

CBMS workbench (virtual), Oct 13 2021

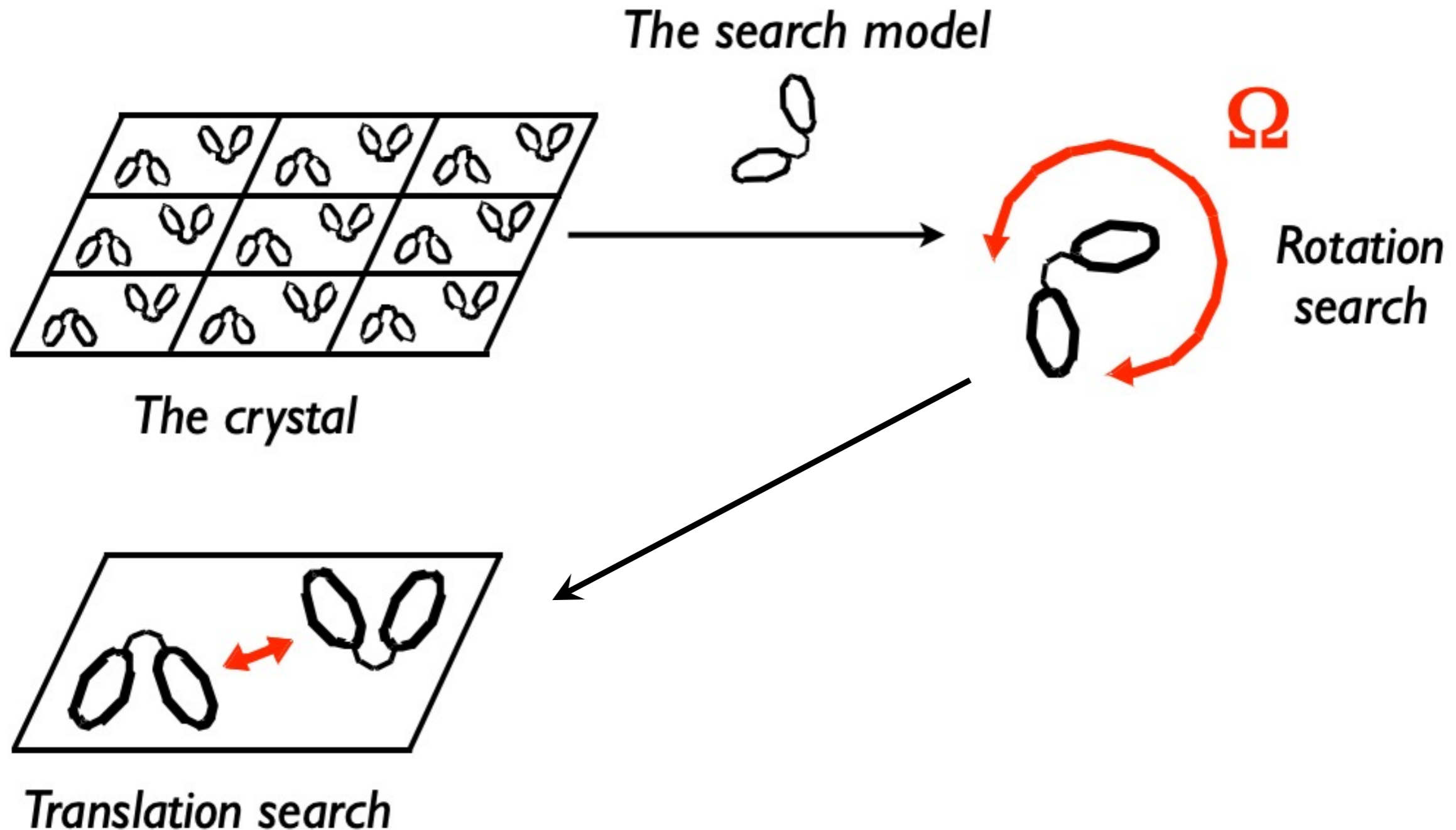


AlphaFold for MR

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Molecular replacement (MR)

Use a previously known structure to get phase estimates



AlphaFold

AI scientists from Google DeepMind won CASP14 (Critical Assessment of Structural Prediction competition)

Amino acid sequence



Structural model

The average rmsd is ~ 1.6 Å!

The code is available on GitHub and can be run on google Colab:

- <https://github.com/deepmind/alphafold>
- <https://colab.research.google.com/github/deepmind/alphafold/blob/main/notebooks/AlphaFold.ipynb>

AlphaFold

Amino acid sequence



- 1) Do *multiple sequence alignment* (MSA)
 - find parts of the sequence more likely to mutate and correlations between them
 - find proteins that may have a similar structure (“templates”)
 - guess which amino acids are likely to be in contact with each other

2) Neural network 1: identify which parts of the MSA are more informative

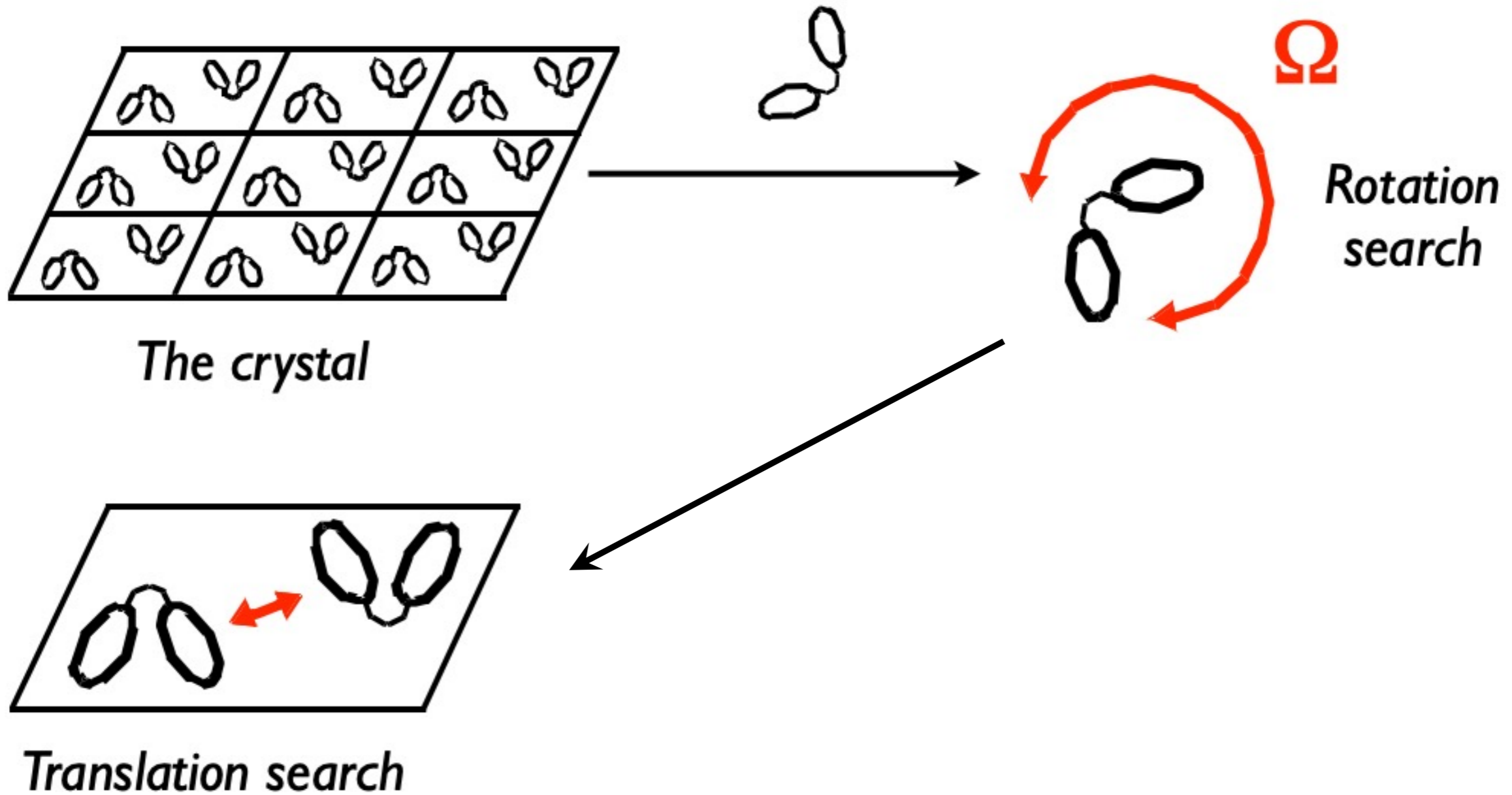
3) Neural network 2: build a model



Structural model

Use AlphaFold model for MR

AlphaFold model

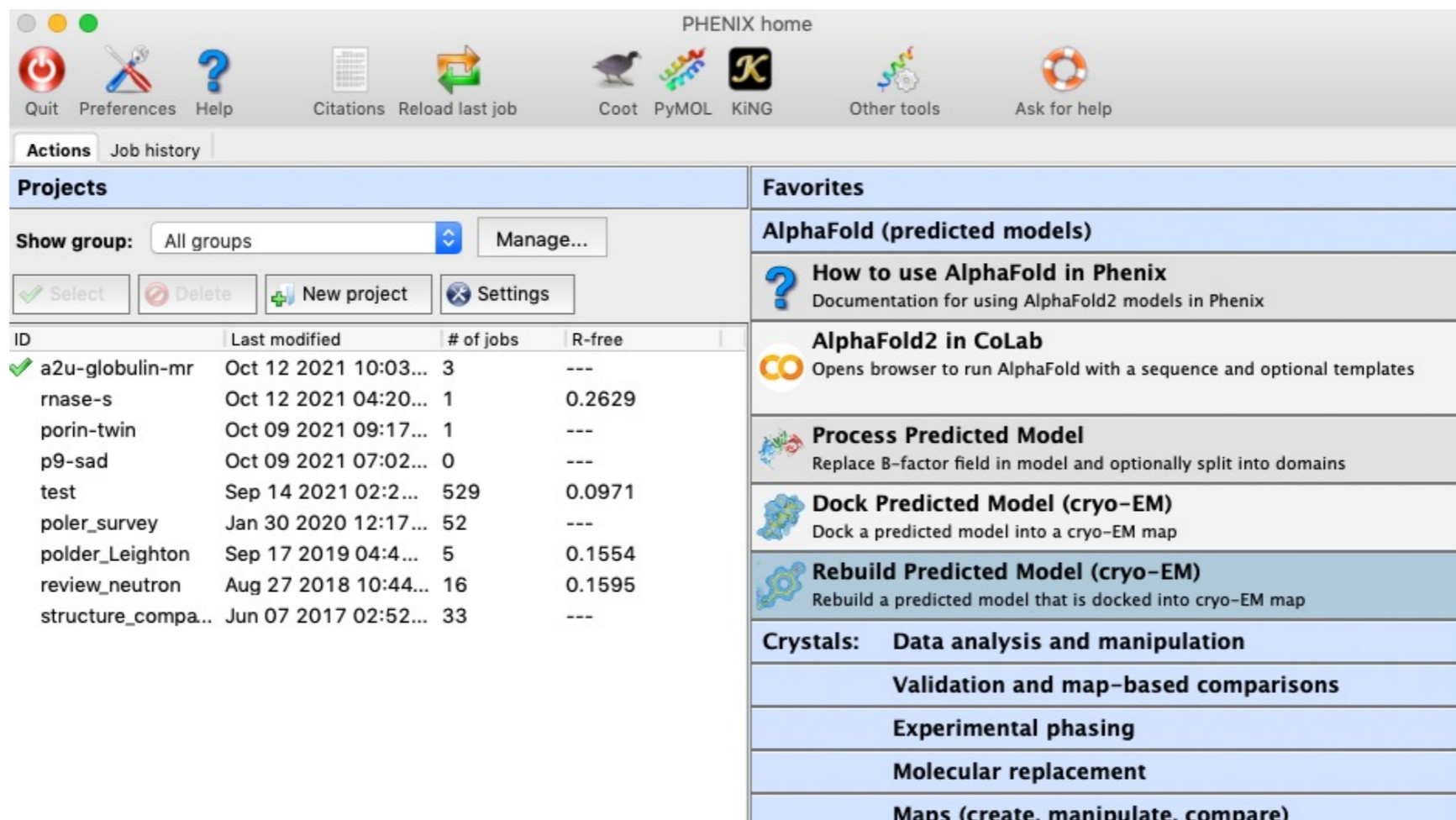


AlphaFold for MR

Use the tutorial data for the A2U-globulin structure (MR tutorial)

1) Run the tutorial with supplied search model

2) With the sequence, do a prediction and run MR again



The screenshot shows the PHENIX home interface. The top menu bar includes: Quit, Preferences, Help, Citations, Reload last job, Coot, PyMOL, KING, Other tools, and Ask for help. Below the menu bar are two tabs: 'Actions' and 'Job history'. The main content area is divided into two panels. The left panel, titled 'Projects', has a 'Show group:' dropdown set to 'All groups' and a 'Manage...' button. Below this are buttons for 'Select', 'Delete', 'New project', and 'Settings'. A table lists various projects with columns for ID, Last modified, # of jobs, and R-free. The right panel, titled 'Favorites', contains several links and buttons for actions like 'How to use AlphaFold in Phenix', 'AlphaFold2 in CoLab', 'Process Predicted Model', 'Dock Predicted Model (cryo-EM)', and 'Rebuild Predicted Model (cryo-EM)'. At the bottom, there is a 'Crystals:' section with sub-sections for 'Data analysis and manipulation', 'Validation and map-based comparisons', 'Experimental phasing', 'Molecular replacement', and 'Maps (create, manipulate, compare)'.

ID	Last modified	# of jobs	R-free
✓ a2u-globulin-mr	Oct 12 2021 10:03...	3	---
rnase-s	Oct 12 2021 04:20...	1	0.2629
porin-twin	Oct 09 2021 09:17...	1	---
p9-sad	Oct 09 2021 07:02...	0	---
test	Sep 14 2021 02:2...	529	0.0971
poler_survey	Jan 30 2020 12:17...	52	---
polder_Leighton	Sep 17 2019 04:4...	5	0.1554
review_neutron	Aug 27 2018 10:44...	16	0.1595
structure_compa...	Jun 07 2017 02:52...	33	---

The Project



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Liebschner D, *et al.*, Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in *Phenix*. *Acta Cryst.* 2019 **D75**:861–877

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Phenix Testers & Users

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