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ANTHEPROT: IBM PC and Apple Macintosh versions

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We have translated the ANTHEPROT package (Deléage *et al.*, 1988) on the Apple Macintosh and the IBM PC microcomputers.

IBM PC version

The translation has been realized on an IBM-PC-compatible computer. The program has also been checked on the IBM PS/2 series. Options are given for graphic cards (EGA, CGA, VGA, Hercules). The input of sequences is made via an editor which allows the sequences to be corrected. All the graphics can be displayed on the screen together with a movable cursor on the curve. The coordinates of this cursor are displayed at the same time above the profile as well as the given amino acid position (see Figure 1). This improvement allows the user to identify both the amino acid (with its position) and its corresponding value. Facilities have also been included to permit the plot of proteins of any length by means of variable scaling factors. A new option predicts the amphiphilicity of α-helices and β-sheets (Eisenberg *et al.*, 1982). The possibility of displaying the helical wheel (orthogonal projection of α-helices) is also offered. The secondary structure prediction methods have been translated with the possibility of predicting a set or subset of proteins and of saving the predicted states into a single file. For the HOMOL and DIRINFO programs, the possibility of scanning the α-helix, β-sheet, β-turn and coil potentials is given by a graphic display. The GOR method has been implemented as described by Gibrat *et al.* (1987) using the new set of parameters.

Macintosh version

The software has been tested on the Macintosh 512/800, +, SE and II versions. The programs used a matrix printer (Apple Imagewriter II) connected with either a direct output or an AppleTalk network. All the applications have been developed using most of the facilities (windows, button and mouse). Control variables have been included to avoid unexecutable subroutines in the course of the programs. Text outputs can be obtained on screen, printer, disk or clipboard. The clipboard output is particularly useful since the data can be formatted with a word processor and used in a spreadsheet or in graphics software. The graphic output (see Figure 2) can be delivered on screen and/or printer. All the options are selectable by the mouse and only some numerical values have to be selected from the keyboard.

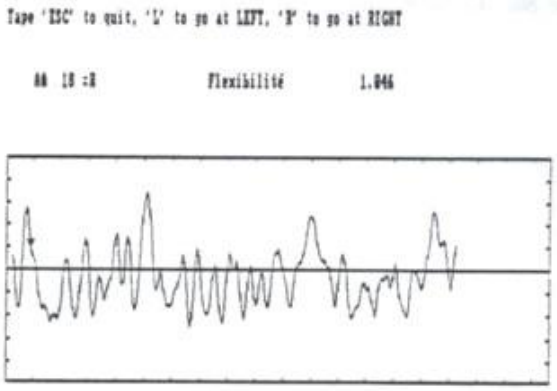

Fig. 1. Profile for local flexibility (Karplus and Schulz, 1985) of lactate dehydrogenase using a spanning window of seven residues (IBM version). The position of the cursor (at Arg 18) is indicated by a star and the corresponding value for flexibility is 1.046. The amino acid scale is 20 and the flexibility is graduated by 0.0375.

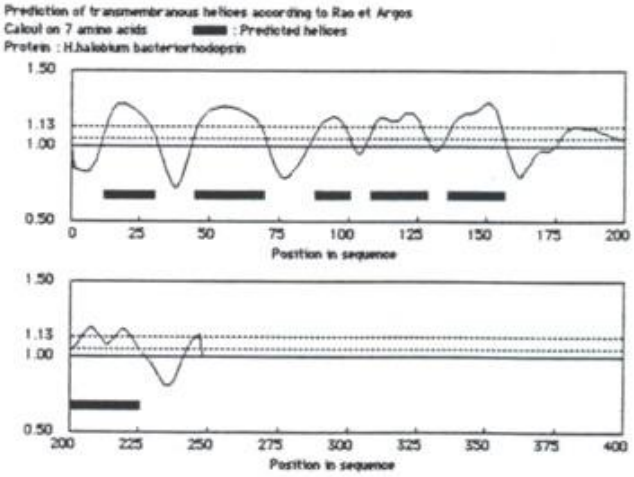

Fig. 2. Smooth profile for predicted intramembranous helices for *Halobium* bacteriorhodopsin with a spanning window of seven residues (Rao and Argos, 1986). The predicted helices are shown under the curve as black boxes (Macintosh version).

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