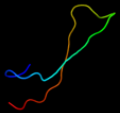
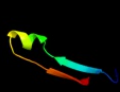
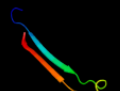
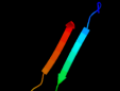
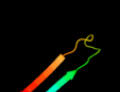
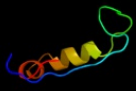
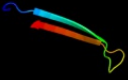
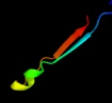
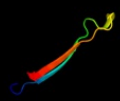
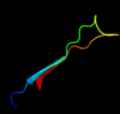
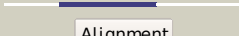
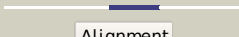
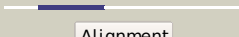
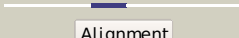


| #  | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                            |
|----|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">dlv8ha1</a> | <br>Alignment   |    | 29.3       | 13     | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> SoxZ-like                                                                                                                                                                 |
| 2  | <a href="#">c1mgtA</a>  | <br>Alignment   |    | 16.1       | 12     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (o6-methylguanine-dna methyltransferase);<br><b>PDBTitle:</b> crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1 |
| 3  | <a href="#">c3lf4B</a>  | <br>Alignment   |    | 9.9        | 20     | <b>PDB header:</b> fluorescent protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> fluorescent timer precursor blue102;<br><b>PDBTitle:</b> crystal structure of fluorescent timer precursor blue102                                                                               |
| 4  | <a href="#">c2gw4D</a>  | <br>Alignment   |    | 9.6        | 28     | <b>PDB header:</b> luminescent protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> kaede;<br><b>PDBTitle:</b> crystal structure of stony coral fluorescent protein kaede, red form                                                                                                 |
| 5  | <a href="#">c2zmcwC</a> | <br>Alignment |  | 8.8        | 32     | <b>PDB header:</b> luminescent protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> fluorescent protein;<br><b>PDBTitle:</b> crystal structure of monomeric kusabira-orange (mko),2 orange-emitting gfp-like protein, at ph 6.0                                                     |
| 6  | <a href="#">d1moua</a>  | <br>Alignment |  | 8.8        | 16     | <b>Fold:</b> GFP-like<br><b>Superfamily:</b> GFP-like<br><b>Family:</b> Fluorescent proteins                                                                                                                                                                                    |
| 7  | <a href="#">c1w2tE</a>  | <br>Alignment |  | 8.3        | 16     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> E: <b>PDB Molecule:</b> beta fructosidase;<br><b>PDBTitle:</b> beta-fructosidase from thermotoga maritima in complex with2 raffinose                                                                                              |
| 8  | <a href="#">c3evpA</a>  | <br>Alignment |  | 8.0        | 20     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> circular-permuted green fluorescent protein;<br><b>PDBTitle:</b> crystal structure of circular-permuted egfp                                                                                      |
| 9  | <a href="#">c3cfhB</a>  | <br>Alignment |  | 7.8        | 21     | <b>PDB header:</b> fluorescent protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> gfp-like photoswitchable fluorescent protein;<br><b>PDBTitle:</b> photoswitchable red fluorescent protein psrfp, off-state                                                                      |
| 10 | <a href="#">d2rh7a1</a> | <br>Alignment |  | 7.8        | 16     | <b>Fold:</b> GFP-like<br><b>Superfamily:</b> GFP-like<br><b>Family:</b> Fluorescent proteins                                                                                                                                                                                    |
| 11 | <a href="#">d1lc0a2</a> | <br>Alignment |  | 7.8        | 26     | <b>Fold:</b> FwdE/GAPDH domain-like<br><b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br><b>Family:</b> Biliverdin reductase                                                                                                              |

|    |                         |           |                                                                                     |     |    |                                                                                                                                                                                                                                                                           |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|-----|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">d2b5ea3</a> | Alignment |    | 7.7 | 19 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> PDI-like                                                                                                                                                                          |
| 13 | <a href="#">c2z6zA_</a> | Alignment |    | 7.7 | 28 | <b>PDB header:</b> fluorescent protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> fluorescent protein dronpa;<br><b>PDBTitle:</b> crystal structure of a photoswitchable gfp-like protein2 dronpa in the bright-state                                                       |
| 14 | <a href="#">d1xqma_</a> | Alignment |    | 7.7 | 20 | <b>Fold:</b> GFP-like<br><b>Superfamily:</b> GFP-like<br><b>Family:</b> Fluorescent proteins                                                                                                                                                                              |
| 15 | <a href="#">d1ggxa_</a> | Alignment |    | 7.5 | 20 | <b>Fold:</b> GFP-like<br><b>Superfamily:</b> GFP-like<br><b>Family:</b> Fluorescent proteins                                                                                                                                                                              |
| 16 | <a href="#">c2c9jG_</a> | Alignment |    | 7.5 | 24 | <b>PDB header:</b> luminescent protein<br><b>Chain:</b> G: <b>PDB Molecule:</b> green fluorescent protein fp512;<br><b>PDBTitle:</b> structure of the fluorescent protein cmfp512 at 1.35a from2 cerianthus membranaceus                                                  |
| 17 | <a href="#">c2otbB_</a> | Alignment |    | 7.5 | 24 | <b>PDB header:</b> fluorescent protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> gfp-like fluorescent chromoprotein cfp484;<br><b>PDBTitle:</b> crystal structure of a monomeric cyan fluorescent protein2 in the fluorescent state                                        |
| 18 | <a href="#">c3ai5A_</a> | Alignment |  | 7.3 | 20 | <b>PDB header:</b> fluorescent protein, transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> yeast enhanced green fluorescent protein, ubiquitin;<br><b>PDBTitle:</b> crystal structure of yeast enhanced green fluorescent protein-2 ubiquitin fusion protein          |
| 19 | <a href="#">c3gb3B_</a> | Alignment |  | 7.3 | 16 | <b>PDB header:</b> fluorescent protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> killerred;<br><b>PDBTitle:</b> x-ray structure of genetically encoded photosensitizer2 killerred in native form                                                                           |
| 20 | <a href="#">c1yzwB_</a> | Alignment |  | 7.3 | 24 | <b>PDB header:</b> luminescent protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> gfp-like non-fluorescent chromoprotein;<br><b>PDBTitle:</b> the 2.1a crystal structure of the far-red fluorescent2 protein hcrcd: inherent conformational flexibility of the3 chromophore |
| 21 | <a href="#">d1vkna2</a> | Alignment | not modelled                                                                        | 7.1 | 30 | <b>Fold:</b> FwdE/GAPDH domain-like<br><b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br><b>Family:</b> GAPDH-like                                                                                                                  |
| 22 | <a href="#">c3rwaE_</a> | Alignment | not modelled                                                                        | 7.1 | 20 | <b>PDB header:</b> fluorescent protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> fluorescent protein fp480;<br><b>PDBTitle:</b> crystal structure of circular-permuted mkate                                                                                               |
| 23 | <a href="#">d1ne2a_</a> | Alignment | not modelled                                                                        | 6.9 | 18 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> Ta1320-like                                                                                               |
| 24 | <a href="#">c3akoG_</a> | Alignment | not modelled                                                                        | 6.9 | 20 | <b>PDB header:</b> fluorescent protein<br><b>Chain:</b> G: <b>PDB Molecule:</b> venus;<br><b>PDBTitle:</b> crystal structure of the reassembled venus                                                                                                                     |
| 25 | <a href="#">d2q49a2</a> | Alignment | not modelled                                                                        | 6.9 | 40 | <b>Fold:</b> FwdE/GAPDH domain-like<br><b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br><b>Family:</b> GAPDH-like                                                                                                                  |
| 26 | <a href="#">c2oxgE_</a> | Alignment | not modelled                                                                        | 6.5 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> soxz protein;<br><b>PDBTitle:</b> the soxyz complex of paracoccus pantotrophus                                                                                                              |
| 27 | <a href="#">c2g3dB_</a> | Alignment | not modelled                                                                        | 6.4 | 20 | <b>PDB header:</b> luminescent protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> green fluorescent protein;<br><b>PDBTitle:</b> structure of s65g y66a gfp variant after spontaneous2 peptide hydrolysis                                                                   |
| 28 | <a href="#">c3cglE_</a> | Alignment | not modelled                                                                        | 5.9 | 24 | <b>PDB header:</b> fluorescent protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> gfp-like fluorescent chromoprotein dsfp483;<br><b>PDBTitle:</b> crystal structure and raman studies of dsfp483, a cyan fluorescent2 protein from discosoma striata                        |

|    |                         |                                                                                             |              |     |    |                                                                                                                                                                                                                                                                        |
|----|-------------------------|---------------------------------------------------------------------------------------------|--------------|-----|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">c3t9aA_</a> |  Alignment  | not modelled | 5.9 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> inositol pyrophosphate kinase;<br><b>PDBTitle:</b> crystal structure of the catalytic domain of human diphosphoinositol2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0 |
| 30 | <a href="#">c2ib5H_</a> |  Alignment | not modelled | 5.8 | 20 | <b>PDB header:</b> luminescent protein<br><b>Chain:</b> H: <b>PDB Molecule:</b> chromo protein;<br><b>PDBTitle:</b> structural characterization of a blue chromoprotein and its yellow2 mutant from the sea anemone cnidopus japonicus                                 |
| 31 | <a href="#">d1nh8a2</a> |  Alignment | not modelled | 5.7 | 25 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GlnB-like<br><b>Family:</b> ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain                                                                                                         |
| 32 | <a href="#">d1ckma2</a> |  Alignment | not modelled | 5.4 | 40 | <b>Fold:</b> ATP-grasp<br><b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain<br><b>Family:</b> mRNA capping enzyme                                                                                                                                   |
| 33 | <a href="#">d2v0ea1</a> |  Alignment | not modelled | 5.4 | 30 | <b>Fold:</b> GYF/BRK domain-like<br><b>Superfamily:</b> BRK domain-like<br><b>Family:</b> BRK domain-like                                                                                                                                                              |
| 34 | <a href="#">d1mywa_</a> |  Alignment | not modelled | 5.3 | 20 | <b>Fold:</b> GFP-like<br><b>Superfamily:</b> GFP-like<br><b>Family:</b> Fluorescent proteins                                                                                                                                                                           |
| 35 | <a href="#">d1uisa_</a> |  Alignment | not modelled | 5.3 | 16 | <b>Fold:</b> GFP-like<br><b>Superfamily:</b> GFP-like<br><b>Family:</b> Fluorescent proteins                                                                                                                                                                           |