

















## Sequence Feature Settings

Feature Settings

DAS Settings

 Uniprot PDBsum\_protprot cbs\_func uniprot

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

Optimise Order

Invert Selection

Seq sort by Score

Seq Sort by density

OK

Cancel

Load Colours

Save Colours