**TOPO2: Transmembrane Protein Visualization Tool**

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With the number of integral membrane proteins estimated to comprise 25% of all proteins, the need to visualize these proteins to enhance our understanding of their function is an important problem in molecular biology. TOPO2 software has been evolving to provide just such a research tool.

Transmembrane protein topology visualization can be a very time-consuming process when done with conventional drawing software. The TOPO2 program was developed to allow for the rapid creation of such images. TOPO2 is used to visualize transmembrane proteins in the UCSF Pharmacogenetics of Membrane Transporters (PMT) Project.

TOPO2 has an open web site implementation (http://www.sacs.ucsf.edu/TOPO2) as well as being part of the SACS resource at UCSF. While the program doesn’t predict transmembrane segments, it has been coupled with three TMD prediction programs (MEMSAT, HMIMTOP and TMHMM) on the SACS web site to automatically generate images of their predictions.

The public version of TOPO2 (http://www.sacs.ucsf.edu/TOPO2) has been online for four years and has users worldwide. A recent feature added to the public site is the ability to turn off residue characters. In the future, the features developed for PMT will be added as well.

Considerable effort has gone into checking user input for errors. Errors are reported back to the user, along with the reason for the problem and a link to the program’s help page.

TOPO2 is part of the SACS resource. It is available on the command line and through the web. There are two web versions (basic and advanced), and it has been coupled with three TMD prediction programs to show their results graphically.

SACS command line users have access to the PMT development software as well as the standard version. SACS web users can display a plain (basic) or embellished (advanced) image. Their PostScript output can then be printed automatically, if their networked printer is known to the SACS system.