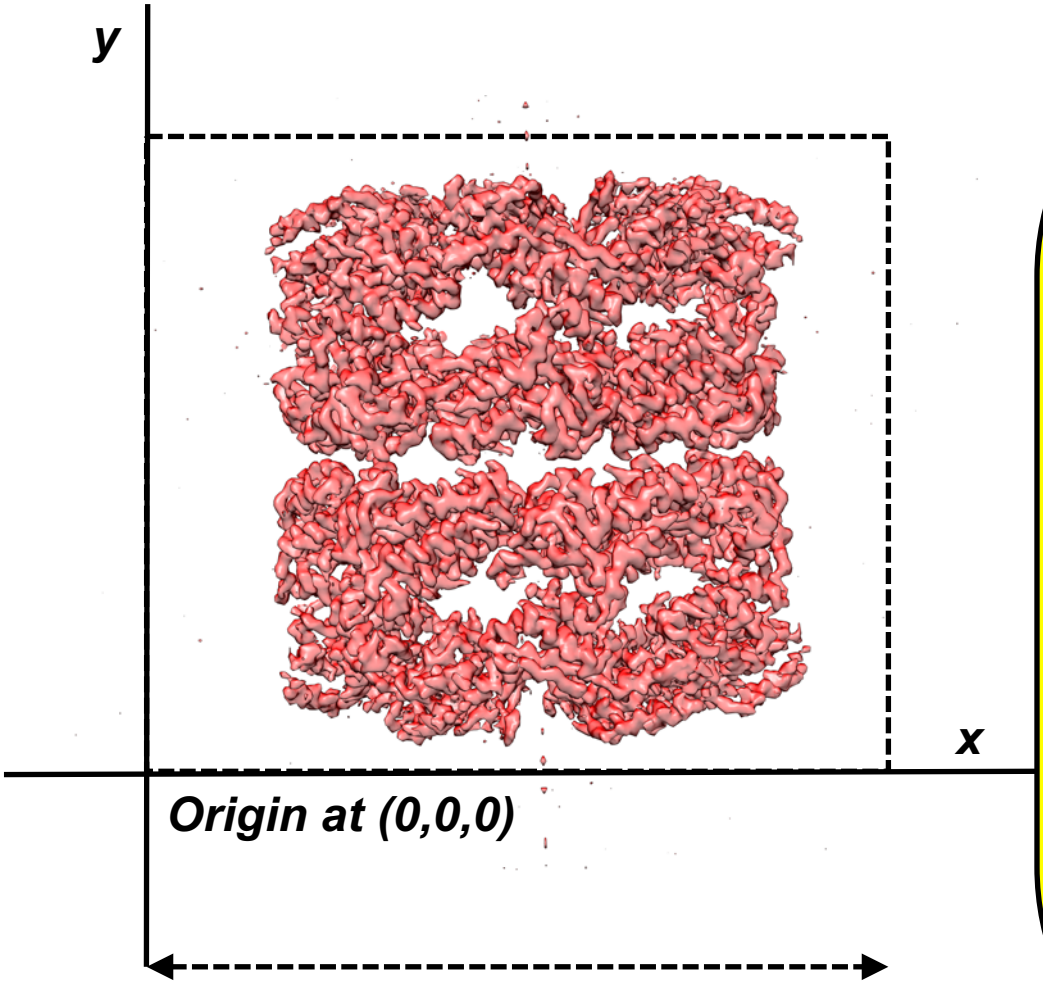
Origin: (-128, -128, -128)

Extent (map size):
256, 256, 256

Unit cell grid:
256 x 256 x 256

Unit cell:
300 Å x 300 Å x 300 Å

Map with origin at (0, 0, 0)



Center: (128, 128, 128)

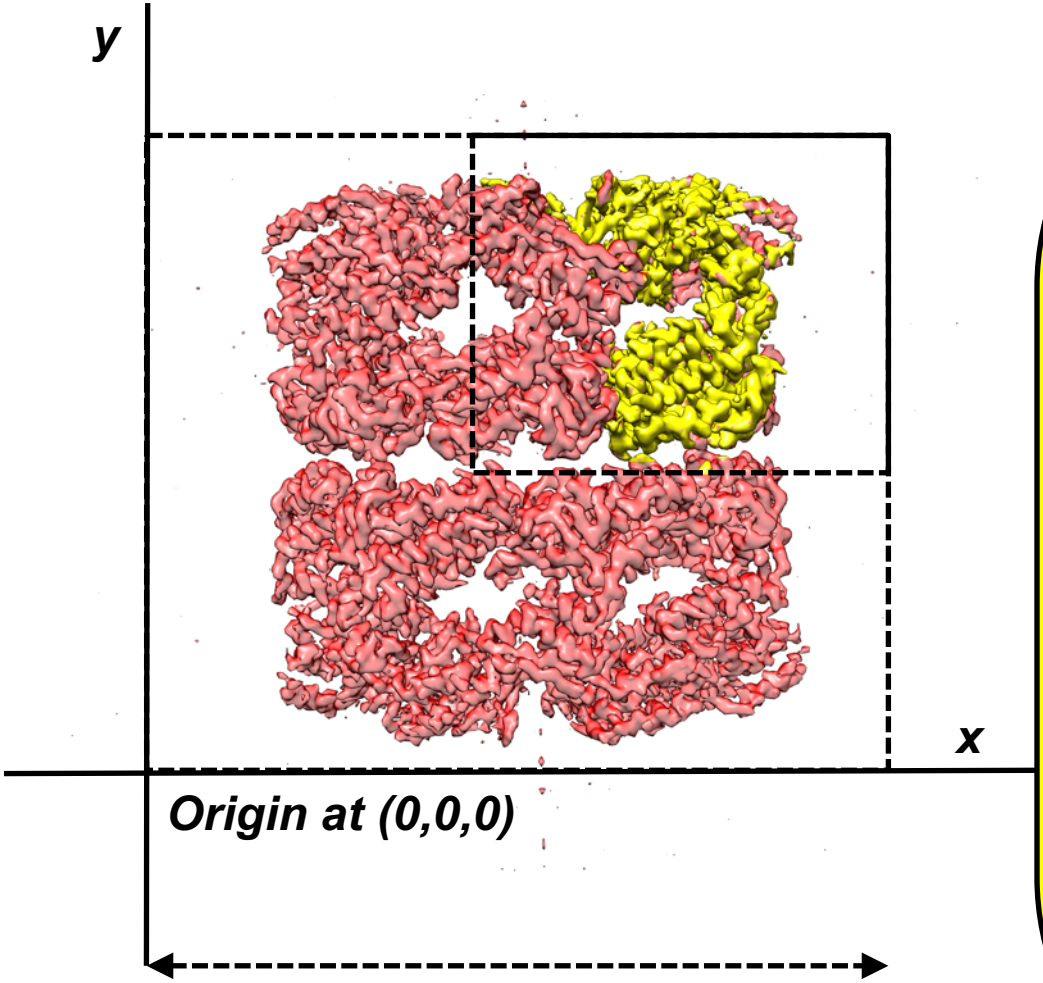
Origin: (0, 0, 0)

Extent (map size):
256, 256, 256

Unit cell grid:
256 x 256 x 256

Unit cell:
300 Å x 300 Å x 300 Å

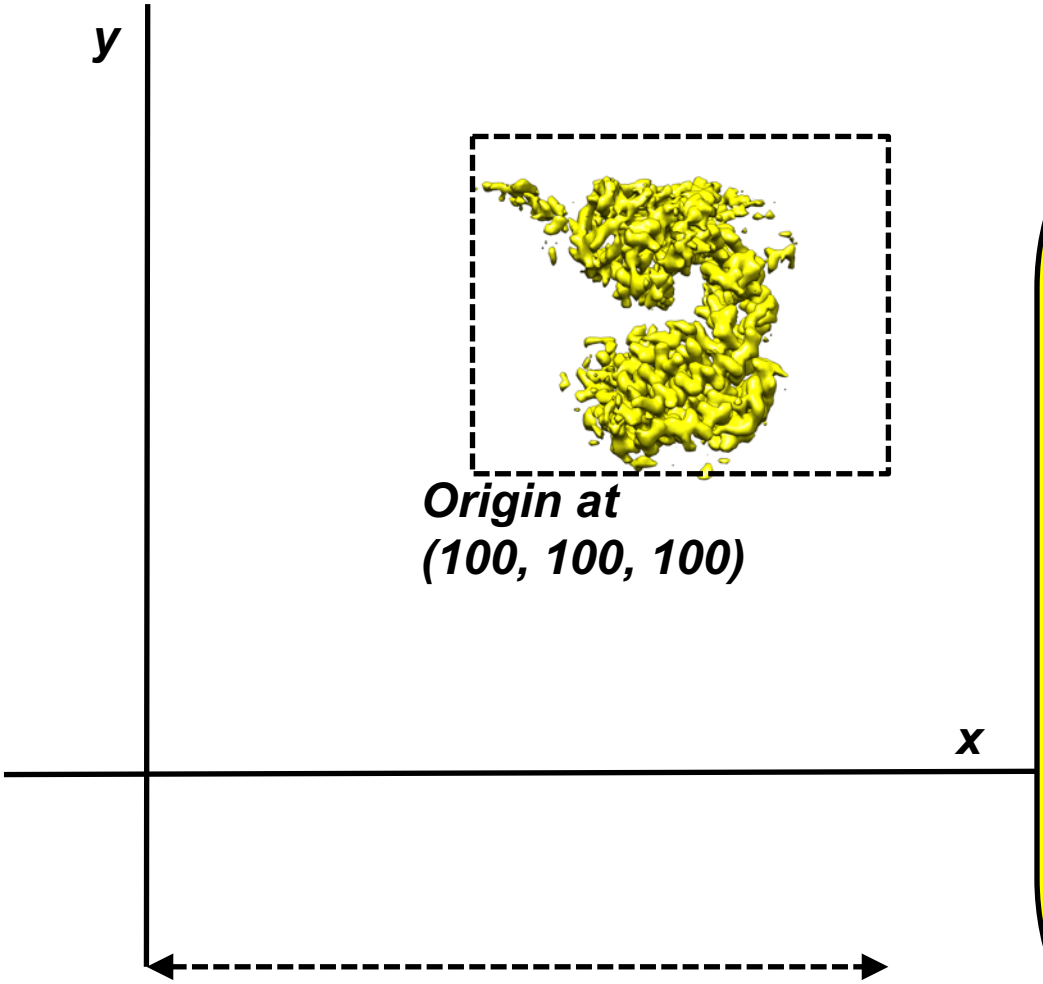
Cutting out part of a map with map_box



Boxed map

Box cut from 100 – 256 in each direction

Displaying map properties with show_map_info



Boxed map

Origin: (100, 100, 100)

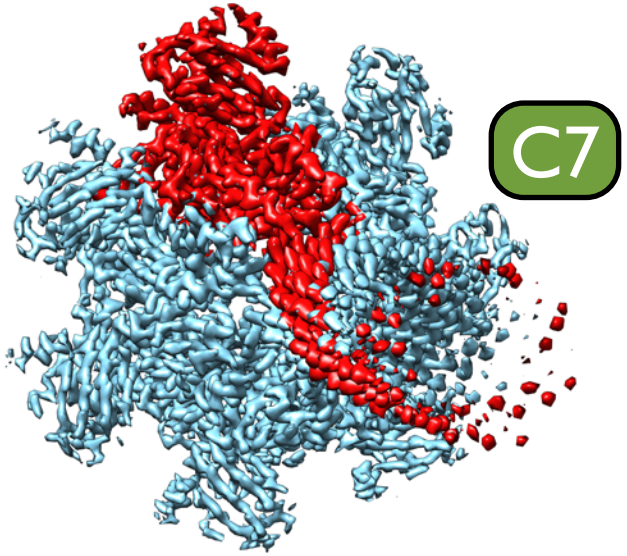
Extent (map size):
156, 156, 156

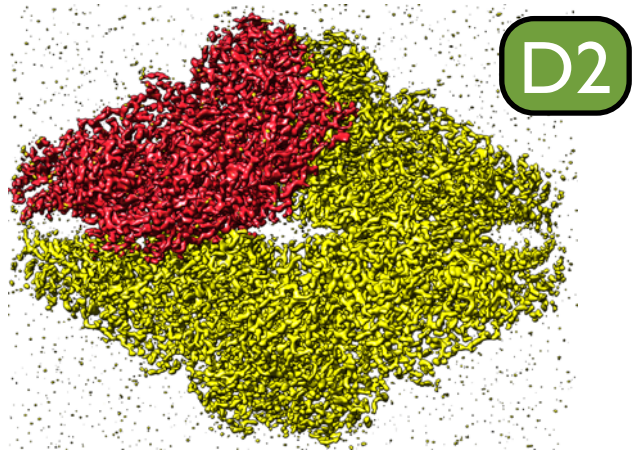
Box map cell:
183 Å x 183 Å x 183 Å

Unit cell grid:
256 x 256 x 256

Unit cell:
300 Å x 300 Å x 300 Å

Finding map symmetry with symmetry_from_map

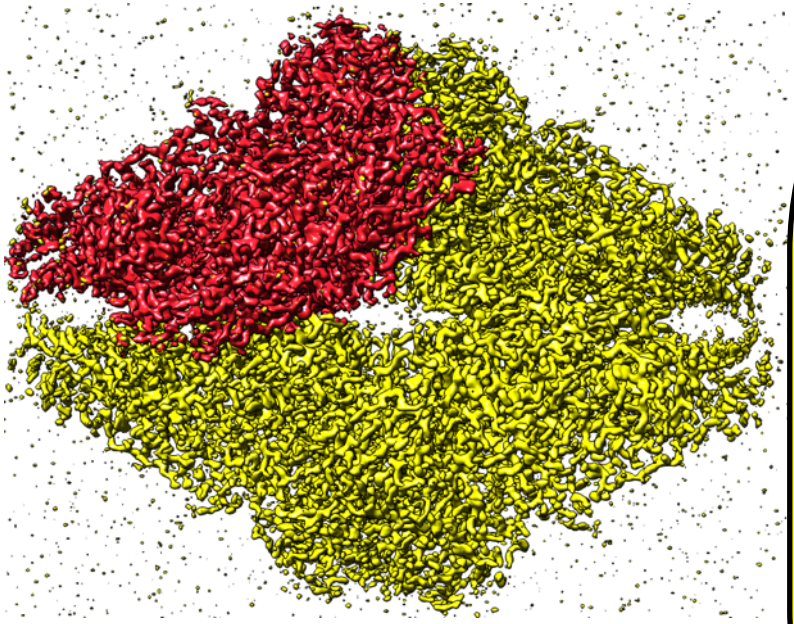




Procedure for finding symmetry:

- Test point group symmetries (e.g., C7, D2, I, O, T)
- Helical symmetry
- Principal rotation axes along z, x, y
- Score based on map correlation for symmetry-related points and number of operators

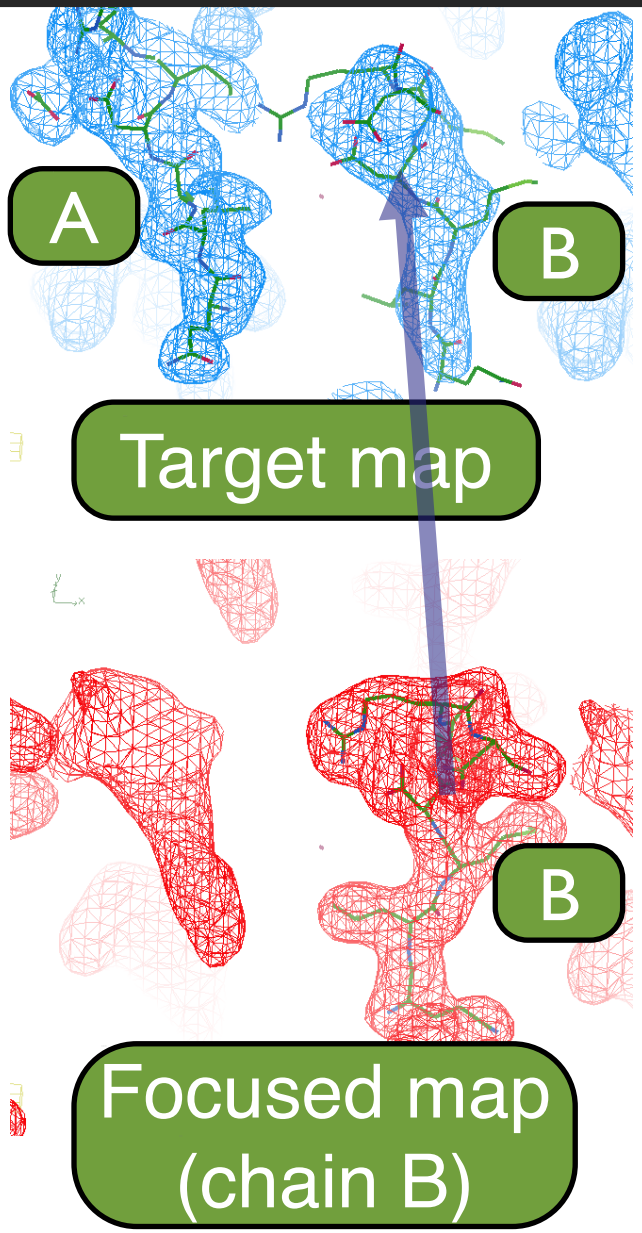
Extracting unique part of map with map_box (extract_unique option)



Procedure:

- Use symmetry of map
- Contour map at level that yields regions about 50 residues in size
- Group symmetry-related regions
- Choose one member of each group
- Optimize compactness and connectivity of unique part of map

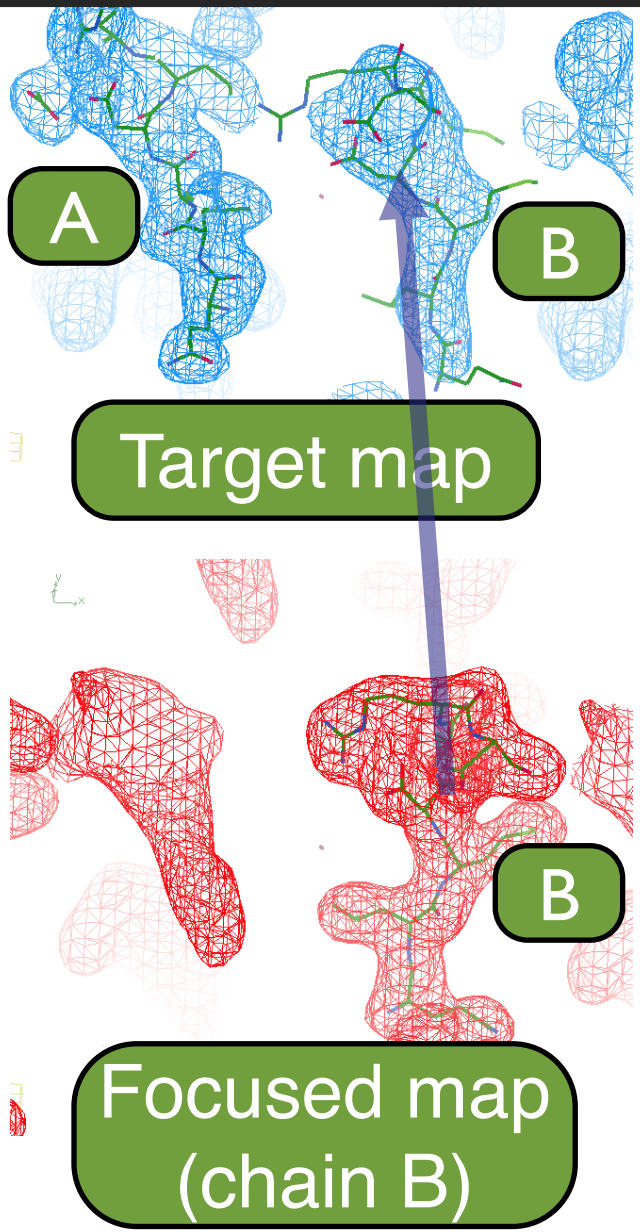
Combining maps with combine_focused_maps



Procedure for combining maps:

- Superimpose density
- Rotation/translation from refined models
- Average target and focused map density
- Weight using map-model correlations

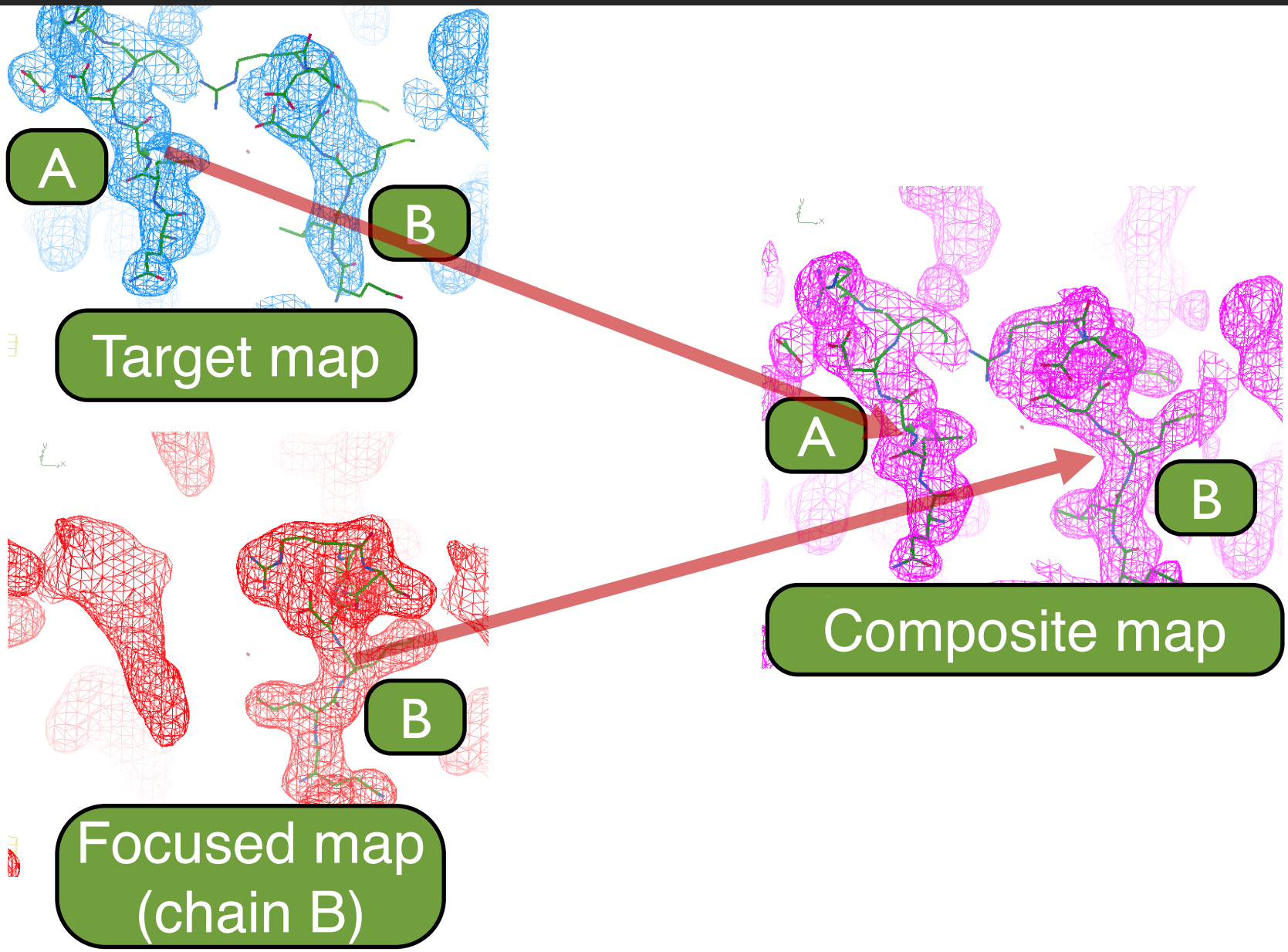
Combining maps with combine_focused_maps



Features

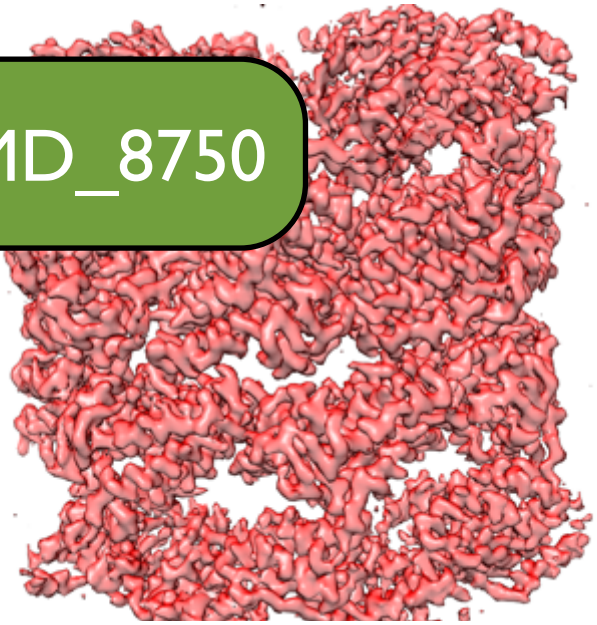
- Averaging of entire chains or local regions
- Application of symmetry to focused map (e.g., superimpose chain B of focused map on chains EFGH of target map)

Combining maps with combine_focused_maps



Docking models with dock-in-map

EMD_8750



1ss8 chain A

Search procedure:

Pure translation

- low-res
- high-res

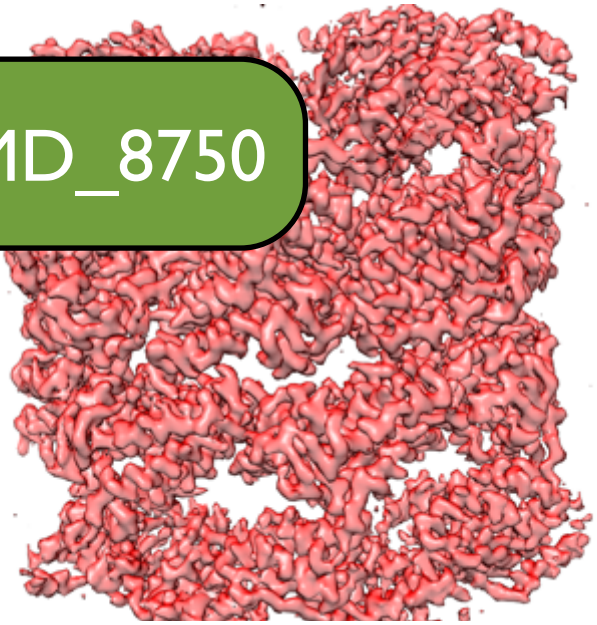
Rotation / translation

- low-res
- high-res

Score based on rigid-body refinement map-model correlation

Docking models with dock-in-map

EMD_8750



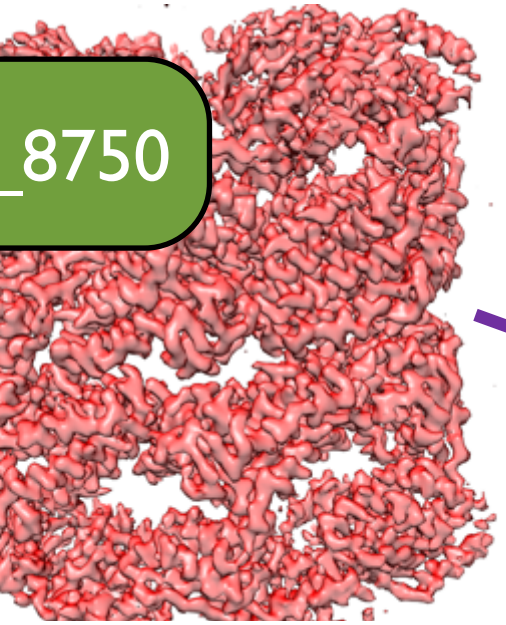
1ss8 chain A

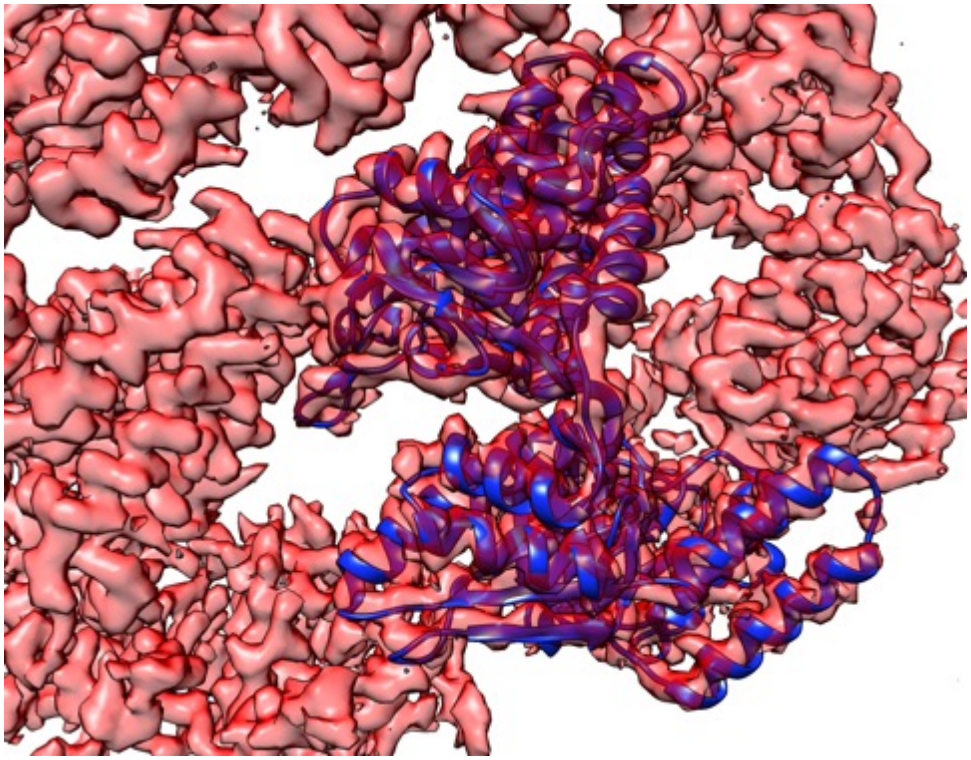
Features

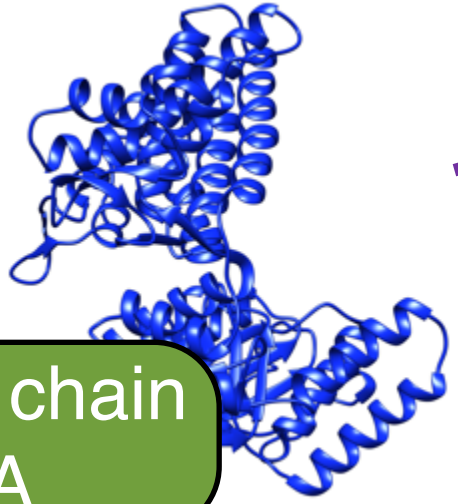
- Multiple chains
- Density search
- Symmetry
- Multiprocessing

Docking models with dock-in-map

EMD_8750



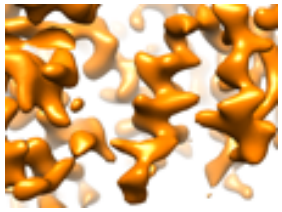




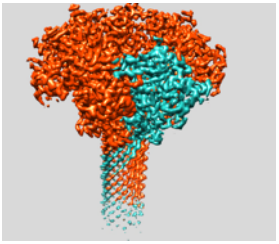
1ss8 chain A

1ss8 chain A docked in map

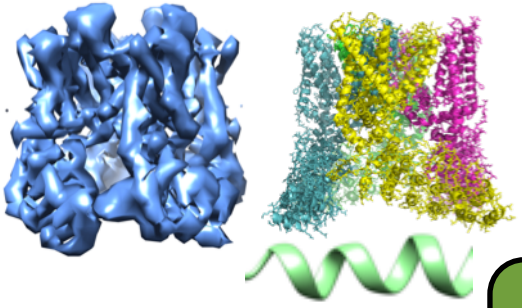
Phenix cryo-EM structure determination tools



Map improvement → Auto-sharpen, Combine-focused-maps

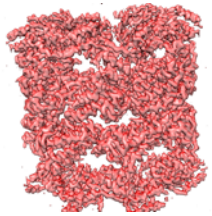


Segmentation → Map-box (extract-unique), Segment-and-split-map

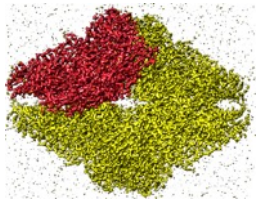


Docking, Auto-building, Flexible fitting, Refinement → Dock-in-map, Map-to-model, Cryo-fit, Real-space-refine

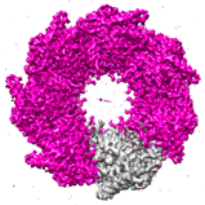
Phenix cryo-EM utilities



Display map properties → Show-map-info



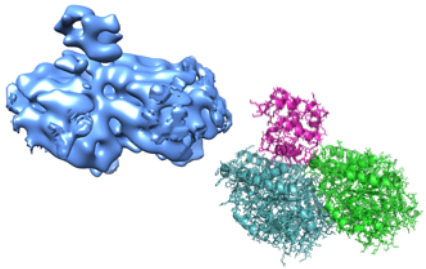
Map manipulation → Map-box, Map-to-structure-factors



Find symmetry → Map-symmetry

MEQASFSLSG

Guess sequence → Sequence-from-map



Validate structure → Mtriage, EMringer, Validation-cryoEM

The Phenix Project

Lawrence Berkeley Laboratory

Paul Adams, Pavel Afonine, Nigel Moriarty, Billy Poon, Oleg Sobolev, Dorothee Liebschner

Los Alamos National Laboratory

Tom Terwilliger, Li-Wei Hung

Cambridge University

Randy Read, Airlie McCoy, Tristan Croll, Rob Oeffner, Kaushik Hatti, Massimo Sammito

Duke University

Jane & David Richardson, Chris Williams, Bradley Hintze, Vincent Chen

An NIH/NIGMS funded Program Project