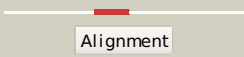

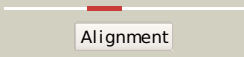

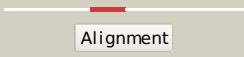

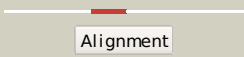



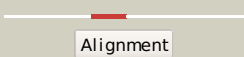

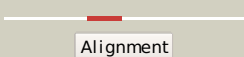



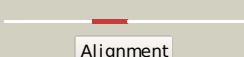

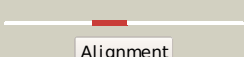

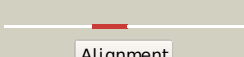










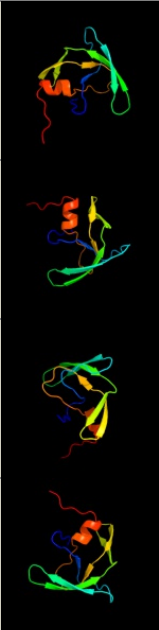
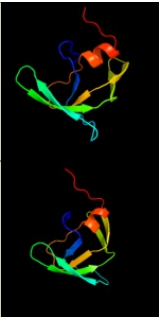


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1c0mA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
2	c3f9kV_	 Alignment		100.0	11	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
3	dlasua_	 Alignment		100.0	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
4	dlc0ma2	 Alignment		100.0	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	c1k6yB_	 Alignment		100.0	15	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
6	c3l2tB_	 Alignment		100.0	21	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)
7	c3hpgC_	 Alignment		100.0	16	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
8	c1ex4A_	 Alignment		99.9	14	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
9	c3dlrA_	 Alignment		99.9	21	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv2 integrase
10	c3nf9A_	 Alignment		99.9	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
11	c3kksB_	 Alignment		99.9	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

12	dlcxqa_	Alignment		99.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
13	dlcxqa_	Alignment		99.9	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
14	dlhyva_	Alignment		99.9	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
15	dlc6va_	Alignment		99.8	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
16	clrthA_	Alignment		99.7	16	PDB header: nucleotidyltransferase Chain: A: PDB Molecule: hiv-1 reverse transcriptase; PDBTitle: high resolution structures of hiv-1 rt from four rt-2 inhibitor complexes
17	clmu2A_	Alignment		99.5	19	PDB header: transferase Chain: A: PDB Molecule: hiv-2 rt; PDBTitle: crystal structure of hiv-2 reverse transcriptase
18	d2zd1b1	Alignment		99.3	16	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
19	c2opqA_	Alignment		99.2	19	PDB header: transferase Chain: A: PDB Molecule: reverse transcriptase/ribonuclease h; PDBTitle: crystal structure of l100i mutant hiv-1 reverse2 transcriptase in complex with gw420867x.
20	c3kk1B_	Alignment		99.2	16	PDB header: transferase/dna Chain: B: PDB Molecule: reverse transcriptase p51 subunit; PDBTitle: hiv-1 reverse transcriptase-dna complex with nucleotide inhibitor gs-2 9148-diphosphate bound in nucleotide site
21	dlmu2a2	Alignment	not modelled	99.1	17	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
22	dlbcoa2	Alignment	not modelled	99.0	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
23	clbcoA_	Alignment	not modelled	98.7	14	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
24	dlztwa1	Alignment	not modelled	98.6	13	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
25	dlhara_	Alignment	not modelled	98.2	17	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
26	c2ehgA_	Alignment	not modelled	98.0	17	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hi; PDBTitle: crystal structure of hyperthermophilic archaeal rnase hi
27	c3hstD_	Alignment	not modelled	97.9	13	PDB header: hydrolase Chain: D: PDB Molecule: protein rv2228c/mt2287; PDBTitle: n-terminal rnase h domain of rv2228c from mycobacterium tuberculosis2 as a fusion protein with maltose binding protein
28	dljl2a_	Alignment	not modelled	97.9	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
						Fold: DNA/RNA polymerases

29	d1rw3a_	Alignment	not modelled	97.8	14	Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
30	c2qkkl_	Alignment	not modelled	97.7	15	PDB header: hydrolase/dna/rna Chain: I: PDB Molecule: ribonuclease h1; PDBTitle: human rnase h catalytic domain mutant d210n in complex with2 14-mer rna/dna hybrid
31	c2kq2A_	Alignment	not modelled	97.5	19	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h-related protein; PDBTitle: solution nmr structure of the apo form of a ribonuclease h2 domain of protein dsy1790 from desulfitobacterium3 hafniense, northeast structural genomics target dhr1a
32	d1jl1aa1	Alignment	not modelled	97.5	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
33	c2hb5A_	Alignment	not modelled	97.4	15	PDB header: hydrolase Chain: A: PDB Molecule: reverse transcriptase/ribonuclease h; PDBTitle: crystal structure of the moloney murine leukemia virus2 rnase h domain
34	d1s9ga1	Alignment	not modelled	97.4	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
35	c3u3gA_	Alignment	not modelled	97.4	16	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h; PDBTitle: structure of lc11-rnase h1 isolated from compost by metagenomic2 approach: insight into the structural bases for unusual enzymatic3 properties of sto-rnase h1
36	c2e41A_	Alignment	not modelled	97.4	18	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hi; PDBTitle: thermodynamic and structural analysis of thermolabile rnase hi from2 shewanella oneidensis mr-1
37	d1rila_	Alignment	not modelled	97.4	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
38	d1s1ta1	Alignment	not modelled	97.4	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
39	d1wsib_	Alignment	not modelled	97.3	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
40	c3h08B_	Alignment	not modelled	97.3	17	PDB header: hydrolase Chain: B: PDB Molecule: rnh (ribonuclease h); PDBTitle: crystal structure of the ribonuclease h1 from chlorobium2 tepidum
41	c3hosA_	Alignment	not modelled	97.2	7	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
42	d1jl1a_	Alignment	not modelled	97.2	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
43	d1mu2a1	Alignment	not modelled	97.2	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
44	d1eeta1	Alignment	not modelled	97.0	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
45	d1ol1wa_	Alignment	not modelled	97.0	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
46	d1nh0a_	Alignment		95.7	14	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
47	d1bdqa_	Alignment		95.2	14	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
48	d1c6ya_	Alignment		94.6	12	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
49	d1siva_	Alignment		94.6	14	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)

50	d3ecga1	Alignment		94.1	16	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
51	d2nmza1	Alignment		94.1	16	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
52	d1kzka_	Alignment	not modelled	93.9	14	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
53	d1sgua_	Alignment	not modelled	93.7	12	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
54	d1rpia_	Alignment	not modelled	93.7	10	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
55	d1zbfal	Alignment	not modelled	93.1	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
56	d1hvca_	Alignment	not modelled	92.7	19	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
57	c3nr6A_	Alignment	not modelled	91.8	19	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: protease p14; PDBTitle: crystal structure of xenotropic murine leukemia virus-related virus2 (xmrv) protease
58	c2rpiA_	Alignment	not modelled	88.3	24	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h; PDBTitle: the nmr structure of the submillisecond folding2 intermediate of the thermus thermophilus ribonuclease h
59	d1az5a_	Alignment	not modelled	86.1	16	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
60	d2fmba_	Alignment	not modelled	86.0	12	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
61	d1nsoa_	Alignment	not modelled	84.2	20	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
62	d4fiva_	Alignment	not modelled	76.2	18	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
63	c3f2kB_	Alignment	not modelled	75.7	5	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
64	c3s8iA_	Alignment	not modelled	75.7	19	PDB header: hydrolase Chain: A: PDB Molecule: protein ddi1 homolog 1; PDBTitle: the retroviral-like protease (rvp) domain of human ddi1
65	d1sqha_	Alignment	not modelled	50.8	7	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Hypothetical protein cg14615-pa
66	c2i1aC_	Alignment	not modelled	48.7	17	PDB header: protein turnover Chain: C: PDB Molecule: dna damage-inducible protein ddi1; PDBTitle: a retroviral protease-like domain in the eukaryotic protein2 ddi1
67	c3lhrA_	Alignment	not modelled	41.3	12	PDB header: transcription regulator Chain: A: PDB Molecule: zinc finger protein 24; PDBTitle: crystal structure of the scan domain from human znf24
68	d1dq3a2	Alignment	not modelled	39.5	8	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: PI-Pfui intein middle domain
69	c2zf8A_	Alignment	not modelled	26.4	18	PDB header: structural protein Chain: A: PDB Molecule: component of sodium-driven polar flagellar motor; PDBTitle: crystal structure of moty
70	c2csdB_	Alignment	not modelled	25.6	3	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
71	d2fi2a1	Alignment	not modelled	23.5	10	Fold: Acyl carrier protein-like Superfamily: Retrovirus capsid dimerization domain-like Family: SCAN domain
72	d2d81a1	Alignment	not modelled	23.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PHB depolymerase-like
73	c3dcgF_	Alignment	not modelled	21.2	22	PDB header: ligase/viral protein Chain: F: PDB Molecule: virion infectivity factor; PDBTitle: crystal structure of the hiv vif bc-box in complex with human elonginb2 and elonginc
74	d1sska_	Alignment	not modelled	21.2	25	Fold: Coronavirus RNA-binding domain Superfamily: Coronavirus RNA-binding domain Family: Coronavirus RNA-binding domain

75	c2de0X_	Alignment	not modelled	20.8	15	PDB header: transferase Chain: X: PDB Molecule: alpha-(1,6)-fucosyltransferase; PDBTitle: crystal structure of human alpha 1,6-fucosyltransferase, fut8
76	c2b9kA_	Alignment	not modelled	19.8	14	PDB header: antibiotic Chain: A: PDB Molecule: antimicrobial peptide Ici; PDBTitle: solution structure of Ici, an amp from bacillus subtilis
77	d2pt0a1	Alignment	not modelled	19.8	14	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Myo-inositol hexaphosphate phosphohydrolase (phytase) Phya
78	c2leza_	Alignment	not modelled	19.3	12	PDB header: signaling protein Chain: A: PDB Molecule: secreted effector protein pipb2; PDBTitle: solution nmr structure of n-terminal domain of salmonella effector2 protein pipb2. northeast structural genomics consortium (nesg) target3 stt318a
79	c2f7tA_	Alignment	not modelled	18.4	8	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
80	c2jeuA_	Alignment	not modelled	18.3	26	PDB header: transcription Chain: A: PDB Molecule: regulatory protein e2; PDBTitle: transcription activator structure reveals redox control of2 a replication initiation reaction
81	c1tueG_	Alignment	not modelled	17.5	16	PDB header: replication Chain: G: PDB Molecule: regulatory protein e2; PDBTitle: the x-ray structure of the papillomavirus helicase in2 complex with its molecular matchmaker e2
82	c2yc2D_	Alignment	not modelled	17.4	10	PDB header: transport protein Chain: D: PDB Molecule: small rab-related gtpase; PDBTitle: intraflagellar transport complex 25-27 from chlamydomonas
83	c2l26A_	Alignment	not modelled	17.0	9	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein rv0899/mt0922; PDBTitle: rv0899 from mycobacterium tuberculosis contains two separated domains
84	d1ecfa1	Alignment	not modelled	16.8	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
85	d1xr7a_	Alignment	not modelled	16.5	26	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
86	d1wwia1	Alignment	not modelled	15.0	9	Fold: Histone-fold Superfamily: Histone-fold Family: Bacterial histone-fold protein
87	d1qqha_	Alignment	not modelled	15.0	18	Fold: E2 regulatory, transactivation domain Superfamily: E2 regulatory, transactivation domain Family: E2 regulatory, transactivation domain
88	d1raja_	Alignment	not modelled	14.9	14	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
89	c4e6sA_	Alignment	not modelled	14.4	10	PDB header: transcription Chain: A: PDB Molecule: zinc finger and scan domain-containing protein 10; PDBTitle: crystal structure of the scan domain from mouse zfp206
90	d1gph11	Alignment	not modelled	14.3	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
91	d1w79a1	Alignment	not modelled	13.8	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
92	d1xr6a_	Alignment	not modelled	13.6	28	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
93	c2kgwA_	Alignment	not modelled	13.4	9	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein a; PDBTitle: solution structure of the carboxy-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
94	d1vqoe2	Alignment	not modelled	13.4	7	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
95	d1baia_	Alignment	not modelled	13.3	18	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
96	c4acoA_	Alignment	not modelled	13.3	23	PDB header: dna binding protein Chain: A: PDB Molecule: centromere dna-binding protein complex cbf3 subunit a; PDBTitle: structure of the budding yeast ndc10 n-terminal domain
97	c3du6A_	Alignment	not modelled	13.3	23	PDB header: transferase Chain: A: PDB Molecule: telomerase reverse transcriptase; PDBTitle: structure of the catalytic subunit of telomerase, tert
98	c3n6mA_	Alignment	not modelled	13.2	13	PDB header: transferase Chain: A: PDB Molecule: rna-dependent rna polymerase; PDBTitle: crystal structure of ev71 rdpr in complex with gtp
99	c1uv7A_	Alignment	not modelled	13.1	26	PDB header: transport Chain: A: PDB Molecule: general secretion pathway protein m; PDBTitle: periplasmic domain of epsm from vibrio cholerae