Cn3D has long been NCBI's structure and structure alignment viewer. With version 4.1, Cn3D now includes a suite of alignment tools that lets the user edit and create multiple alignments using a variety of built-in algorithms that operate on both sequence and structure information. Cn3D's alignment model is well suited to structure-based sequence alignments, and guides the user towards defining a protein family's conserved core, wherein each member sequence contains all the sites that are homologous in both sequence and structure. The program's built-in algorithms assist the discovery of conserved sites and the accurate alignment of new member sequences, both with and without known structure.

Sequence and structure conservation can be visualized directly, helping the user to gauge where strong or weak homology exists, and even where errors in alignment are more likely. Cn3D does not automate alignment creation, since the user must still use some judgment in validating sequence and structure conservation; however, it provides many tools for analyzing sequence and structure relationships in different ways, and for selectively combining this information by building up an alignment iteratively. Alignments can be annotated to highlight important conserved residues, and exported for use in other applications.