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Title:	Tracing polypeptide chains in electron-density maps
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Tools for Easy and Difficult Problems: Tracing polypeptide chains in electron-density maps

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Why automate macromolecular X-ray crystal structure determination? How do you automate something so complicated as this? This talk will try to address these two questions, beginning with a brief introduction to crystallography, and continuing with examples from the PHENIX software package.

Some reasons to automate structure determination are (1) it makes straightforward cases accessible to a wider group of structural biologists, (2) it makes difficult cases more feasible for experts, (3) it can speed up the process, and (4) it can help reduce errors. Many of these advantages are related to the fact that if software is highly automated, then a user can afford to try many different possibilities and choose the most successful. Others come from the incorporation of systematic procedures for evaluation of map or model quality in automated approaches. To automate a process as complicated as macromolecular X-ray crystal structure determination you need (1) tools to carry out each individual step on the process, (2) seamless transfer of information between steps, (3) a way to decide what is good, and (4) a way to make decisions about what to do next.

Examples from the PHENIX software package for highly automated macromolecular structure determination will be used to illustrate how to automate structure determination and to speculate on the future of automation on macromolecular structure determination.

The PHENIX software is available at http://www.phenix-online.org.

Tracing polypeptide chains in electron-density maps

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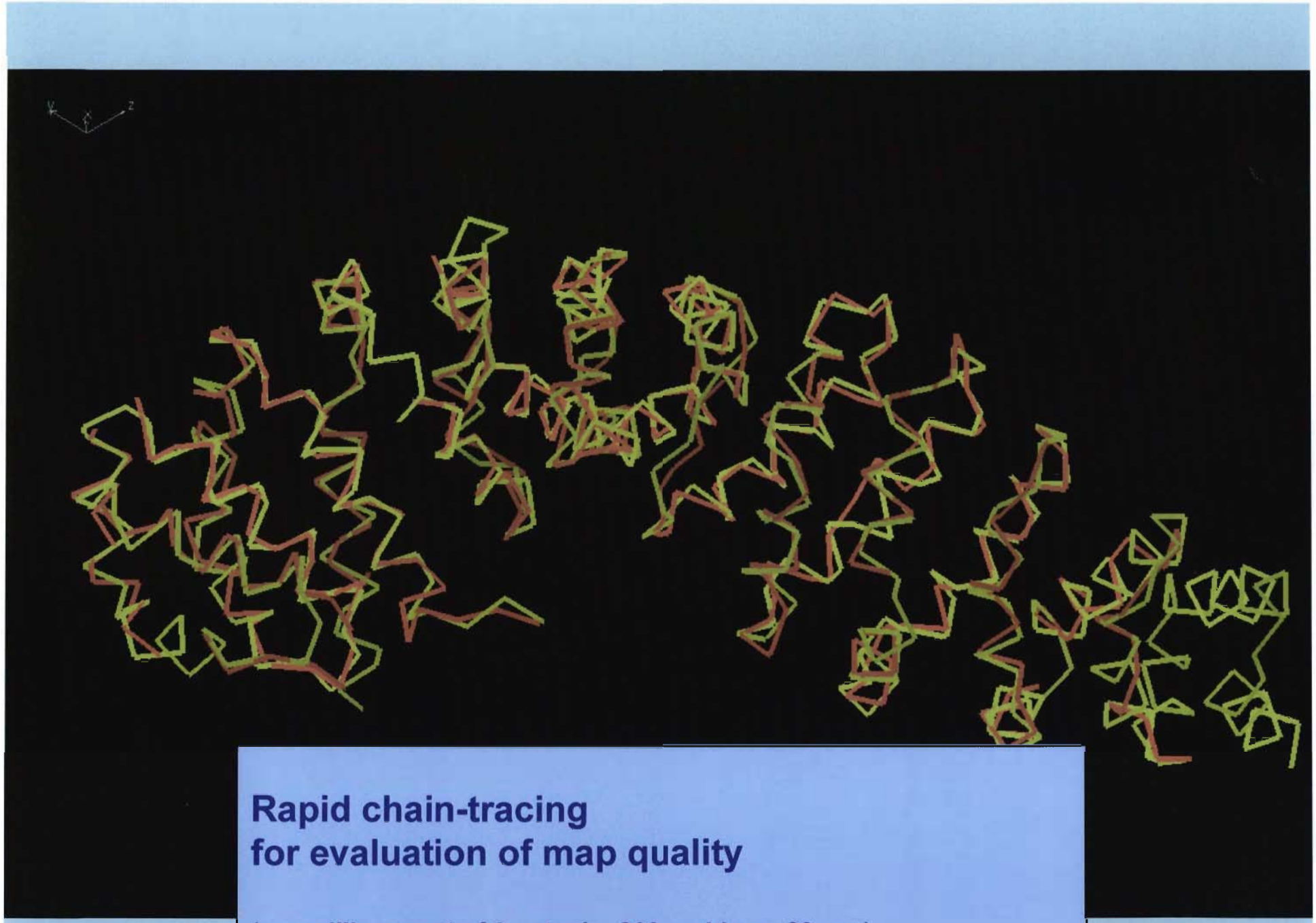
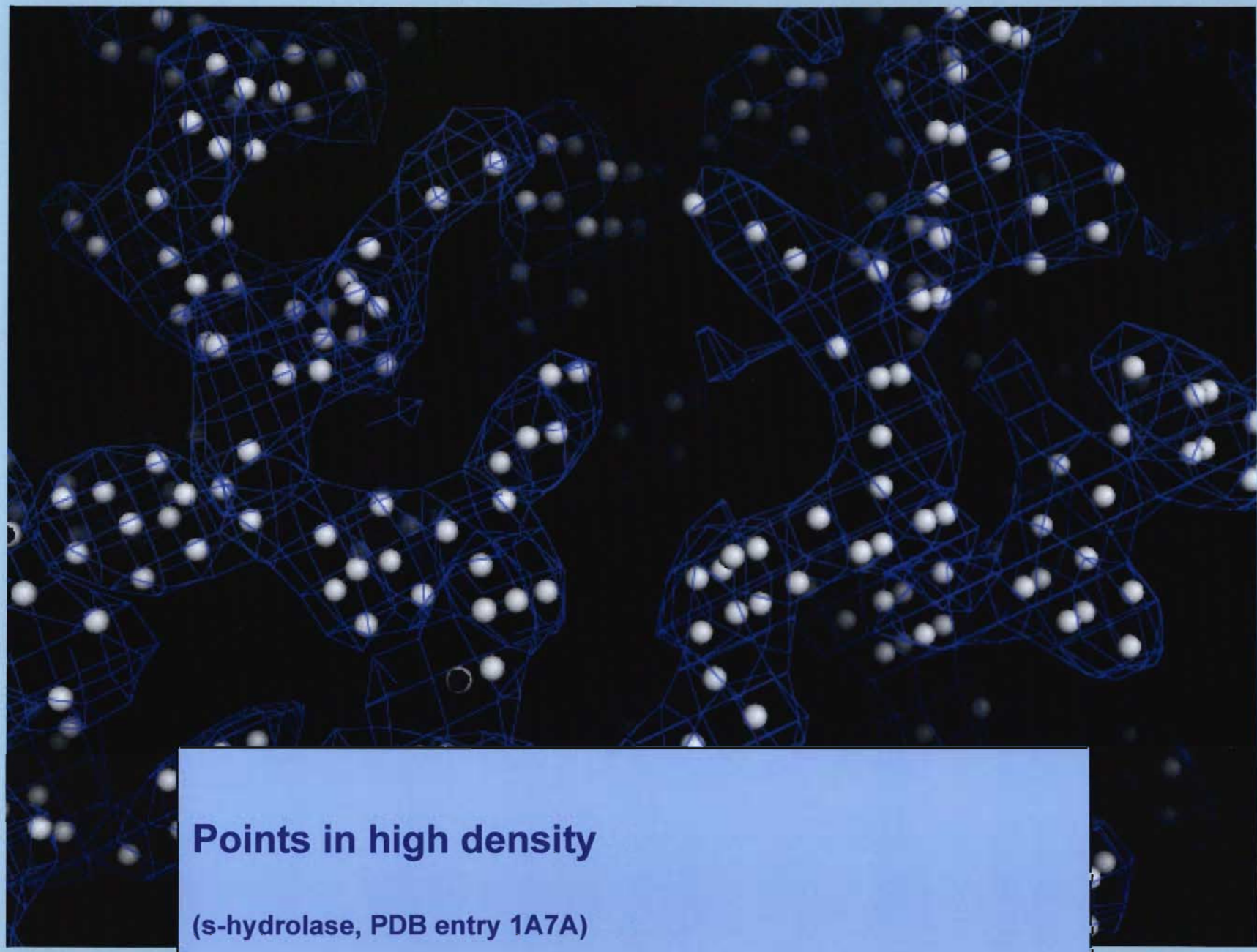


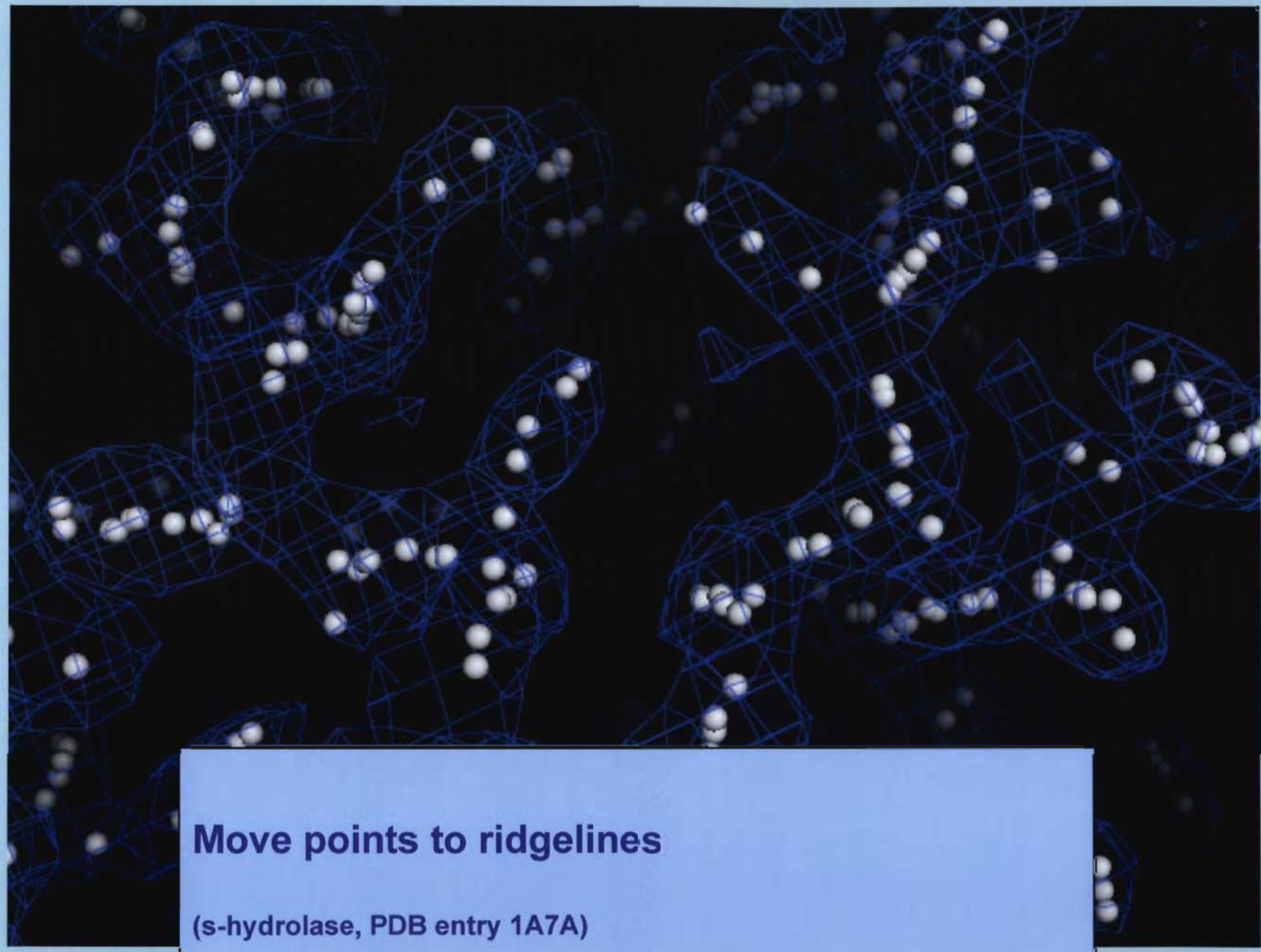
Rapid chain-tracing for evaluation of map quality

(armadillo repeat of β-catenin, 369 residues, 23 sec)



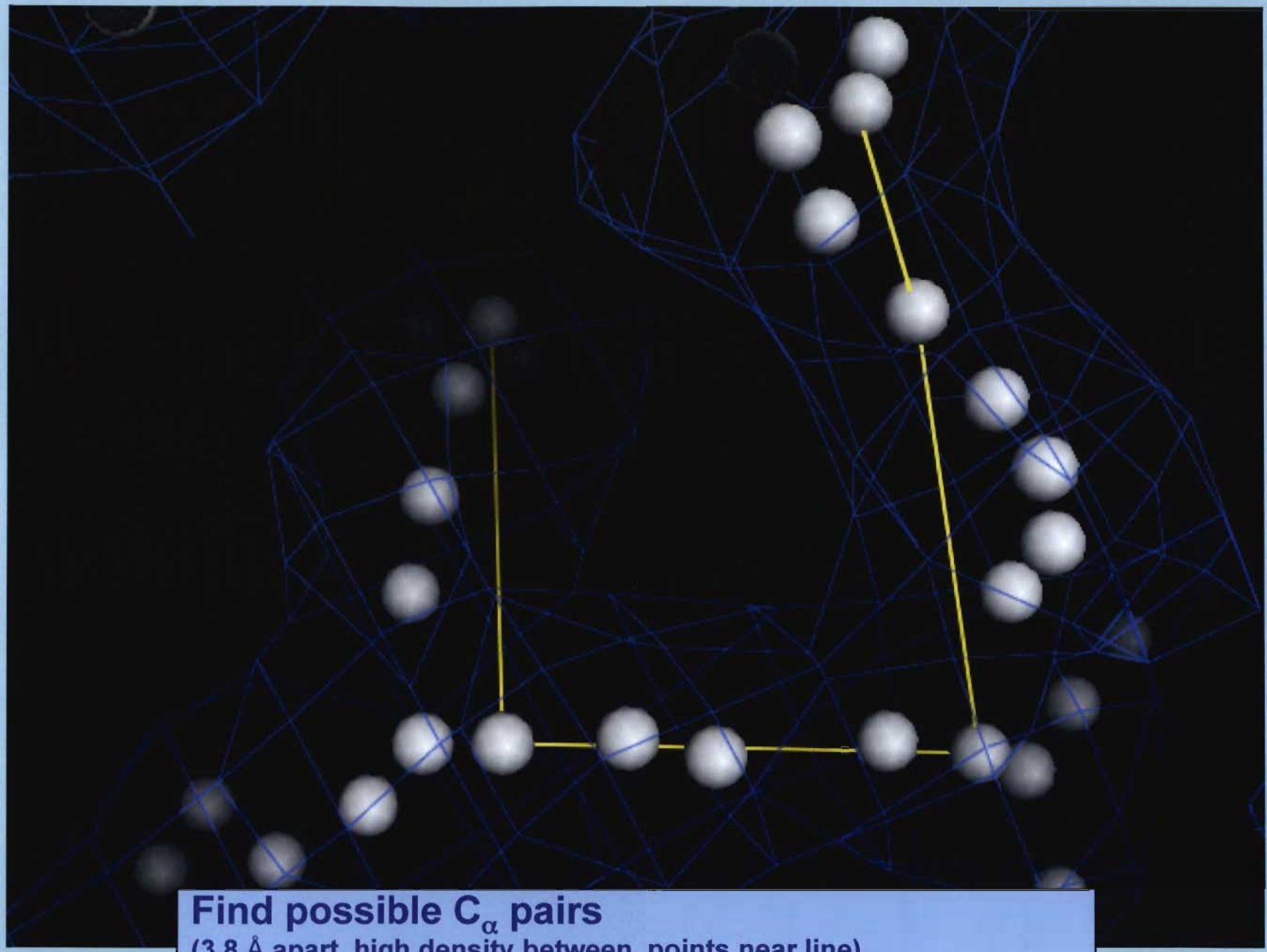
Points in high density

(s-hydrolase, PDB entry 1A7A)



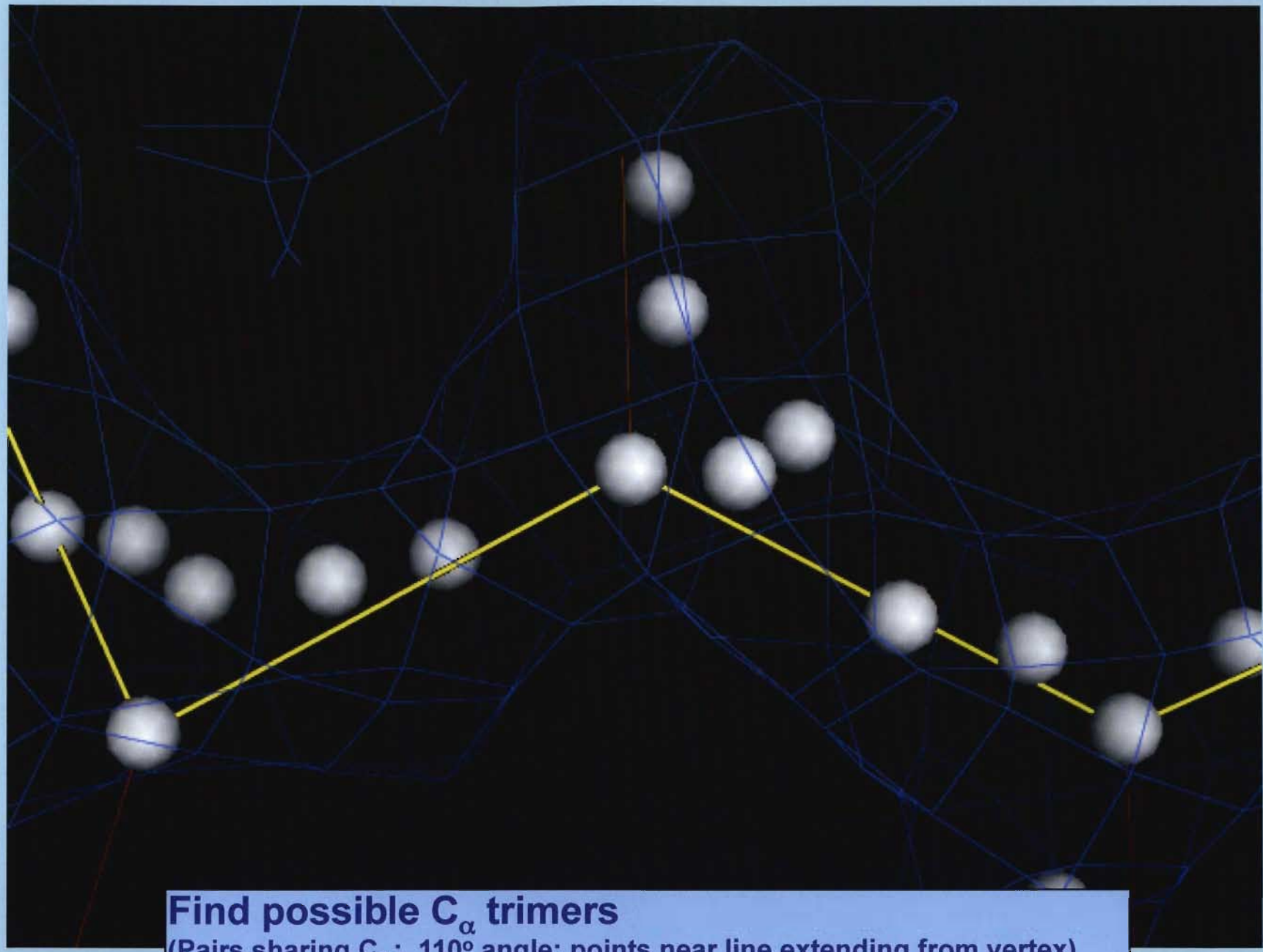
Move points to ridgelines

(s-hydrolase, PDB entry 1A7A)



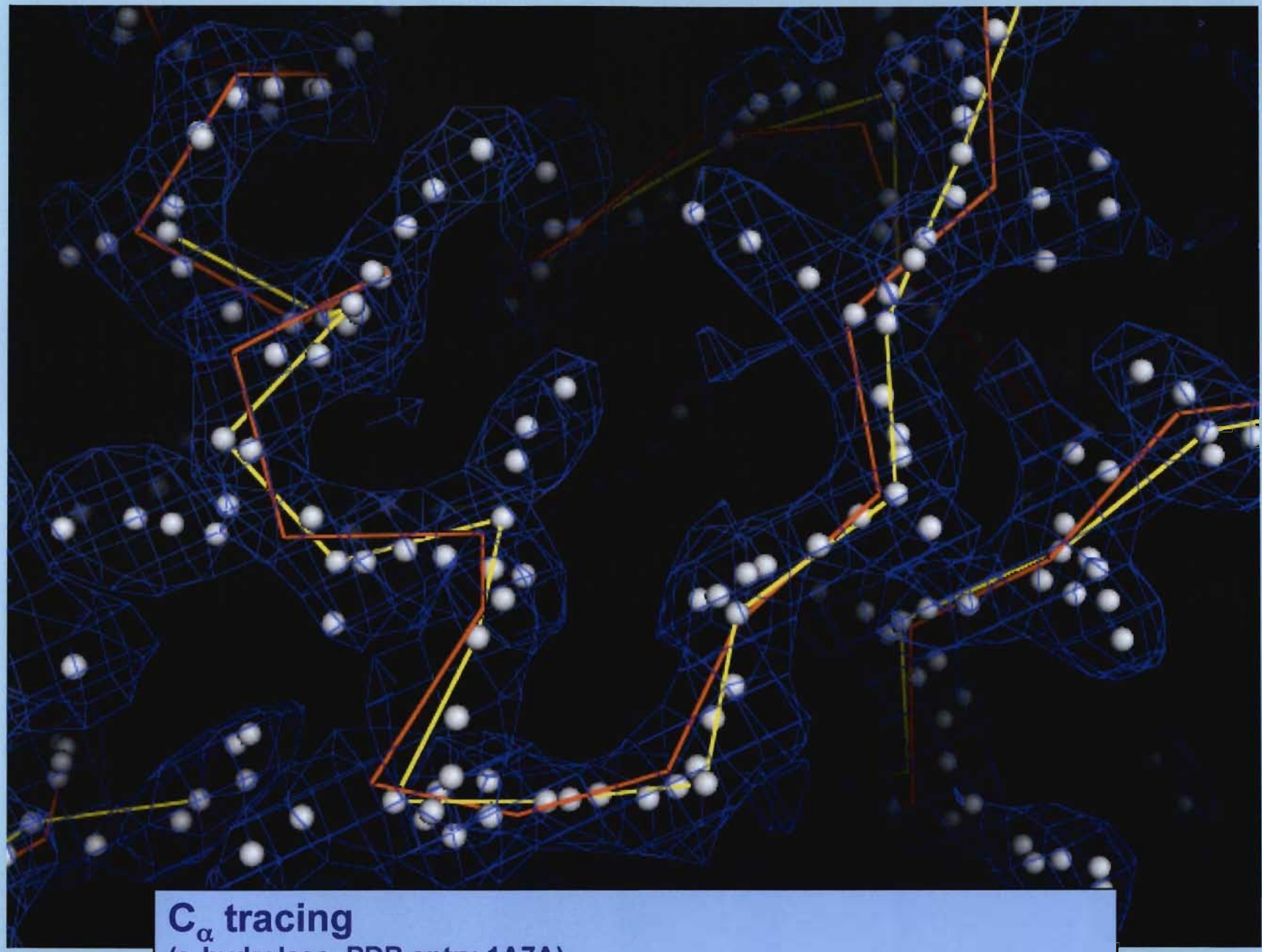
Find possible C_α pairs

(3.8 Å apart, high density between, points near line)



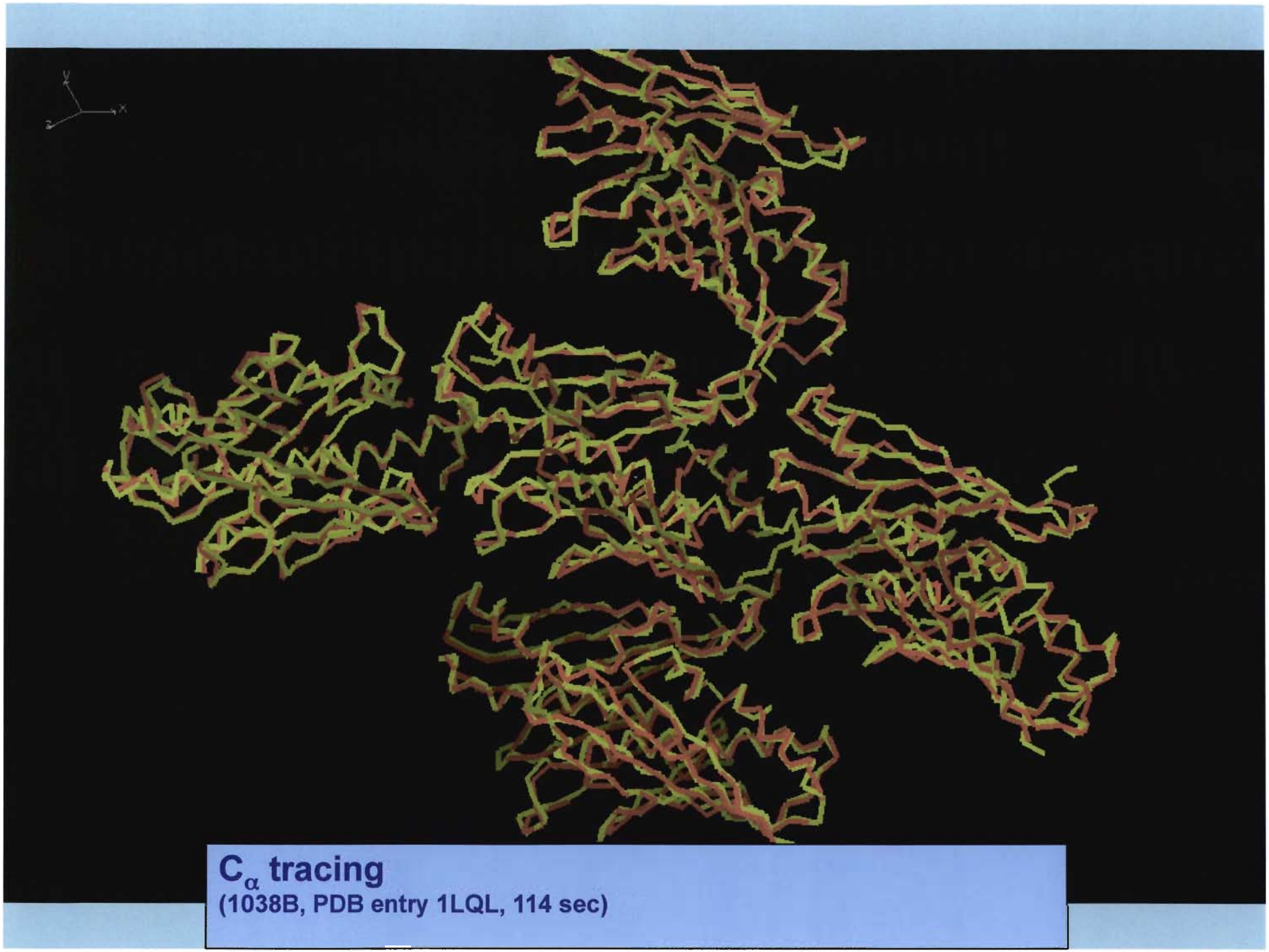
Find possible C_α trimers

(Pairs sharing C_α; 110° angle; points near line extending from vertex)

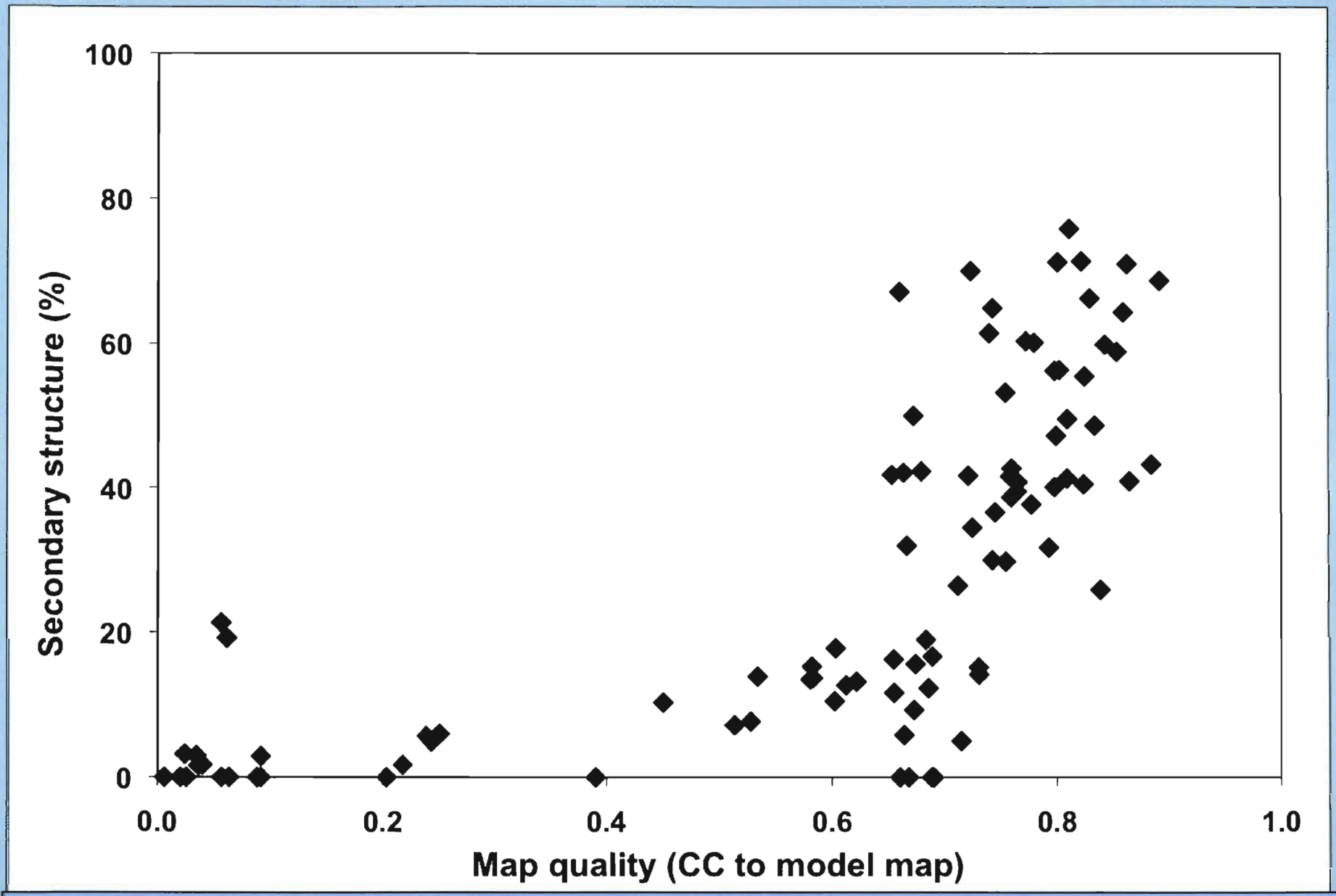


C_α tracing
(s-hydrolase, PDB entry 1A7A)

C_α tracing
(mevalonate kinase, PDB entry 1KKH, 9 sec)



C_α tracing
(1038B, PDB entry 1LQL, 114 sec)



Using secondary structure content to evaluate map quality

The PHENIX Project

Phenix

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