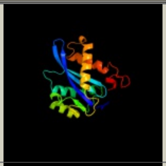
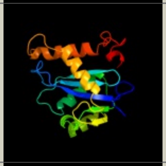
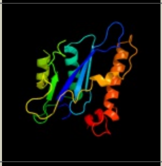
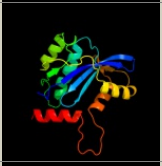
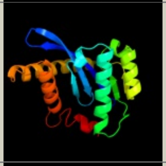
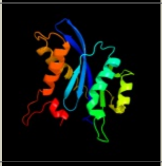
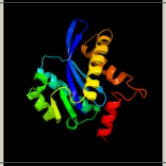
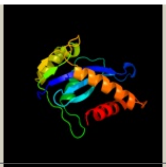
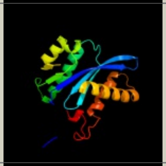
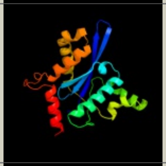
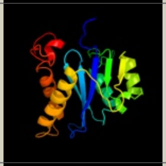
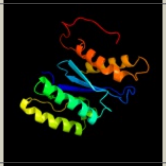
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0CF60
Date	Wed Jan 25 15:20:36 GMT 2012
Unique Job ID	ffc6c777d17e0837

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f9kV_	Alignment		99.8	18	**PDB header:**viral protein, recombination **Chain:** V: **PDB Molecule:**integrase; **PDBTitle:** two domain fragment of hiv-2 integrase in complex with ledgf ibd
2	d1c0ma2	Alignment		99.8	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
3	c1c0mA_	Alignment		99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (integrase); **PDBTitle:** crystal structure of rsv two-domain integrase
4	d1bcoa2	Alignment		99.8	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**mu transposase, core domain
5	d1asua_	Alignment		99.8	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
6	d1exqa_	Alignment		99.8	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
7	c3nf9A_	Alignment		99.7	17	**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
8	c1ex4A_	Alignment		99.7	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** hiv-1 integrase catalytic core and c-terminal domain
9	c1bcoA_	Alignment		99.7	16	**PDB header:**transposase **Chain:** A: **PDB Molecule:**bacteriophage mu transposase; **PDBTitle:** bacteriophage mu transposase core domain
10	c3kksB_	Alignment		99.7	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of catalytic core domain of biv integrase in crystal2 form ii
11	d1c6va_	Alignment		99.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain

12	d1cxqa_	Alignment		99.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
13	c1k6yB_	Alignment		99.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a two-domain fragment of hiv-1 integrase
14	d1hyva_	Alignment		99.6	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
15	c3hpgC_	Alignment		99.6	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**integrase; **PDBTitle:** visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
16	c3l2tB_	Alignment		99.6	12	**PDB header:**recombination/dna **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
17	c3dlrA_	Alignment		99.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the catalytic core domain from pfv2 integrase
18	c3hosA_	Alignment		98.7	17	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
19	c2f7tA_	Alignment		97.4	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mos1 transposase; **PDBTitle:** crystal structure of the catalytic domain of mos1 mariner2 transposase
20	c3f2kB_	Alignment		95.6	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histone-lysine n-methyltransferase setmar; **PDBTitle:** structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
21	c3mwmA_	Alignment	not modelled	44.9	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein; **PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
22	d1mzba_	Alignment	not modelled	43.2	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FUR-like
23	c2fe3B_	Alignment	not modelled	41.5	30	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**peroxide operon regulator; **PDBTitle:** the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
24	c2o03A_	Alignment	not modelled	38.0	27	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
25	c2fu4B_	Alignment	not modelled	36.5	29	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
26	c2w57A_	Alignment	not modelled	36.3	33	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
27	c2xigA_	Alignment	not modelled	34.2	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
28	c3e7lD_	Alignment	not modelled	34.0	17	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna

						binding2 domain
29	c3eyyA_	Alignment	not modelled	33.3	31	**PDB header:**transport **Chain:** A: **PDB Molecule:**putative iron uptake regulatory protein; **PDBTitle:** structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
30	c2kkmA_	Alignment	not modelled	28.5	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation machinery-associated protein 16; **PDBTitle:** solution nmr structure of yeast protein yor252w [residues2 38-178]: northeast structural genomics consortium target3 yt654
31	d2aq0a1	Alignment	not modelled	21.4	35	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
32	d1f1ea_	Alignment	not modelled	19.4	20	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Archaeal histone
33	c1htrP_	Alignment	not modelled	12.4	26	**PDB header:**aspartyl protease **Chain:** P: **PDB Molecule:**progastricsin (pro segment); **PDBTitle:** crystal and molecular structures of human progastricsin at 1.622 angstroms resolution
34	c1u78A_	Alignment	not modelled	10.8	7	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
35	c1yshE_	Alignment	not modelled	10.7	19	**PDB header:**structural protein/rna **Chain:** E: **PDB Molecule:**40s ribosomal protein s13; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
36	d1gdta1	Alignment	not modelled	8.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
37	c1s1hO_	Alignment	not modelled	8.4	31	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**40s ribosomal protein s13; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
38	c3iwfA_	Alignment	not modelled	7.6	7	**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
39	c3u5gK_	Alignment	not modelled	7.6	14	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**40s ribosomal protein s10-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
40	c3oioA_	Alignment	not modelled	7.4	47	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (arac-type dna-binding domain- **PDBTitle:** crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
41	d1pdnc_	Alignment	not modelled	6.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
42	d2gtad1	Alignment	not modelled	6.1	4	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like