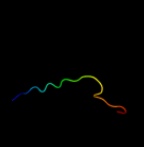


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f9kV_	 Alignment		100.0	13	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
2	c1k6yB_	 Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
3	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
4	c1c0mA_	 Alignment		100.0	11	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
5	c3l2tB_	 Alignment		100.0	17	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)
6	d1c0ma2	 Alignment		100.0	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
7	d1asua_	 Alignment		100.0	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
8	c3dlrA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv2 integrase
9	c1ex4A_	 Alignment		99.9	9	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
10	c3kksB_	 Alignment		99.9	9	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	d1cxqa_	 Alignment		99.9	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain

12	dlhyva_	Alignment		99.9	8	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
13	c3nf9A_	Alignment		99.9	10	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
14	dlxqqa_	Alignment		99.9	8	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
15	dlc6va_	Alignment		99.9	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
16	dlbcoa2	Alignment		98.7	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
17	clbcoA_	Alignment		98.6	13	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
18	c3nngA_	Alignment		97.8	15	PDB header: viral protein Chain: A: PDB Molecule: n-terminal domain of moloney murine leukemia virus PDBTitle: crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3
19	c3hosA_	Alignment		86.9	6	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
20	clvdza_	Alignment		26.7	33	PDB header: hydrolase Chain: A: PDB Molecule: a-type atpase subunit a; PDBTitle: crystal structure of a-type atpase catalytic subunit a from2 pyrococcus horikoshii ot3
21	dle0ea_	Alignment	not modelled	16.7	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
22	dlgvha3	Alignment	not modelled	14.1	38	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavoheemoglobin, C-terminal domain
23	dlk6ya1	Alignment	not modelled	13.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
24	d2b5dx1	Alignment	not modelled	13.1	24	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: AmyC C-terminal domain-like
25	dlwjfa_	Alignment	not modelled	12.6	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
26	dlufaa1	Alignment	not modelled	10.8	33	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: AmyC C-terminal domain-like
27	dlfx0b3	Alignment	not modelled	10.8	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
28	clcl4A_	Alignment	not modelled	10.7	20	PDB header: viral protein Chain: A: PDB Molecule: protein (gag polyprotein); PDBTitle: nucleocapsid protein from mason-pfizer monkey virus (mpmv)
						Fold: Retrovirus zinc finger-like domains

29	d1dsva_	Alignment	not modelled	9.2	27	Superfamily: Retrovirus zinc finger-like domains Family: Retrovirus zinc finger-like domains
30	c2p4eP_	Alignment	not modelled	9.0	17	PDB header: hydrolase Chain: P: PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: crystal structure of pcsk9
31	c2w2mP_	Alignment	not modelled	9.0	17	PDB header: hydrolase/receptor Chain: P: PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: wt pcsk9-deltac bound to wt egf-a of ldlr
32	c2pmwA_	Alignment	not modelled	9.0	17	PDB header: hydrolase Chain: A: PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: the crystal structure of proprotein convertase subtilisin2 kexin type 9 (pcsk9)
33	d1skyb3	Alignment	not modelled	8.6	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
34	c2c61A_	Alignment	not modelled	8.5	18	PDB header: hydrolase Chain: A: PDB Molecule: a-type atp synthase non-catalytic subunit b; PDBTitle: crystal structure of the non-catalytic b subunit of a-type2 atpase from m. maei go1
35	c3l0oB_	Alignment	not modelled	7.9	12	PDB header: hydrolase Chain: B: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
36	d2dlqa3	Alignment	not modelled	7.8	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
37	d1skye3	Alignment	not modelled	7.8	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
38	d1fx0a3	Alignment	not modelled	7.7	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
39	d1iwpA_	Alignment	not modelled	7.7	11	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Diol dehydratase, alpha subunit
40	d2jdia3	Alignment	not modelled	7.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
41	c1kmhA_	Alignment	not modelled	7.6	18	PDB header: hydrolase Chain: A: PDB Molecule: atpase alpha subunit; PDBTitle: crystal structure of spinach chloroplast f1-atpase2 complexed with tentoxin
42	c2eqoA_	Alignment	not modelled	7.5	21	PDB header: transcription Chain: A: PDB Molecule: tnf receptor-associated factor 3-interacting PDBTitle: solution structure of the stn_traf3ip1_nd domain of2 interleukin 13 receptor alpha 1-binding protein-1 [homo3 sapiens]
43	c2dhyA_	Alignment	not modelled	7.3	20	PDB header: immune system Chain: A: PDB Molecule: cue domain-containing protein 1; PDBTitle: solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
44	c1hsjA_	Alignment	not modelled	7.1	12	PDB header: transcription/sugar binding protein Chain: A: PDB Molecule: fusion protein consisting of staphylococcus PDBTitle: sarr mbp fusion structure
45	c2qe7C_	Alignment	not modelled	7.1	18	PDB header: hydrolase Chain: C: PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
46	d1xpua3	Alignment	not modelled	7.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
47	c30aaC_	Alignment	not modelled	7.0	18	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: atp synthase subunit alpha; PDBTitle: structure of the e.coli f1-atp synthase inhibited by subunit epsilon
48	c2oblA_	Alignment	not modelled	6.9	29	PDB header: hydrolase Chain: A: PDB Molecule: escn; PDBTitle: structural and biochemical analysis of a prototypical atpase from the2 type iii secretion system of pathogenic bacteria
49	d2jdid3	Alignment	not modelled	6.9	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
50	d1a6ca2	Alignment	not modelled	6.8	20	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
51	d1d5ya1	Alignment	not modelled	6.7	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
52	d1dq3a2	Alignment	not modelled	6.7	8	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: PI-Pfui intein middle domain
53	c2r9vA_	Alignment	not modelled	6.6	18	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution
54	c2w6fA_	Alignment	not modelled	6.5	18	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase subunit alpha heart isoform, PDBTitle: low resolution structures of bovine mitochondrial f1-

					atpase2 during controlled dehydration: hydration state 2.
55	c2yiuE_	Alignment	not modelled	6.5	18 PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome c1, heme protein; PDBTitle: x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
56	c3a5dM_	Alignment	not modelled	6.5	14 PDB header: hydrolase Chain: M: PDB Molecule: v-type atp synthase beta chain; PDBTitle: inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
57	c1gvhA_	Alignment	not modelled	6.4	38 PDB header: oxidoreductase Chain: A: PDB Molecule: flavoheomprotein; PDBTitle: the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unsuspected geometry of the3 distal heme pocket
58	c2kxsA_	Alignment	not modelled	6.2	19 PDB header: protein binding Chain: A: PDB Molecule: tight junction protein zo-1, linker, peptide of myocardium- PDBTitle: zo1 zu5 domain in complex with grinl1a peptide
59	c2jizD_	Alignment	not modelled	5.9	36 PDB header: hydrolase Chain: D: PDB Molecule: atp synthase subunit beta; PDBTitle: the structure of f1-atpase inhibited by resveratrol.
60	c2dpyA_	Alignment	not modelled	5.9	29 PDB header: hydrolase Chain: A: PDB Molecule: flagellum-specific atp synthase; PDBTitle: crystal structure of the flagellar type iii atpase flii
61	c2w6jD_	Alignment	not modelled	5.8	36 PDB header: hydrolase Chain: D: PDB Molecule: atp synthase subunit beta, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
62	c1w0jB_	Alignment	not modelled	5.8	21 PDB header: hydrolase Chain: B: PDB Molecule: atp synthase alpha chain heart isoform, PDBTitle: beryllium fluoride inhibited bovine f1-atpase
63	c1fx0B_	Alignment	not modelled	5.7	36 PDB header: hydrolase Chain: B: PDB Molecule: atp synthase beta chain; PDBTitle: crystal structure of the chloroplast f1-atpase from spinach
64	dlvk9a_	Alignment	not modelled	5.7	13 Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Hypothetical protein TM1506
65	dlgxha_	Alignment	not modelled	5.7	19 Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
66	c1ee8A_	Alignment	not modelled	5.6	38 PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
67	dlayia_	Alignment	not modelled	5.5	14 Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
68	clskyE_	Alignment	not modelled	5.4	29 PDB header: atp synthase Chain: E: PDB Molecule: f1-atpase; PDBTitle: crystal structure of the nucleotide free alpha3beta3 sub-complex of2 f1-atpase from the thermophilic bacillus ps3
69	dlxgsa1	Alignment	not modelled	5.4	13 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Methionine aminopeptidase, insert domain
70	c2no8A_	Alignment	not modelled	5.3	14 PDB header: immune system Chain: A: PDB Molecule: colicin-e2 immunity protein; PDBTitle: nmr structure analysis of the colicin immunity protein im2
71	c3a5dB_	Alignment	not modelled	5.3	29 PDB header: hydrolase Chain: B: PDB Molecule: v-type atp synthase alpha chain; PDBTitle: inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase