

### Sequence Feature Settings

Feature Settings | DAS Settings

EMBL       uniprot       PDBsum\_ligands

Feature Type	Colour	Display
cleaved_initiator_methionine		<input checked="" type="checkbox"/>
polypeptide_region		<input checked="" type="checkbox"/>
natural_variant_site		<input type="checkbox"/>
glycosylated_residue		<input checked="" type="checkbox"/>
PO4 contact		<input checked="" type="checkbox"/>
OXY contact		<input checked="" type="checkbox"/>
HEM contact		<input checked="" type="checkbox"/>
metal_binding		<input checked="" type="checkbox"/>
turn		<input checked="" type="checkbox"/>
alpha_helix		<input checked="" type="checkbox"/>
mature_protein_region		<input checked="" type="checkbox"/>

Invert Selection

Optimise Order

OK    Cancel    Load Colours    Save Colours

Colour    Calculate    Web Service

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c g c c c c g g g c t c c g c g c c a g c c a a t g a g e g c g c c c g g e c g g g g c g t g c 54
g c c c c a a g c a t a a a c c c t g g c g e g c t e g c g g e c c g g e a c t c t t c t g g t 108
a g a c t c a g a g a g a a c c c a c c a t g g t g c t g t c t c c t g c c g a c a a g a c c a 162
a g g c c g c c t g g g g t a a g g t c g g c c g c e a c g c t g g c g a g t a t g g t g c g g 216
t g g a g a g g t g a g g c t c c c t c c c c t g c t e c g a c c c g g g c t c t c g c c c g 270
c c c a c a g g c c a c c c t c a a c c g t c c t g g c c c g g a c c c a a a c c c c a c c c 324
c t g c t t c t c c c c g a g g a t g t t c c t g t c c t t c c c c a c c a c c a a g a c c t 378
c g c a c t t c g a c c t g a g c c a c g g c t c t g c c c a a g t t a a g g c c a c g g c a 432
t g g c g a c g c g t g a c c a a c g c c t g g c g c a c g t g g a c g a c a t g c c e a 486

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EMBL|V00488/1-1138 487 a c g c g c t g t c e g c c c t g a g c g a c c t g c a c g c g c a c a a g b t f c g g t g g a e c c g g 540
EMBL|V00488/1-1138 541 t c a a c t t c a a g g t g a g c g g c g g g c c g g g a g c g a t c t g g g t c g a g g g g c g a g a t g 594
EMBL|V00488/1-1138 595 g c g c t t c c t c t c a g g g c a g a g g a t c a c g c g g g t t g c g g g a g g t g t a g c g a g g 648
EMBL|V00488/1-1138 649 c g g c g g c g e g g c t t g g g c c g a c t g a c c c t c t t c t c t g c a c a g c t c c t a a g c c a 702
EMBL|V00488/1-1138 703 c t g c c t g t g t g t g a c c c t g g c g c c c a c t c c c c c c g g a g t t c a c c c c t g c g g t 756
EMBL|V00488/1-1138 757 g c a c g c t t c c c t g g a c a a g t t c c t g g c t t c t g t g a c a c c g t g t g a c c t c c a a 810
EMBL|V00488/1-1138 811 a t a c c g t t a a g c t g g a g c c t c g g t a g c c g t t c c t c t g c c c g c t g g g c c t c c c a 864
EMBL|V00488/1-1138 865 a c g g g c e c t c t c c c c t c c t t g c a c c g g c c c t t c c t g g t c t t t g a a t a a g t c t 918

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