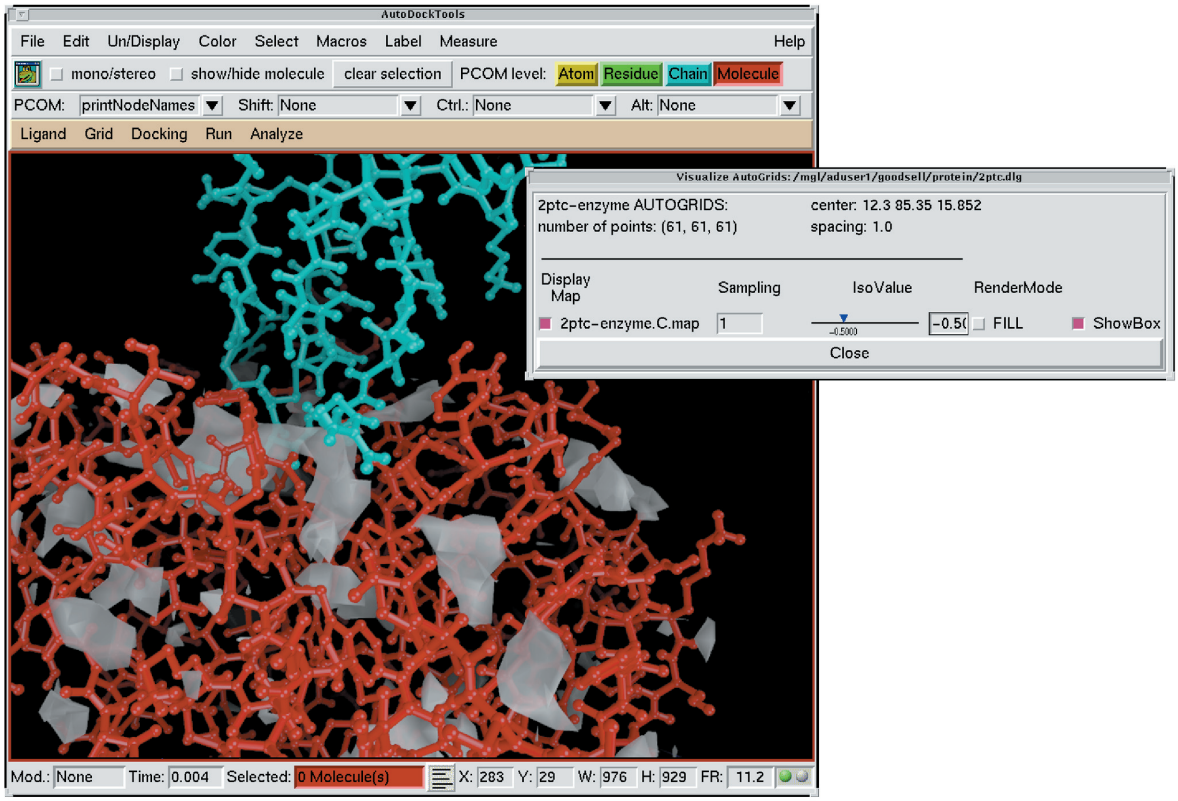

FIGURE 2. In this figure, AutoGrid has been used to calculate affinity grid values around the target molecule. White contours surround regions in space that are particularly favorable for carbon atom binding. The crystallographic conformation of bovine pancreatic trypsin inhibitor is shown in cyan. Notice how it binds in a pocket that is filled with favorable affinity values.

Protein–Protein Interactions: A Molecular Cloning *Manual*, 2nd Ed., © 2005 by Cold Spring Harbor Laboratory Press, Chapter 45, Figure 2.