

# Version History

The present released version is 4.1.2 (18 January 1996).

Major changes since the first release of 'FoldIt (light)' (version 3.7.3, July 1994) are the following:

Version 4.0.0 (4 April 1995):

- A given structure now requires much less RAM memory (3.3K instead of 4.5K per residue) and less disk space (-13%).

CAUTION: The binaries (.FIT) created by the preceding version of 'FoldIt (light)' will not be read by the present version. You will be obliged to rebuild the .FIT files again from the original text files! (sorry)

- Nucleic acids are now fully recognized: up to 400 bases can be read.
- Water molecules are handled as separated entities: up to 1000 molecules can be read.
- Structure elements can be identified on the fly by simply moving the cursor over a structure image: with the OptionKey or the ControlKey down, atom names or residues names are automatically displayed.
- Application now keeps its color palette when the image window is saved to disk.
- Up to 50 atoms can be selected.
- Protein residues, bases, hetero-atoms or water can be selectively read.
- Once in memory, these 4 entities can be made visible or can be hidden.
- The 'Save As.../.PDB' menu item now produces complete files, including hetero-atoms.
- Keyboard short cuts are available to change the rotation axis and the display mode.
- The Help document (what you are reading) can now be printed. Items are easily accessed thanks to the links of the Content window. It is advised to put an alias of this document in your system 'Apple Menu Items'.

Version 4.0.1 (16 April 1995):

- Bug in turning atom list resolved.
- Improvement of image & text menu item availability.
- Bug in 'Save As.../.PDB' for structures built from scratch resolved.
- Slight speed improvement by limiting how often WaitNextEvent is called.

Version 4.0.2 (26 May 1995):

- A small line is drawn in the bottom left corner of the image window to materialize the bottom image region where a click rotates the structure around the Z-axis.
- Saved images have the original color background.
- User friendly 'Pen Settings' dialog.
- Any color depth can be used.

Version 4.0.3 (30 May 1995):

- Preferences dialog.
- General use of GWorlds (+ dynamic memory allocation).
- Use of QuickTime features: Motion speed increased by using DragAlignedWindow.
- Cmd-Up & Down arrows act on EDmap.

Version 4.0.4 (7 July 1995):

- Maximum number of H-bond windows=10.
- Windows menu.
- Image window & dialogs set to fit portable computer screens.
- Problem of international keyboards addressed.
- All windows (including utility windows) make use of GWorlds.
- Bug occurring when turning a bond on 'no FPU' versions.

Version 4.0.5 (17 August 1995):

- Version number of '.FIT' files is changed because of a bug on files containing hetero-atoms.
- Menu item 'Show I-bonds'.
- Multiple selection (hydrophobic, hydrophilic, positively & negatively charged).

Version 4.0.6+4.0.7 (14+18 September 1995):

- Menu item 'FoldIt Commands'.
- Bug if report length exceeds 32K; possibility to write results to disk.
- Aware of presence of a FPU unit.
- Pixel distance between stereo pairs.
- Color code if BFactor display.
- Bugs when free memory is tight.
- Write to disk when report is too long.

Version 4.0.8 (13 October 1995):

- Dynamic settings apply to stereo images.

Version 4.1.0 (30 October 1995):

- SetPort problem related to Image window (thanks to François ANTIER).
- Bug in SaveStructPDB for HETATOM.
- Deselecting atoms now also deselects clash arrays;
- Beta testing of PPC version (Thanks to Roberto SOLARO); format of text files downloaded with Netscape and Mosaic.
- Edit text in atInfo windows displayed correctly.
- User items work correctly with PPC.
- Apple events for MW & THINK;
- PPC VERSION SEEMS TO WORK PROPERLY: A REAL MILESTONE.

Version 4.1.1 (24 December 1995):

- Balloon help.
- Smooth zooming + zooming stops when keys are released.
- Bugs in popup menus.
- Speed test improves by about 10%.
- Help in line (thanks to R. Fronabarger).

Version 4.1.2 (18 January 1996):

- Custom line drawing routine for extra speed (thanks to 'Rotater' by Craig Kloeden): speed test improves by about 250%!!!
- Simulation of site directed mutagenesis.