

*Model-building using cryo-EM and crystallographic maps*

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Currently many structures are being determined at resolutions in the range of 3 Å to 4.5 Å. Recent developments in cryo-electron microscopy have spurred a rapid increase in the number of large structures and many crystal structures continue to be determined in this range of resolutions. Model-building at resolutions lower than about 3 Å remains challenging due to the lack of detail in the density maps. Additional difficulties are presented by cases where both protein and RNA are present and the interpretation of density must include the choice of chain type.

We have developed tools for low-resolution model-building using either X-ray or cryo-EM maps. The phenix.map\_to\_model tool divides a map into small contiguous regions of density, builds protein or RNA into each, optimizes geometry by finding segments that appear to have secondary structure, combines all the models of each chain type together, identifies which chain type fits each part of a map best, and combines all these together into a partial model for the structure. Any symmetry present in the structure can be included in the model-building process.

All the tools needed to carry out this low-resolution model-building are available in current versions of Phenix and can be obtained from the Phenix web site at <http://www.phenix-online.org>.

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