



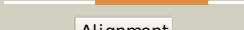

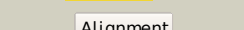







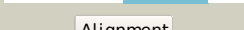

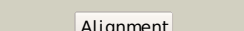
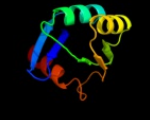
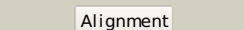



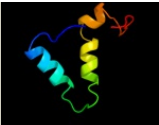
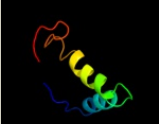


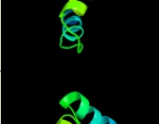






Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0CE52
Date	Thu Jan 5 11:30:20 GMT 2012
Unique Job ID	08704bce25c266ce

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	 Alignment		98.2	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	 Alignment		97.5	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
3	d1cxqa_	 Alignment		84.2	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
4	c3hefB_	 Alignment		79.7	14	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit
5	d1asua_	 Alignment		70.0	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
6	c3nf9A_	 Alignment		47.7	14	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: integrase; PDBTitle: structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
7	d1a9xa1	 Alignment		39.7	16	Fold: Carbamoyl phosphate synthetase, large subunit connection domain Superfamily: Carbamoyl phosphate synthetase, large subunit connection domain Family: Carbamoyl phosphate synthetase, large subunit connection domain
8	d1c0ma2	 Alignment		35.3	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
9	c1c0mA_	 Alignment		30.6	19	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
10	d1slma1	 Alignment		29.6	27	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
11	c3ohwB_	 Alignment		22.4	16	PDB header: protein binding Chain: B: PDB Molecule: phycobilisome lcm core-membrane linker polypeptide; PDBTitle: x-ray structure of phycobilisome lcm core-membrane linker polypeptide2 (fragment 721-860) from synechocystis sp. pcc 6803, northeast3 structural genomics consortium target sgr209e

12	c2ky4A_	Alignment		22.4	16	PDB header: photosynthesis Chain: A: PDB Molecule: phycobilisome linker polypeptide; PDBTitle: solution nmr structure of the pbs linker domain of phycobilisome2 linker polypeptide from anabaena sp. northeast structural genomics3 consortium target nsr123e
13	c2l3wA_	Alignment		20.8	20	PDB header: photosynthesis Chain: A: PDB Molecule: phycobilisome rod linker polypeptide; PDBTitle: solution nmr structure of the pbs linker domain of phycobilisome rod2 linker polypeptide from synechococcus elongatus, northeast structural3 genomics consortium target snr168a
14	d1k78a1	Alignment		19.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
15	c3pruD_	Alignment		19.4	13	PDB header: photosynthesis Chain: D: PDB Molecule: phycobilisome 32.1 kda linker polypeptide, phycocyanin- PDBTitle: crystal structure of phycobilisome 32.1 kda linker polypeptide,2 phycocyanin-associated, rod 1 (fragment 14-158) from synechocystis3 sp. pcc 6803, northeast structural genomics consortium target sgr182a
16	c2l06A_	Alignment		18.7	22	PDB header: protein binding Chain: A: PDB Molecule: phycobilisome lcm core-membrane linker polypeptide; PDBTitle: solution nmr structure of the pbs linker polypeptide domain (fragment2 254-400) of phycobilisome linker protein apce from synechocystis sp.3 pcc 6803. northeast structural genomics consortium target sgr209c
17	d1hyva_	Alignment		18.2	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
18	c1q2iA_	Alignment		17.8	28	PDB header: antitumor protein Chain: A: PDB Molecule: pnc27; PDBTitle: nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
19	d1exqa_	Alignment		16.0	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
20	c3pvpA_	Alignment		15.9	14	PDB header: dna binding protein/dna Chain: A: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
21	c3f9kV_	Alignment	not modelled	15.1	14	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
22	d1su3a1	Alignment	not modelled	14.8	28	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
23	c2o8kA_	Alignment	not modelled	14.2	27	PDB header: transcription/dna Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
24	c3u1nC_	Alignment	not modelled	14.2	12	PDB header: hydrolase Chain: C: PDB Molecule: sam domain and hd domain-containing protein 1; PDBTitle: structure of the catalytic core of human samhd1
25	c1k6yB_	Alignment	not modelled	12.7	19	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
26	c1x6iB_	Alignment	not modelled	12.2	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ygfy; PDBTitle: crystal structure of ygfy from escherichia coli
27	c1bg1A_	Alignment	not modelled	10.9	11	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
28	d2fug11	Alignment	not modelled	9.9	19	Fold: Bromodomain-like Superfamily: Nqo1C-terminal domain-like Family: Nqo1C-terminal domain-like
29	d1nkua_	Alignment	not modelled	9.1	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase I (Tag)

30	d2d1ha1	Alignment	not modelled	8.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
31	c3iwfa_	Alignment	not modelled	8.3	4	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
32	c2kvcA_	Alignment	not modelled	8.2	20	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
33	d1sfka_	Alignment	not modelled	7.6	19	Fold: Flavivirus capsid protein C Superfamily: Flavivirus capsid protein C Family: Flavivirus capsid protein C
34	d1slma2	Alignment	not modelled	7.4	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
35	d1c6va_	Alignment	not modelled	7.3	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
36	d1vcoa2	Alignment	not modelled	6.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
37	d1r6ra_	Alignment	not modelled	5.9	10	Fold: Flavivirus capsid protein C Superfamily: Flavivirus capsid protein C Family: Flavivirus capsid protein C
38	c1r6rA_	Alignment	not modelled	5.9	10	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: solution structure of dengue virus capsid protein reveals a2 new fold
39	c1yvlB_	Alignment	not modelled	5.7	9	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
40	c1ud0B_	Alignment	not modelled	5.6	20	PDB header: chaperone Chain: B: PDB Molecule: 70 kda heat-shock-like protein; PDBTitle: crystal structure of the c-terminal 10-kda subdomain of hsc70
41	d1h3fa1	Alignment	not modelled	5.6	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
42	c2vkpA_	Alignment	not modelled	5.6	12	PDB header: protein-binding Chain: A: PDB Molecule: btb/poz domain-containing protein 6; PDBTitle: crystal structure of btb domain from btbdb6
43	c3d3kD_	Alignment	not modelled	5.4	12	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
44	c1m6vE_	Alignment	not modelled	5.4	16	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
45	d1jlva_	Alignment	not modelled	5.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV
46	c2lkyA_	Alignment	not modelled	5.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msme_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b