

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlcxqa_	 Alignment		96.9	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
2	dlhyva_	 Alignment		96.7	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
3	dlexqa_	 Alignment		96.5	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
4	diasua_	 Alignment		96.0	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	clex4A_	 Alignment		94.8	16	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
6	dlc6va_	 Alignment		94.2	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
7	c1k6yB_	 Alignment		94.2	14	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
8	c3f9kV_	 Alignment		93.2	12	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
9	dlc0ma2	 Alignment		93.1	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
10	c3nf9A_	 Alignment		92.6	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
11	c1c0mA_	 Alignment		89.5	16	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase

12	c3dlrA_	Alignment		88.7	12	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv2 integrase
13	c1bcoA_	Alignment		84.0	10	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
14	d1kcoa2	Alignment		69.1	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
15	c3kksB_	Alignment		66.1	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
16	c2k8fB_	Alignment		45.4	29	PDB header: transferase/transcription Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: structural basis for the regulation of p53 function by p300
17	c3he5D_	Alignment		36.2	30	PDB header: de novo protein Chain: D: PDB Molecule: synzip2; PDBTitle: heterospecific coiled-coil pair synzip2:synzip1
18	c3hpgC_	Alignment		34.1	15	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
19	c1q2iA_	Alignment		20.7	27	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
20	c3l2tB_	Alignment		18.9	8	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	d2olua2	Alignment	not modelled	18.4	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
22	c2l14B_	Alignment	not modelled	18.0	29	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
23	d1nvpd2	Alignment	not modelled	16.6	38	Fold: Transcription factor IIA (TFIIA), beta-barrel domain Superfamily: Transcription factor IIA (TFIIA), beta-barrel domain Family: Transcription factor IIA (TFIIA), beta-barrel domain
24	d1st9a_	Alignment	not modelled	16.5	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
25	c3dwbC_	Alignment	not modelled	14.4	18	PDB header: transferase Chain: C: PDB Molecule: penicillin-binding protein 2; PDBTitle: identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer PDB header: hydrolase Chain: B: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: crystal structure of aminopeptidase (m18 family) from thermotoga2 maritima
26	c2glfB_	Alignment	not modelled	13.4	11	PDB header: hydrolase Chain: B: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: crystal structure of aminopeptidase (m18 family) from thermotoga2 maritima
27	d1nh2d2	Alignment	not modelled	12.1	25	Fold: Transcription factor IIA (TFIIA), beta-barrel domain Superfamily: Transcription factor IIA (TFIIA), beta-barrel domain Family: Transcription factor IIA (TFIIA), beta-barrel domain
28	c3dacB_	Alignment	not modelled	10.8	36	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 PDB header: cell cycle

29	c3dacP_	Alignment	not modelled	10.7	36	Chain: P: PDB Molecule: cellular tumor antigen p53; PDBTitle: structure of the human mdmx protein bound to the p53 tumor2 suppressor transactivation domain
30	c2vknA_	Alignment	not modelled	10.4	4	PDB header: membrane protein Chain: A: PDB Molecule: protein ssu81; PDBTitle: yeast sho1 sh3 domain complexed with a peptide from pbs2
31	c1nvpD_	Alignment	not modelled	10.3	15	PDB header: transcription/dna Chain: D: PDB Molecule: transcription initiation factor iia gamma chain; PDBTitle: human tfiia/tbp/dna complex
32	d1qnta2	Alignment	not modelled	9.8	20	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
33	d1e42a2	Alignment	not modelled	9.7	6	Fold: Subdomain of clathrin and coatamer appendage domain Superfamily: Subdomain of clathrin and coatamer appendage domain Family: Clathrin adaptor appendage, alpha and beta chain-specific domain
34	c3a2aC_	Alignment	not modelled	9.5	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
35	c3bpjD_	Alignment	not modelled	7.6	9	PDB header: translation Chain: D: PDB Molecule: eukaryotic translation initiation factor 3 subunit j; PDBTitle: crystal structure of human translation initiation factor 3, subunit 12 alpha
36	c3pp5A_	Alignment	not modelled	7.0	19	PDB header: structural protein Chain: A: PDB Molecule: brk1; PDBTitle: high-resolution structure of the trimeric scar/wave complex precursor2 brk1
37	c2juia_	Alignment	not modelled	7.0	33	PDB header: toxin Chain: A: PDB Molecule: plne; PDBTitle: three-dimensional structure of the two peptides that2 constitute the two-peptide bacteriocin plantaracin ef
38	c3pf6C_	Alignment	not modelled	6.8	29	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein pp-luz7_gp033; PDBTitle: the structure of uncharacterized protein pp-luz7_gp033 from2 pseudomonas phage luz7.
39	d1y7ea2	Alignment	not modelled	6.6	11	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
40	d1v6fa_	Alignment	not modelled	6.4	9	Fold: Gelsolin-like Superfamily: Actin depolymerizing proteins Family: Cofilin-like
41	d1nc7a_	Alignment	not modelled	6.4	24	Fold: Hypothetical protein TM1070 Superfamily: Hypothetical protein TM1070 Family: Hypothetical protein TM1070
42	d1tlea2	Alignment	not modelled	6.1	20	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Subtilase propeptides/inhibitors
43	d2bg1a1	Alignment	not modelled	6.1	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
44	c3p8cE_	Alignment	not modelled	5.9	19	PDB header: protein binding Chain: E: PDB Molecule: probable protein brick1; PDBTitle: structure and control of the actin regulatory wave complex
45	c2gljR_	Alignment	not modelled	5.7	11	PDB header: hydrolase Chain: R: PDB Molecule: PDBTitle: crystal structure of aminopeptidase i from clostridium2 acetobutylicum
46	d1ce7b2	Alignment	not modelled	5.5	31	Fold: beta-Trefoil Superfamily: Ricin B-like lectins Family: Ricin B-like
47	d2je8a2	Alignment	not modelled	5.4	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain