

Foldit Standalone Reference Sheet

(Modifier abbreviations: C=Control/Command, A=Alt, S=Shift)

Import File Extensions

Main PDB file	.pdb
Main FASTA file	.fasta
Guide PDB	.second.pdb
Template PDB	.template.pdb
Constraints	.cnstr
Params	.params
Score function weights	.wts
Score function patch	.wts_patch
Electron density	.density
Symmetry	.sym
Flags file (command line args)	.cmdline

Viewport Mouse Controls

Near clip	CA+drag
Far clip	CS+drag
Fog	AS+drag

Save/Load Keys

Import PDB/FASTA/etc files	CAS+I
Export PDB file	CAS+X
Load session	CAS+L
Save session	CAS+S

View Option Keys

CPK coloring	CS+C
CPK + hydrogens	CS+V
Active site view	CS+X
Isosurface	C+I

Behavior Options: Minimizer DOFs

Low	Minimize torsions only
Medium	Minimize torsions only, PLUS peptide bond lengths/angles
High	Minimize torsions and ALL bond lengths/angles*
Auto (default)	Minimize torsions only, PLUS bad** peptide bond lengths/angles

*Technically not "cartesian" minimization, but produces in similar behavior

**At each residue, if *cart_bonded* > 5.0 REU, also minimize bond lengths/angles at the peptide bond

Advanced Keys

Measure distance/angle/dihedral
Print constraints to log
Print score components to log

CAS+C
CAS+J
CAS+T

Dialog Panel Keys

Information panel	tab
Alignment panel	L
Rama map panel	Actions

Miscellaneous Keys

Run DSSP	Actions
Focus on residue / protein	Q
Focus and clip on residue	S+Q
Cycle through rotamers	arrow keys