

The release of LAFIRE

May, 1, 2004 : beta-version 1.0 (only Japanese)

May, 28, 2004 : beta-version 1.0(+) (only Japanese)

June, 14, 2004 : beta-version 1.0(++)(only Japanese)

June, 22, 2004 : beta-version 1.1 (only Japanese)

July, 09, 2004 : beta-version 1.2 (only Japanese)

August, 1, 2004 : beta-version 2.0

August,30, 2004 : beta-version 2.1

January, 1, 2005 : version 1.0

January, 5, 2006 : version 2.2

January, 30, 2006 : version 2.3

The version 2.3 has been improved:

1. Debugging same bugs including cis-Pro processing.
2. Simplifying the preparation of PDB file for initial model (see Manual 4-2-3).
3. Flipping side chain of Asn, Gln, and His based on difference of B-factor.
4. Using sigma-weighted Fo-Fc map during building.
5. Enabling refinement of DNA/RNA without building and fitting.

August, 8, 2006 : version 2.4

The new version (v2.4) has been improved in the following points:

1. Debugging same bugs, such as the fitting of side-chain of PHE and TYR.
2. Adding an output structure with lowest free R factor in the stage of torsion angle optimization.
3. Adding rigid-body, coordinates and B-factors refinement after sequence-check at the beginning.

January, 7 2007 : version 2.5 (manual 2.4)

The new version (v2.5) has been improved mainly by debugging

January, 1 2008 : version 2.6 (manual 2.6)

The new version (v2.6) has been improved:

1. The large density blobs occupied by the water molecules can be detected in the final stage (see Manual 4-4-3,4-6-5).
2. Adding fitting function when pickup water molecules (jump=4, see Manual 4-2-7).
3. It is available for CNS1.2
4. Debugging