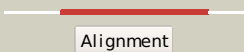

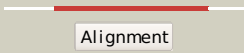



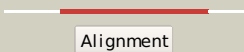

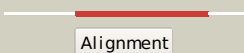

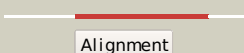

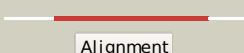

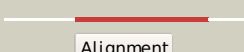

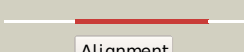

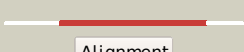

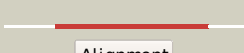






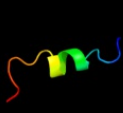
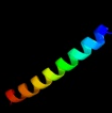
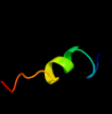


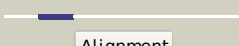
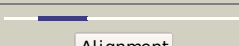


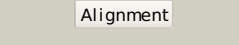
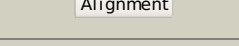
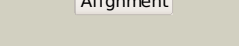
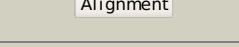
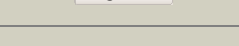
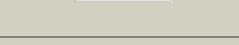
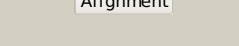
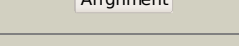
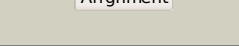
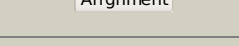
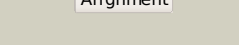
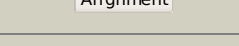




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlhyva_	 Alignment		97.0	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
2	dlcxqa_	 Alignment		96.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
3	dlexqa_	 Alignment		96.2	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
4	c1ex4A_	 Alignment		95.0	16	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
5	c1k6yB_	 Alignment		95.0	15	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
6	c3f9kV_	 Alignment		94.3	14	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
7	dlasua_	 Alignment		93.8	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
8	dlc6va_	 Alignment		93.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
9	c3nf9A_	 Alignment		91.1	16	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
10	c1c0mA_	 Alignment		90.9	18	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
11	dlc0ma2	 Alignment		90.7	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain

12	c3dlrA_	Alignment		89.3	11	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv2 integrase
13	c1bcoA_	Alignment		80.3	10	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
14	c3kksB_	Alignment		69.6	13	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal2 form ii
15	d1bcoa2	Alignment		60.2	11	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
16	c3hpgC_	Alignment		47.7	14	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
17	c2k8fB_	Alignment		42.7	26	PDB header: transferase/transcription Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: structural basis for the regulation of p53 function by p300
18	c3he5D_	Alignment		31.1	30	PDB header: de novo protein Chain: D: PDB Molecule: synzip2; PDBTitle: heterospecific coiled-coil pair synzip2:synzip1
19	c2l14B_	Alignment		17.5	26	PDB header: protein binding Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: structure of cbp nuclear coactivator binding domain in complex with2 p53 tad
20	c3l2tB_	Alignment		13.3	11	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)
21	c1q2iA_	Alignment	not modelled	13.3	21	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
22	c3dacB_	Alignment	not modelled	9.6	33	PDB header: cell cycle Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: structure of the human mdmx protein bound to the p53 tumor2 suppressor transactivation domain
23	c2qlfB_	Alignment	not modelled	9.5	11	PDB header: hydrolase Chain: B: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: crystal structure of aminopeptidase (m18 family) from thermotoga2 maritima
24	c3dacP_	Alignment	not modelled	9.4	33	PDB header: cell cycle Chain: P: PDB Molecule: cellular tumor antigen p53; PDBTitle: structure of the human mdmx protein bound to the p53 tumor2 suppressor transactivation domain
25	d1v6fa_	Alignment	not modelled	9.4	9	Fold: Gelsolin-like Superfamily: Actin depolymerizing proteins Family: Cofilin-like
26	c3a2aC_	Alignment	not modelled	9.3	69	PDB header: transport protein Chain: C: PDB Molecule: voltage-gated hydrogen channel 1; PDBTitle: the structure of the carboxyl-terminal domain of the human voltage-2 gated proton channel hv1
27	d1flga_	Alignment	not modelled	7.8	23	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
28	d1xb4a1	Alignment	not modelled	7.7	43	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain

29	d1e42a2		not modelled	7.4	5	Fold: Subdomain of clathrin and coatomer appendage domain Superfamily: Subdomain of clathrin and coatomer appendage domain Family: Clathrin adaptor appendage, alpha and beta chain-specific domain
30	c1xb4C		not modelled	7.1	43	PDB header: unknown function Chain: C: PDB Molecule: hypothetical 23.6 kda protein in yuh1-ura8 PDBTitle: crystal structure of subunit vps25 of the endosomal2 trafficking complex escrt-ii
31	c2obnA		not modelled	7.1	21	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution
32	d2bg1a1		not modelled	7.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
33	d1lyva		not modelled	6.6	22	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
34	c3t38B		not modelled	6.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum thioredoxin-dependent arsenate reductase2_cg_arsc1'
35	d1ce7b2		not modelled	6.4	31	Fold: beta-Trefoil Superfamily: Ricin B-like lectins Family: Ricin B-like
36	c2zmeD		not modelled	6.2	43	PDB header: protein transport Chain: D: PDB Molecule: vacuolar protein-sorting-associated protein 25; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
37	c1o7dE		not modelled	6.1	31	PDB header: hydrolase Chain: E: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
38	d1y7ea2		not modelled	6.1	11	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
39	c3cuqD		not modelled	6.0	43	PDB header: protein transport Chain: D: PDB Molecule: vacuolar protein-sorting-associated protein 25; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
40	c2zkrl		not modelled	5.9	16	PDB header: ribosomal protein/rna Chain: L: PDB Molecule: rna expansion segment es20; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
41	d2c5wb1		not modelled	5.7	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
42	c3aa0C		not modelled	5.6	63	PDB header: protein binding Chain: C: PDB Molecule: 21mer peptide from leucine-rich repeat-containing protein PDBTitle: crystal structure of actin capping protein in complex with the cp-2 binding motif derived from carnit
43	c2wmyH		not modelled	5.4	19	PDB header: hydrolase Chain: H: PDB Molecule: putative acid phosphatase wzb; PDBTitle: crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
44	c3lk2T		not modelled	5.2	63	PDB header: protein binding Chain: T: PDB Molecule: leucine-rich repeat-containing protein 16a; PDBTitle: crystal structure of capz bound to the uncapping motif from carnit
45	d1vqqa3		not modelled	5.2	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
46	c3pp5A		not modelled	5.1	19	PDB header: structural protein Chain: A: PDB Molecule: brk1; PDBTitle: high-resolution structure of the trimeric scar/wave complex precursor2 brk1
47	d2olua2		not modelled	5.1	24	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase