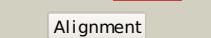
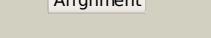
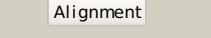
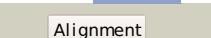


# Phyre<sup>2</sup>

Email	I.a.kelley@imperial.ac.uk
Description	P76071
Date	Thu Jan 5 12:18:09 GMT 2012
Unique Job ID	f7a224221019c692

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_			98.3	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Transposase inhibitor (Tn5 transposase)
2	d1b7ea_			96.9	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Transposase inhibitor (Tn5 transposase)
3	d1asua_			87.3	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
4	d1cxqa_			84.1	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
5	c3nf9A_			69.3	14	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
6	d1a9xa1			47.7	14	<b>Fold:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Superfamily:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Family:</b> Carbamoyl phosphate synthetase, large subunit connection domain
7	d1c0ma2			43.7	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
8	c3f9kv_			43.6	13	<b>PDB header:</b> viral protein, recombination <b>Chain:</b> V: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> two domain fragment of hiv-2 integrase in complex with ledgf ibd
9	c1bcoA_			35.9	15	<b>PDB header:</b> transposase <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriophage mu transposase; <b>PDBTitle:</b> bacteriophage mu transposase core domain
10	c1k6yB_			24.1	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of a two-domain fragment of hiv-1 integrase
11	c3hefB_			23.1	15	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gene 1 protein; <b>PDBTitle:</b> crystal structure of the bacteriophage sf6 terminase small2 subunit

12	<a href="#">d1hyva</a>			21.4	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
13	<a href="#">c1c0mA</a>			16.1	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (integrase); <b>PDBTitle:</b> crystal structure of rsv two-domain integrase
14	<a href="#">d1exqa</a>			15.6	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
15	<a href="#">d1slma1</a>			15.6	22	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> MMP N-terminal domain
16	<a href="#">c3nzqB</a>			13.4	17	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> biosynthetic arginine decarboxylase; <b>PDBTitle:</b> crystal structure of biosynthetic arginine decarboxylase adc (spea2) from escherichia coli, northeast structural genomics consortium3 target er600
17	<a href="#">c3n2oA</a>			10.7	32	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> biosynthetic arginine decarboxylase; <b>PDBTitle:</b> x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
18	<a href="#">d1c6va</a>			10.0	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
19	<a href="#">d1k78a1</a>			8.7	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
20	<a href="#">d1bcoa2</a>			8.1	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> mu transposase, core domain
21	<a href="#">d1sfka</a>		not modelled	7.7	13	<b>Fold:</b> Flavivirus capsid protein C <b>Superfamily:</b> Flavivirus capsid protein C <b>Family:</b> Flavivirus capsid protein C
22	<a href="#">c1bg1A</a>		not modelled	7.5	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> A; <b>PDB Molecule:</b> protein (transcription factor stat3b); <b>PDBTitle:</b> transcription factor stat3b/dna complex
23	<a href="#">c3pvpA</a>		not modelled	7.0	16	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A; <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
24	<a href="#">d2vol1</a>		not modelled	6.6	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
25	<a href="#">d1s1ma2</a>		not modelled	6.4	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
26	<a href="#">d2fm9a1</a>		not modelled	6.4	6	<b>Fold:</b> SipA N-terminal domain-like <b>Superfamily:</b> SipA N-terminal domain-like <b>Family:</b> SipA N-terminal domain-like
27	<a href="#">d6paxa1</a>		not modelled	6.3	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
28	<a href="#">c3ostA</a>		not modelled	6.1	18	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> serine/threonine-protein kinase kcc4; <b>PDBTitle:</b> structure of the kinase associated-1 (ka1) from kcc4p

29	<a href="#">d2ve8a1</a>		not modelled	5.9	36	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FtsK C-terminal domain-like
30	<a href="#">c1ex4A_</a>		not modelled	5.9	17	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> hiv-1 integrase catalytic core and c-terminal domain
31	<a href="#">c3nzpA_</a>		not modelled	5.8	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> arginine decarboxylase; <b>PDBTitle:</b> crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53