

# Sequence Feature Settings

Feature Settings    DAS Settings

PDBsum\_protprot     cbs\_total     Uniprot

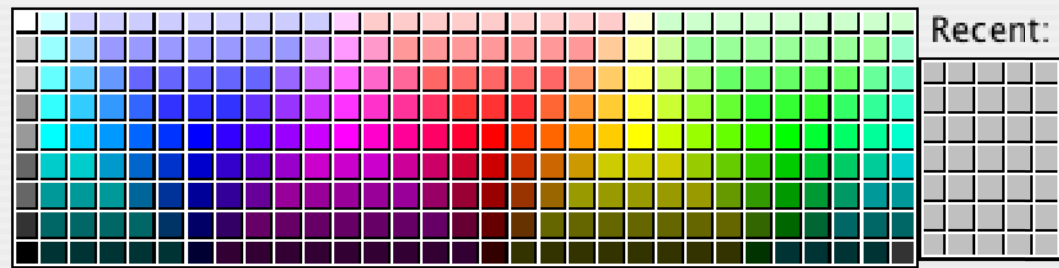
Feature Type	Colour	Display
modified residue		<input checked="" type="checkbox"/>
sequence variant		<input checked="" type="checkbox"/>
metal ion-binding site		<input checked="" type="checkbox"/>
sequence conflict		<input checked="" type="checkbox"/>
turn		<input checked="" type="checkbox"/>
helix		<input checked="" type="checkbox"/>
strand		<input checked="" type="checkbox"/>
signal peptide		<input checked="" type="checkbox"/>
transit peptide		<input checked="" type="checkbox"/>
domain		<input checked="" type="checkbox"/>
chain		<input checked="" type="checkbox"/>

- Optimise Order
- Invert Selection
- Seq sort by Score
- Seq Sort by density

OK    Cancel    Load Colours    Save Colours

# Select new Colour

Swatches    HSB    RGB



Preview

Sample Text    Sample Text   

          Sample Text    Sample Text          Sample Text    Sample Text

OK    Cancel    Reset