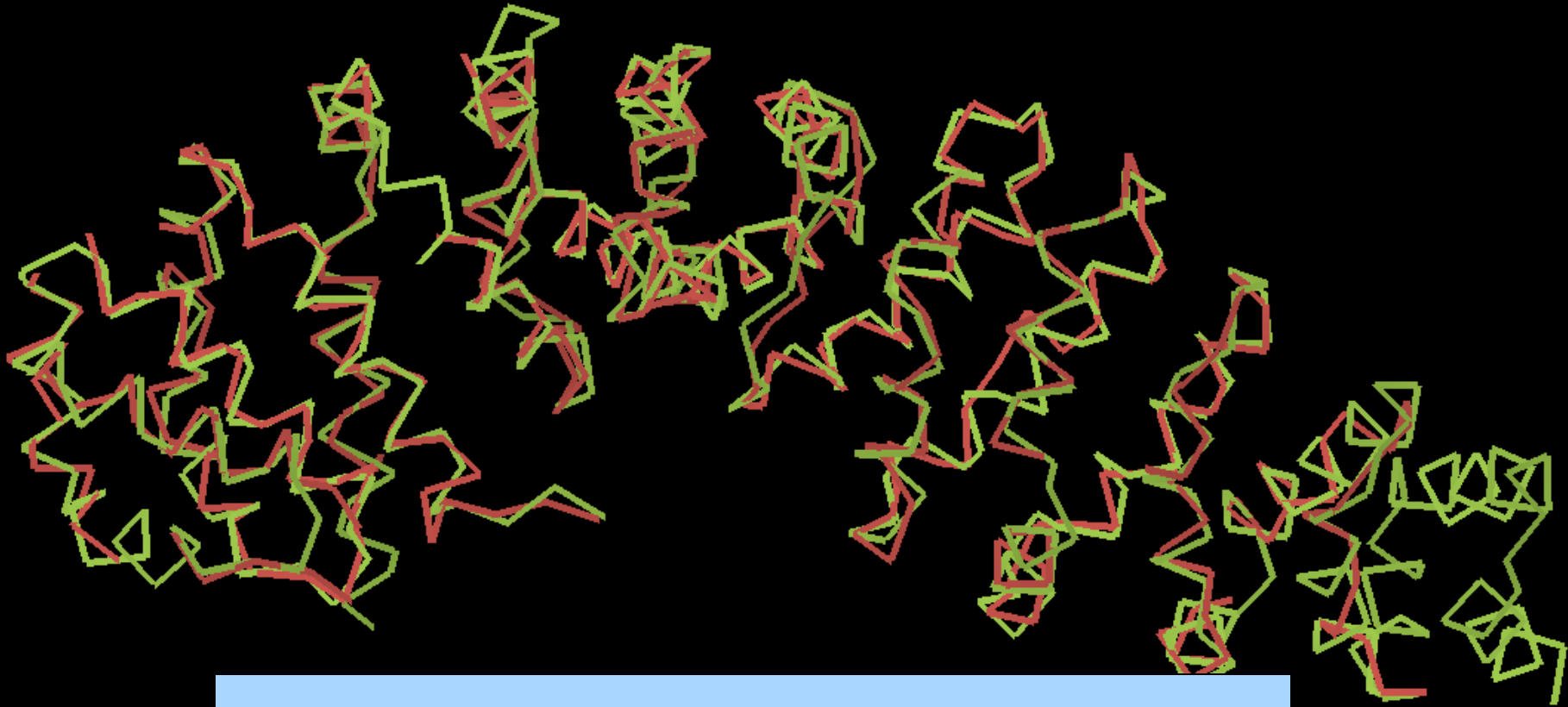


# Tracing polypeptide chains in electron-density maps

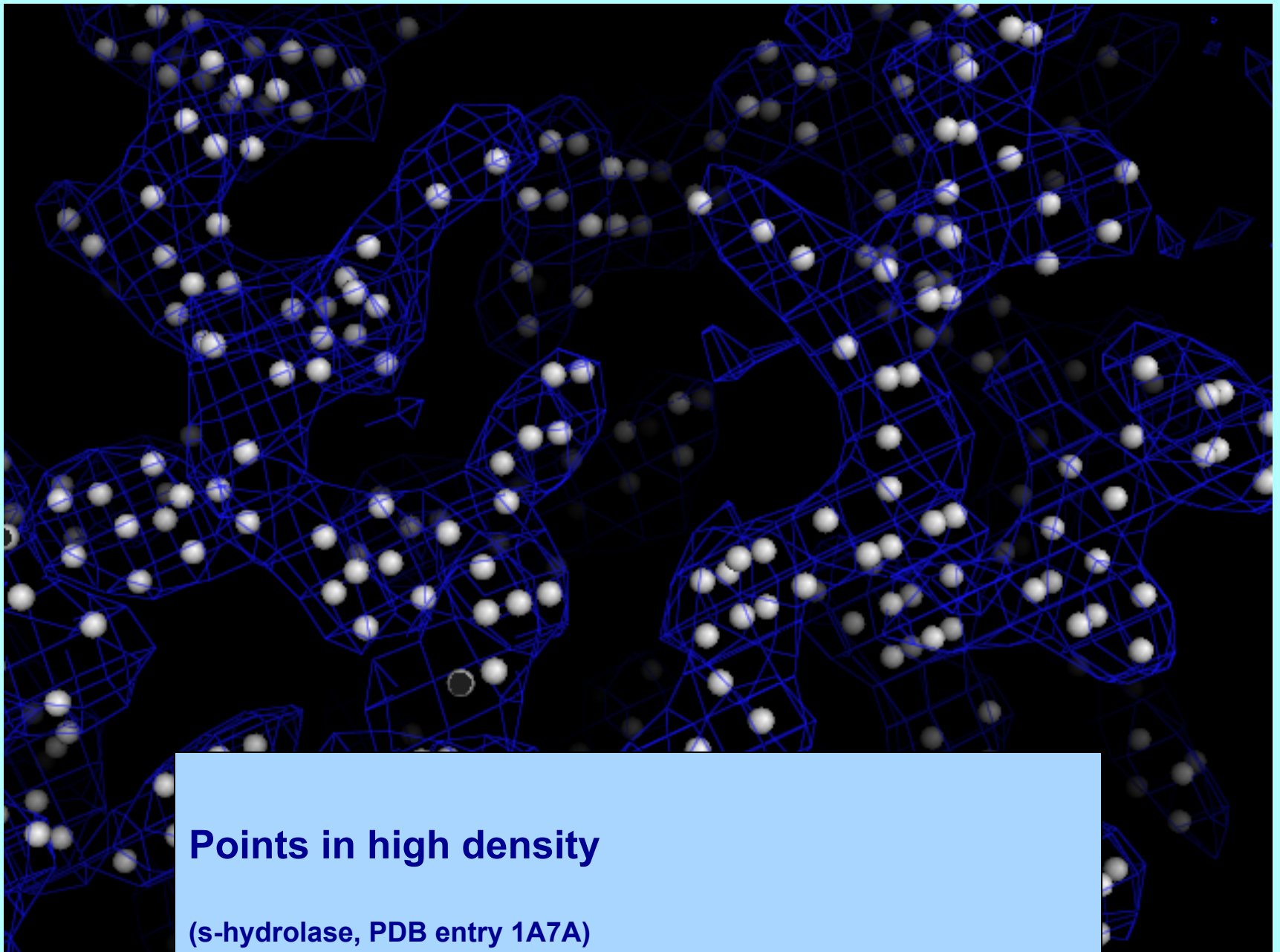
**Tom Terwilliger**  
Los Alamos National Laboratory

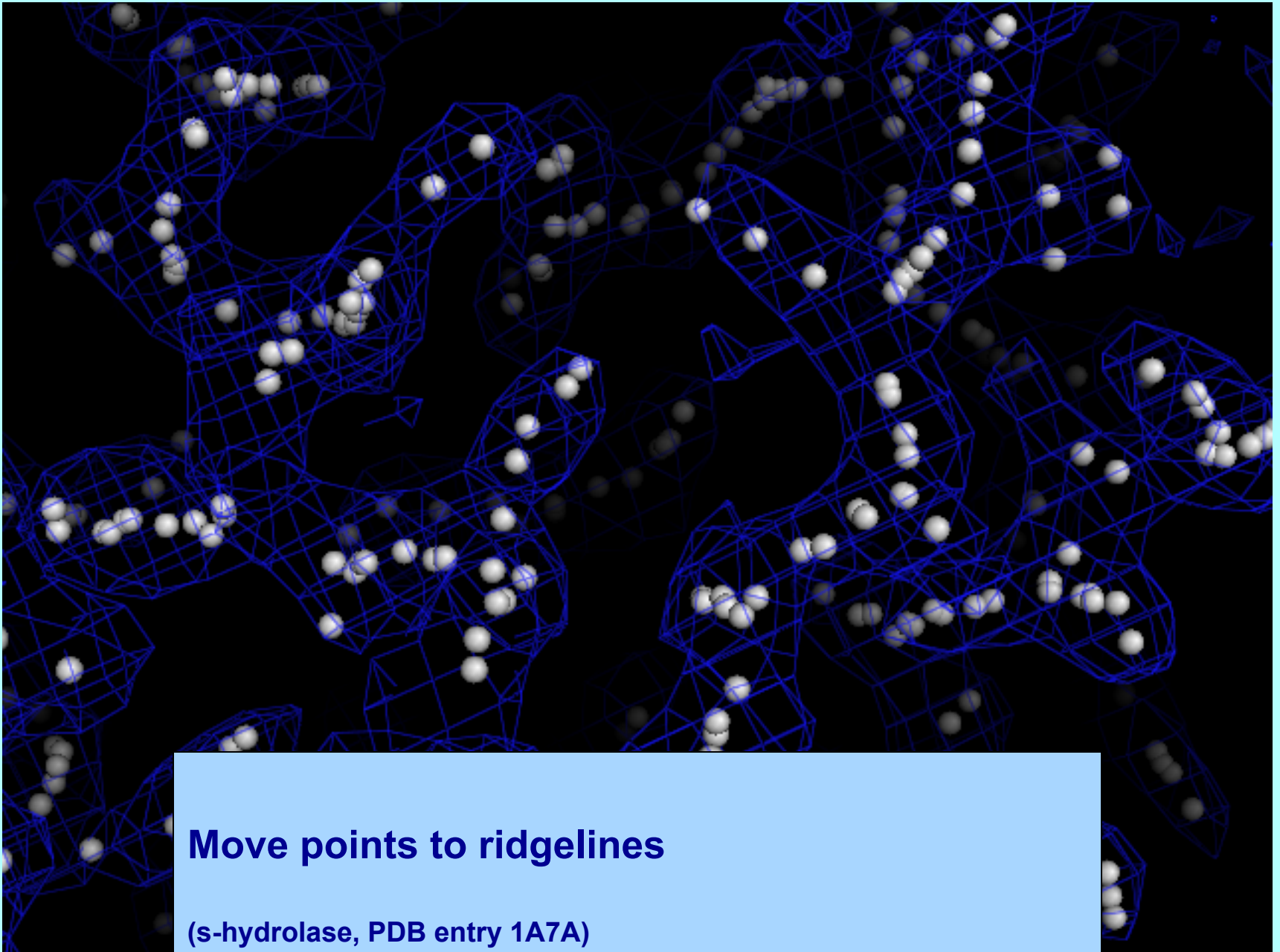




**Rapid chain-tracing  
for evaluation of map quality**

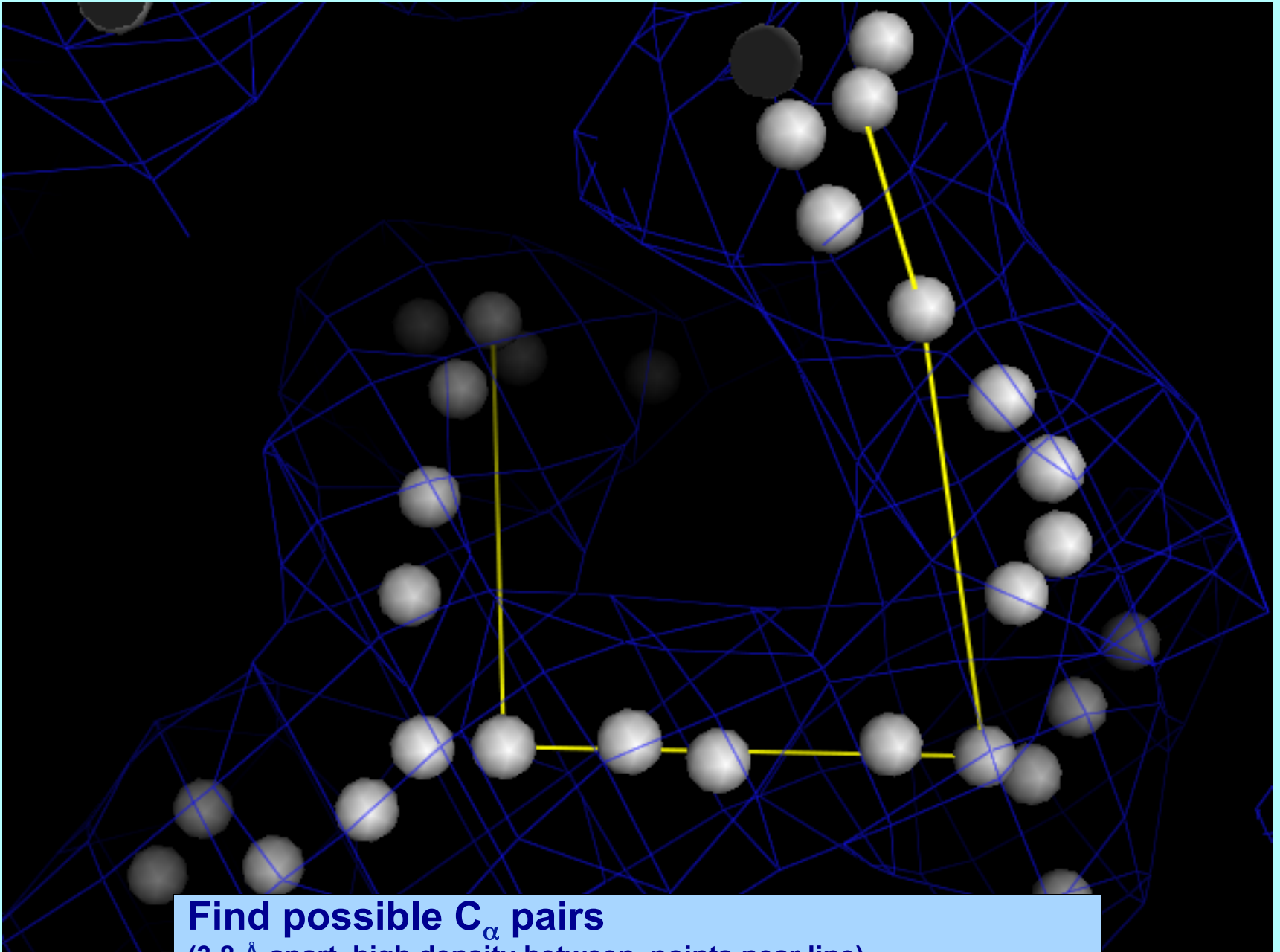
(armadillo repeat of  $\beta$ -catenin, 369 residues, 23 sec)



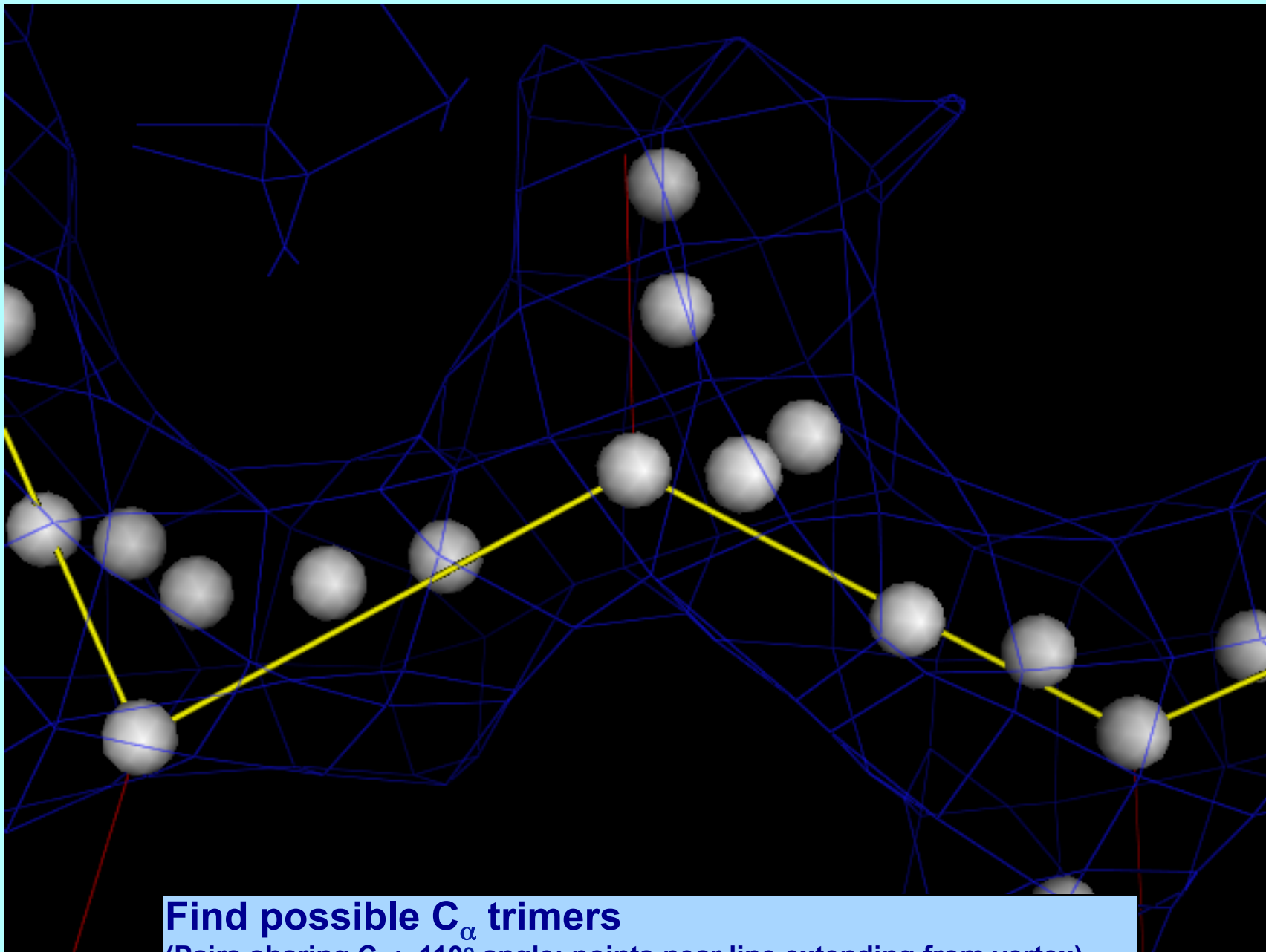


**Move points to ridgelines**

(s-hydrolase, PDB entry 1A7A)

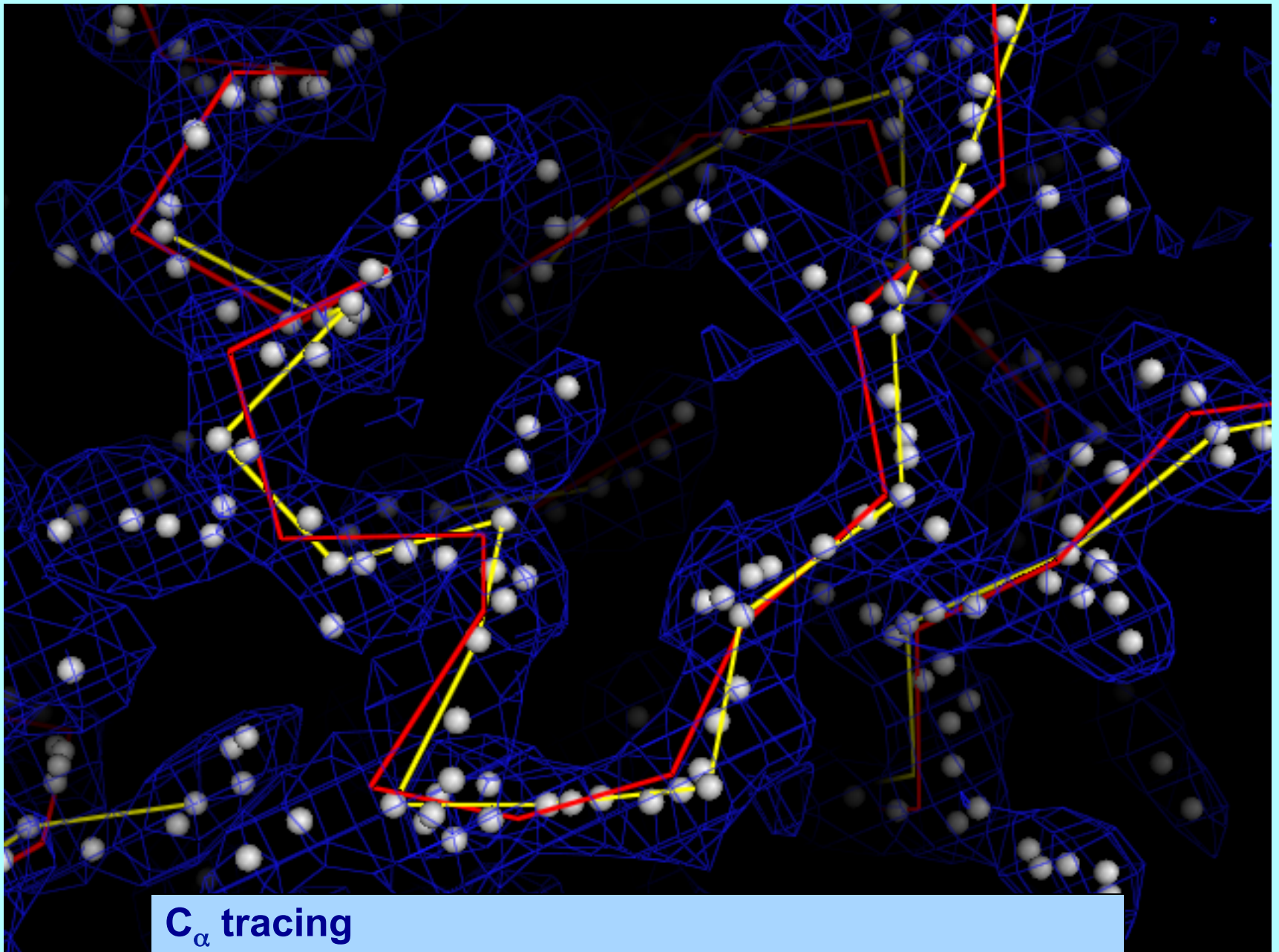


**Find possible  $C_{\alpha}$  pairs**  
(3.8 Å apart, high density between, points near line)



**Find possible  $C_{\alpha}$  trimers**

(Pairs sharing  $C_{\alpha}$ ;  $110^{\circ}$  angle; points near line extending from vertex)

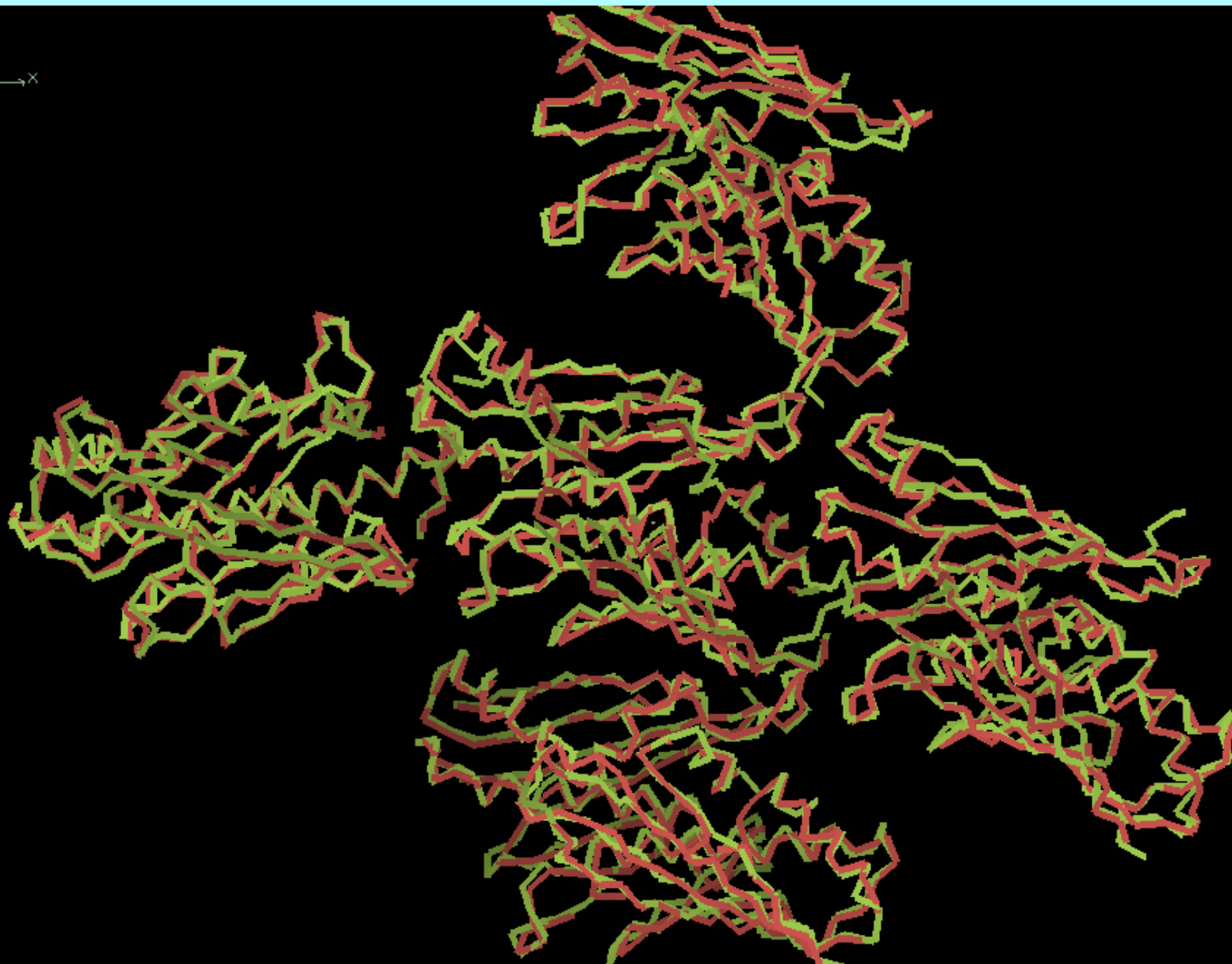
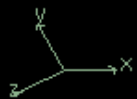


**C<sub>α</sub> tracing**  
(s-hydrolase, PDB entry 1A7A)

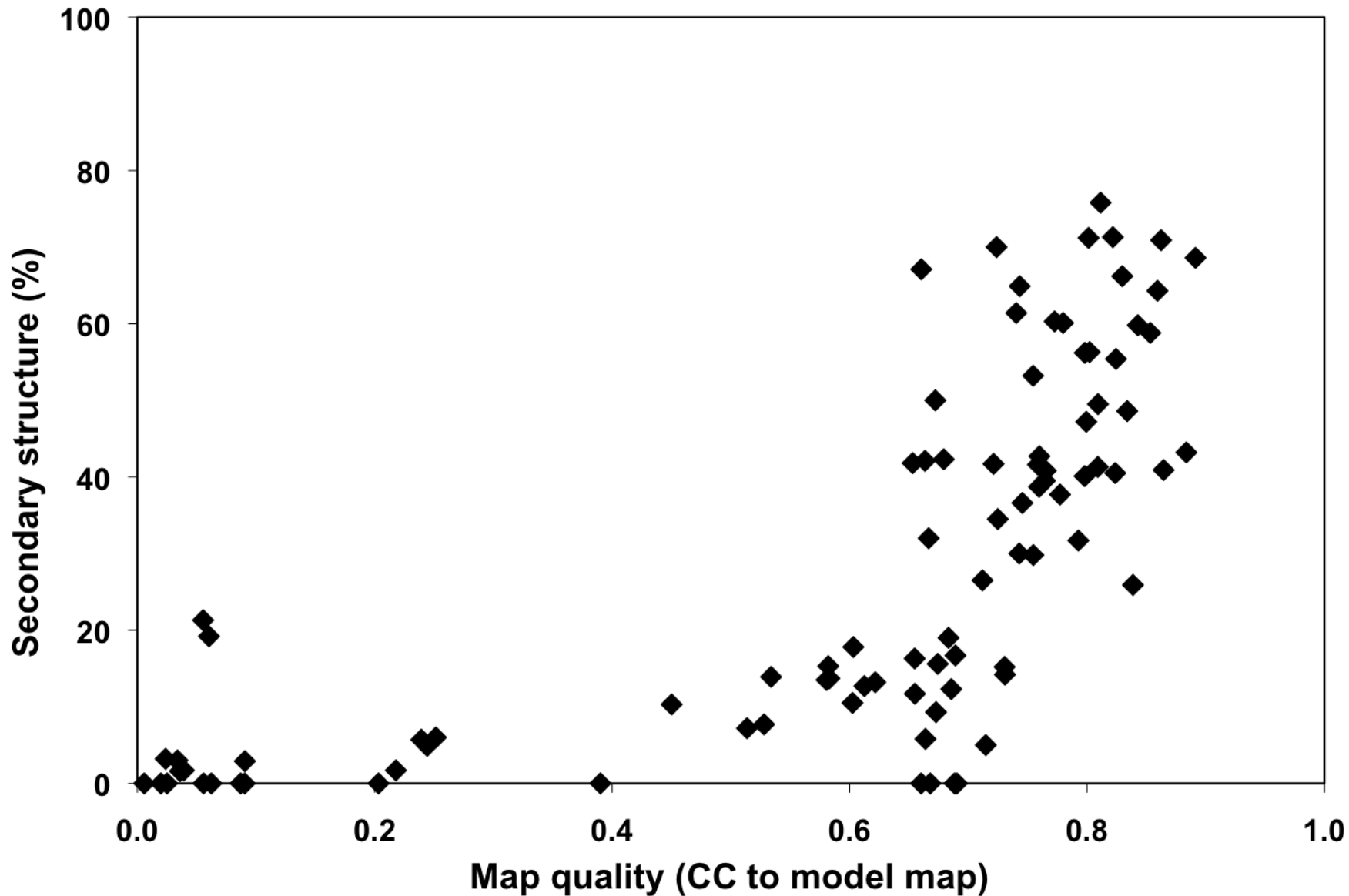


**C<sub>α</sub> tracing**  
(mevalonate kinase, PDB entry 1KKH, 9 sec)





**C<sub>α</sub> tracing**  
(1038B, PDB entry 1LQL, 114 sec)



**Using secondary structure content to evaluate map quality**

# The PHENIX Project



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An NIH/NIGMS funded  
Program Project