# Phyre$^2$

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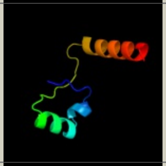
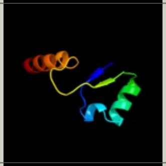
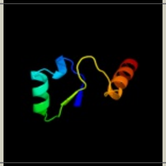
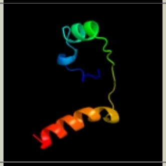
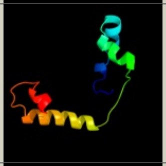
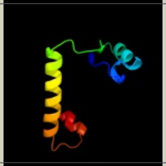
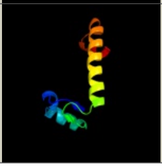
| Description | Q9JMS8 |
| Date | Thu Jan 5 12:38:04 GMT 2012 |
| Unique Job ID | fd8fb85c20e08c6b |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3f9kV_ | Alignment |  | 99.4 | 17 | **PDB header:**viral protein, recombination<br>**Chain:** V: **PDB Molecule:**integrase;<br>**PDBTitle:** two domain fragment of hiv-2 integrase in complex with ledgf ibd |
| 2 | d1asua_ | Alignment |  | 99.3 | 22 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**Retroviral integrase, catalytic domain |
| 3 | c3nf9A_ | Alignment |  | 99.3 | 16 | **PDB header:**hydrolase/hydrolase inhibitor<br>**Chain:** A: **PDB Molecule:**integrase;<br>**PDBTitle:** structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design |
| 4 | c1c0mA_ | Alignment |  | 99.2 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein (integrase);<br>**PDBTitle:** crystal structure of rsv two-domain integrase |
| 5 | d1cxqa_ | Alignment |  | 98.9 | 20 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**Retroviral integrase, catalytic domain |
| 6 | d1c0ma2 | Alignment |  | 98.8 | 20 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**Retroviral integrase, catalytic domain |
| 7 | c1ex4A_ | Alignment |  | 98.8 | 13 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**integrase;<br>**PDBTitle:** hiv-1 integrase catalytic core and c-terminal domain |
| 8 | c1k6yB_ | Alignment |  | 98.6 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**integrase;<br>**PDBTitle:** crystal structure of a two-domain fragment of hiv-1 integrase |
| 9 | d1hyva_ | Alignment |  | 98.5 | 14 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**Retroviral integrase, catalytic domain |
| 10 | c3hpgC_ | Alignment |  | 98.5 | 15 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**integrase;<br>**PDBTitle:** visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces |
| 11 | c3kksB_ | Alignment |  | 98.3 | 20 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**integrase;<br>**PDBTitle:** crystal structure of catalytic core domain of biv integrase in crystal2 form ii |

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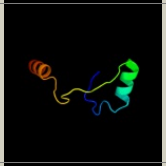
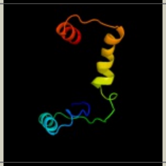
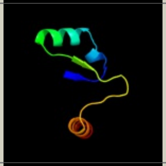
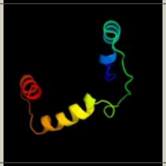
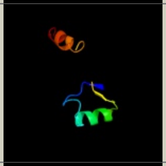
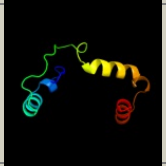
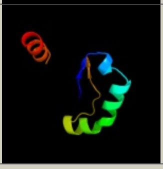
|---|---|---|---|---|---|---|
| 12 | d1bcoa2 | Alignment |  | 98.3 | 13 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**mu transposase, core domain |
| 13 | d1exqa_ | Alignment |  | 98.3 | 10 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**Retroviral integrase, catalytic domain |
| 14 | c1bcoA_ | Alignment |  | 97.8 | 13 | **PDB header:**transposase<br>**Chain:** A: **PDB Molecule:**bacteriophage mu transposase;<br>**PDBTitle:** bacteriophage mu transposase core domain |
| 15 | c3hosA_ | Alignment |  | 97.8 | 7 | **PDB header:**transferase, dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**transposable element mariner, complete cds;<br>**PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg |
| 16 | c3l2tB_ | Alignment |  | 97.7 | 18 | **PDB header:**recombination/dna<br>**Chain:** B: **PDB Molecule:**integrase;<br>**PDBTitle:** crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir) |
| 17 | c2f7tA_ | Alignment |  | 97.7 | 9 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**mos1 transposase;<br>**PDBTitle:** crystal structure of the catalytic domain of mos1 mariner2 transposase |
| 18 | d1c6va_ | Alignment |  | 97.4 | 19 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**Retroviral integrase, catalytic domain |
| 19 | c3f2kB_ | Alignment |  | 97.3 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**histone-lysine n-methyltransferase setmar;<br>**PDBTitle:** structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar |
| 20 | c3dlrA_ | Alignment |  | 95.1 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**integrase;<br>**PDBTitle:** crystal structure of the catalytic core domain from pfv2 integrase |
| 21 | c2i8bB_ | Alignment | not modelled | 38.3 | 29 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**minor nucleoprotein vp30;<br>**PDBTitle:** crystal structure of the c-terminal domain of ebola virus vp30 |
| 22 | d1b7ea_ | Alignment | not modelled | 14.6 | 8 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**Transposase inhibitor (Tn5 transposase) |
| 23 | c1dkgB_ | Alignment | not modelled | 14.0 | 6 | **PDB header:**complex (hsp24/hsp70)<br>**Chain:** B: **PDB Molecule:**nucleotide exchange factor grpe;<br>**PDBTitle:** crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak |
| 24 | c3en9B_ | Alignment | not modelled | 11.3 | 12 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**o-sialoglycoprotein endopeptidase/protein kinase;<br>**PDBTitle:** structure of the methanococcus jannaschii kae1-bud32 fusion2 protein |
| 25 | c3lo0A_ | Alignment | not modelled | 7.6 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**inorganic pyrophosphatase;<br>**PDBTitle:** crystal structure of inorganic pyrophosphatase from2 ehrlichia chaffeensis |
| 26 | c2vkcA_ | Alignment | not modelled | 7.5 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**nedd4-binding protein 2;<br>**PDBTitle:** solution structure of the b3bp smr domain |
| 27 | c3fq3H_ | Alignment | not modelled | 7.4 | 30 | **PDB header:**hydrolase<br>**Chain:** H: **PDB Molecule:**inorganic pyrophosphatase:bacterial/archaeal inorganic<br>**PDBTitle:** crystal structure of inorganic phosphatase from brucella melitensis |
| 28 | d1i40a_ | Alignment | not modelled | 6.6 | 27 | **Fold:**OB-fold<br>**Superfamily:**Inorganic pyrophosphatase<br>**Family:**Inorganic pyrophosphatase |

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| 29 | d2prda_ | Alignment | not modelled | 6.5 | 20 | **Fold:**OB-fold<br>**Superfamily:**Inorganic pyrophosphatase<br>**Family:**Inorganic pyrophosphatase |
| 30 | d1udea_ | Alignment | not modelled | 6.4 | 27 | **Fold:**OB-fold<br>**Superfamily:**Inorganic pyrophosphatase<br>**Family:**Inorganic pyrophosphatase |
| 31 | c3d63B_ | Alignment | not modelled | 6.0 | 27 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**inorganic pyrophosphatase;<br>**PDBTitle:** crystal structure of inorganic pyrophosphatase from burkholderia2 pseudomallei |
| 32 | d1twla_ | Alignment | not modelled | 5.9 | 27 | **Fold:**OB-fold<br>**Superfamily:**Inorganic pyrophosphatase<br>**Family:**Inorganic pyrophosphatase |