# Fold menu

• Helix Settings..., Predict Helix, HCA, CF: (not available)
• Turn Bond: (item enabled only if a torsion atom has been selected by double-clicking on an atom with the Option key down)
If the 'Show Clash Between Atoms During Torsion' has been set in the File/Preferences dialog, clashed atoms are marked as torsion proceeds.
* ClockWise, CounterCW: (âŒ˜S, âŒ˜/) Torsion direction around the torsion atom.
* Go Crazy: randomly(?) turn all bonds of a structure.
• Step Folding: Display residue after residue the folding of a structure (use âŒ˜Y to do this). If the OptionKey is down when choosing this menu item, the folding is not automatic but occurs stepwise (use âŒ˜Y to enter one residue at a time).
Structural information concerning each residue is given:
region (region of Ramachandran plot): pack (helix region), packG (symetrical of helix region), extd (sheet region), extdG (symetrical of sheet region), out (none of the preceeding);
state : alpha, 310, strand, turn, coil;
phi : phi angle in degree.
psi : psi angle in degree.
chi1 : chi1 angle in degree.
OBded: indicates to what atom(s) main chain oxygen is H-bonded (Bded= bonded).
NBded: indicates to what atom(s) main chain nitrogen is H-bonded.
SCBded: indicates to what atom(s) side chain atoms are H-bonded.
• Fold Into Helix.