Phyre2

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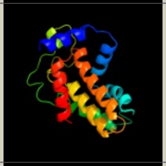
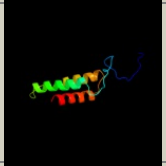
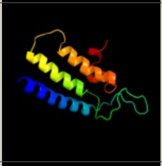
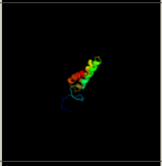
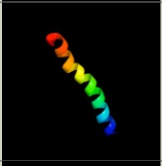
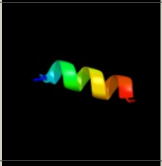
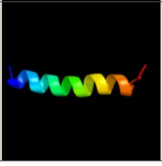
| Description | P75806 |
| Date | Thu Jan 5 12:14:25 GMT 2012 |
| Unique Job ID | 13e3ede5e4510c81 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1d2ta_ | Alignment |  | 99.8 | 10 | **Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Family:**Type 2 phosphatidic acid phosphatase, PAP2 |
| 2 | c2akcC_ | Alignment |  | 99.8 | 18 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**class a nonspecific acid phosphatase phon;<br>**PDBTitle:** crystal structure of tungstate complex of the phon protein2 from s. typhimurium |
| 3 | d1qi9a_ | Alignment |  | 98.3 | 27 | **Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Family:**Haloperoxidase (bromoperoxidase) |
| 4 | d1vnsa_ | Alignment |  | 98.0 | 26 | **Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Family:**Chloroperoxidase |
| 5 | c1vngA_ | Alignment |  | 97.9 | 25 | **PDB header:**haloperoxidase<br>**Chain:** A: **PDB Molecule:**vanadium chloroperoxidase;<br>**PDBTitle:** chloroperoxidase from the fungus curvularia inaequalis:2 mutant h404a |
| 6 | d1up8a_ | Alignment |  | 97.5 | 21 | **Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Family:**Haloperoxidase (bromoperoxidase) |
| 7 | d1qhba_ | Alignment |  | 97.3 | 24 | **Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Family:**Haloperoxidase (bromoperoxidase) |
| 8 | c2kncB_ | Alignment |  | 13.7 | 10 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**integrin beta-3;<br>**PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex |
| 9 | c2cg4B_ | Alignment |  | 8.6 | 13 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**regulatory protein asnc;<br>**PDBTitle:** structure of e.coli asnc |
| 10 | d1eh9a2 | Alignment |  | 8.1 | 43 | **Fold:**Glycosyl hydrolase domain<br>**Superfamily:**Glycosyl hydrolase domain<br>**Family:**alpha-Amylases, C-terminal beta-sheet domain |
| 11 | c2l34A_ | Alignment |  | 7.7 | 15 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**tyro protein tyrosine kinase-binding protein;<br>**PDBTitle:** structure of the dap12 transmembrane homodimer |

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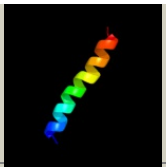
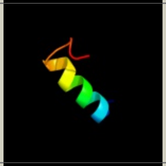
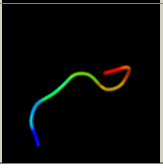
|---|---|---|---|---|---|---|
| 12 | c2l34B_ | Alignment |  | 7.7 | 15 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein;<br>**PDBTitle:** structure of the dap12 transmembrane homodimer |
| 13 | d2cg4a1 | Alignment |  | 6.5 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 14 | d1dsva_ | Alignment |  | 5.6 | 43 | **Fold:**Retrovirus zinc finger-like domains<br>**Superfamily:**Retrovirus zinc finger-like domains<br>**Family:**Retrovirus zinc finger-like domains |

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| 15 | d2r4qa1 | Alignment |  | 5.5 | 18 | **Fold:**Phosphotyrosine protein phosphatases I-like<br>**Superfamily:**PTS system IIB component-like<br>**Family:**PTS system, Fructose specific IIB subunit-like |