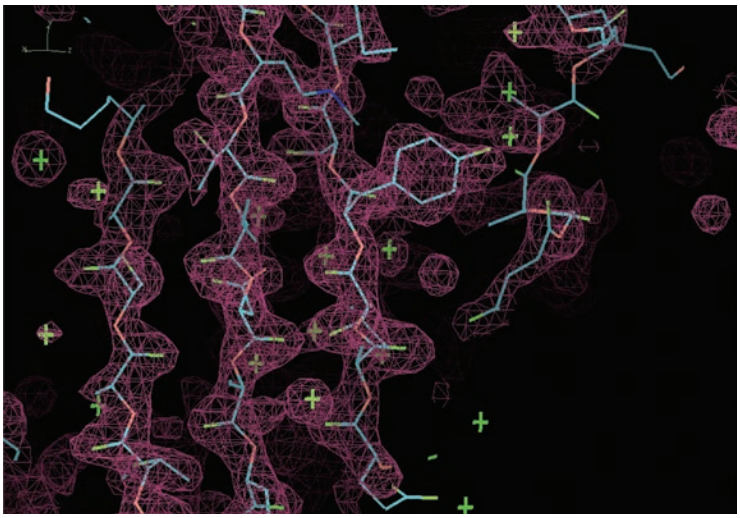

## Kenneth Trueblood Award

ACA President **Cheryl Klein** presented the **Trueblood Award** to **Tom Terwilliger**. The Trueblood award is for, "*exceptional achievement in computational or chemical crystallography*". Terwilliger noted that Kenneth Trueblood was known for both his contributions to crystallographic computing and for his teaching and helpfulness to others and that Trueblood's humanity and science is an inspiration to him.

Terwilliger's lecture, "*Molecular replacement and model-building using distant homology models as templates*," showed how to extend the reach of molecular replacement by using complementary information from the structure-modeling field and by using the local similarities of the search model to the structure to be determined. In the talk there was a running theme: the search models used in molecular replacement are often locally similar to the structure to be solved, even when the structures are rather different as a whole. He presented examples where search models had local details - helices, short loops, supersecondary structures - that were essentially identical to the corresponding parts of the final models, but where these would be offset be several Å when the structures are superimposed.

One part of Terwilliger's talk focused on how the information used in the structure-modeling field, *e.g.* **Rosetta** model-building, is complementary to that used in macromolecular crystallography. In the crystallographic context, automated model-building basically consists of identification of patterns of density in a map ('*I see a helix, let's put a helix there*'). In contrast, he pointed out, in the structure modeling field the key approach is identification of physically plausible conformations of the macromolecule. Terwilliger showed how powerful this structure-modeling approach can be by taking an automatically-determined NMR model of a structure, and, *without crystallographic data*, carrying out **Rosetta** remodeling of the structure, obtaining a model that was far closer than the NMR model to a 1.7 Å crystal structure of the same protein. Terwilliger then described how he worked with David Baker, the lead developer of **Rosetta**, and his postdoctoral researcher Frank DiMaio to combine tools from the **Phenix** crystallographic software with tools from the **Rosetta** software. He showed how **Rosetta** modeling with a scoring term based on fit to electron density developed by DiMaio could slightly improve crystallographic models *even* if they were too different from the target structure for standard automated model-building. In the series of cases Terwilliger showed, this improvement was enough to allow automated model-building to succeed.

**AutoBuild model cycle 2 Map CC: 0.78 R/Rfree=0.26/0.31**



***From Tom Terwilliger: Model and density-modified map for cab55348 at 1.9 Å resolution calculated by phenix.mr_rosetta (1) starting with glucuronoyl esterase Cip2 (PDB entry 3pic, 32% sequence identity, 2.1 Å rmsd from final model) correctly placed in the unit cell. Data and starting model kindly provided by P. Raj Pokkuluri (Argonne National Laboratory).***

***Terwilliger, T. C., DiMaio, F., Read, R. J., Baker, D., Bunkóczi, G., Adams, P. D., Grosse-Kunstleve, R. W., Afonine, P. V., Echols, N. (2012).phenix.mr_rosetta: Molecular replacement and model rebuilding with Phenix and Rosetta. J. Struct. Funct. Genomics 13, 81-90.***

The second part of Terwilliger's talk focused on the theme of local similarity despite global differences between structurally-related proteins. He presented a method he called, "*morphing*", in which a starting model after molecular replacement is distorted (morphed) to improve its match to an electron density map. The surprising element in this part of the talk is that a really poor electron density map can be used to morph a model with amazing accuracy. Terwilliger explained how this can be by pointing out that morphing involves very few parameters, so only a little information needs to be present in the map to identify the right shifts for a local part of the model. He showed how morphing can be used as an early step in model-building after molecular replacement and that morphing can allow structures more distant from the target structure to be solved with molecular replacement.

*Connie Rajnak - with the able last minute assistance of Tom Terwilliger*