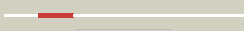
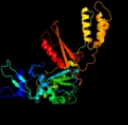


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1c0mA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
2	d1asua_	 Alignment		100.0	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
3	c3f9kV_	 Alignment		100.0	10	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
4	d1c0ma2	 Alignment		100.0	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	c3l2tB_	 Alignment		100.0	20	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	c1ex4A_	 Alignment		100.0	14	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
7	c1k6yB_	 Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
8	c3hpgC_	 Alignment		99.9	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
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	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
11	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

12	dlcxqa_	Alignment		99.9	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
13	dlexqa_	Alignment		99.9	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
14	dlhyva_	Alignment		99.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
15	dlc6va_	Alignment		99.9	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
16	clrthA_	Alignment		99.5	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	21	PDB header: transferase Chain: A: PDB Molecule: hiv-2 rt; PDBTitle: crystal structure of hiv-2 reverse transcriptase
18	d2zd1b1	Alignment		99.3	14	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
19	c3kk1B_	Alignment		99.3	15	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
20	dlmu2a2	Alignment		99.2	17	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
21	dlbcoa2	Alignment	not modelled	99.1	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
22	clbcoA_	Alignment	not modelled	98.9	15	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
23	c2opqA_	Alignment	not modelled	98.8	14	PDB header: transferase Chain: A: PDB Molecule: reverse transcriptase/ribonuclease h; PDBTitle: crystal structure of I100i mutant hiv-1 reverse2 transcriptase in complex with gw420867x.
24	dlzta1	Alignment	not modelled	98.6	12	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
25	dlhara_	Alignment	not modelled	98.2	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
26	c2ehgA_	Alignment	not modelled	98.1	15	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hi; PDBTitle: crystal structure of hyperthermophilic archaeal rnase hi
27	c3hstD_	Alignment	not modelled	98.1	11	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	97.9	14	Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
30	c2qkkl_	Alignment	not modelled	97.8	15	PDB header: hydrolase/dna/rna Chain: I: PDB Molecule: ribonuclease h1; PDBTitle: human rnae h catalytic domain mutant d210n in complex with2 14-mer rna/dna hybrid
31	c2kq2A_	Alignment	not modelled	97.7	18	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 desulfotobacterium3 hafniense, northeast structural genomics target dhr1a
32	d1s9ga1	Alignment	not modelled	97.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
33	c3u3gA_	Alignment	not modelled	97.6	18	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h; PDBTitle: structure of lc11-rnae h1 isolated from compost by metagenomic2 approach: insight into the structural bases for unusual enzymatic3 properties of sto-rnae h1
34	c2hb5A_	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: A: PDB Molecule: reverse transcriptase/ribonuclease h; PDBTitle: crystal structure of the moloney murine leukemia virus2 rnae h domain
35	d1wsib_	Alignment	not modelled	97.5	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
36	d1jlal1	Alignment	not modelled	97.5	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
37	d1s1ta1	Alignment	not modelled	97.5	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
38	c2e4lA_	Alignment	not modelled	97.5	21	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hi; PDBTitle: thermodynamic and structural analysis of thermolabile rnae hi from2 shewanella oneidensis mr-1
39	d1jl1a_	Alignment	not modelled	97.5	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
40	c3h08B_	Alignment	not modelled	97.4	16	PDB header: hydrolase Chain: B: PDB Molecule: rnh (ribonuclease h); PDBTitle: crystal structure of the ribonuclease h1 from chlorobium2 tepidum
41	d1rl1a_	Alignment	not modelled	97.3	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
42	d1mu2a1	Alignment	not modelled	97.3	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
43	d1ol1wa_	Alignment	not modelled	97.2	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
44	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
45	d1eeta1	Alignment	not modelled	97.2	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
46	d1zbfa1	Alignment	not modelled	94.7	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
47	c2rpiA_	Alignment	not modelled	90.1	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
48	c3f2kB_	Alignment	not modelled	80.0	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
49	d1sqha_	Alignment	not modelled	70.7	8	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Hypothetical protein cg14615-pa
50	c3du6A_	Alignment	not modelled	60.0	19	PDB header: transferase Chain: A: PDB Molecule: telomerase reverse transcriptase; PDBTitle: structure of the catalytic subunit of telomerase, tert
51	d2d81a1	Alignment	not modelled	48.3	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PHB depolymerase-like
52	c2zf8A_	Alignment	not modelled	46.2	21	PDB header: structural protein Chain: A: PDB Molecule: component of sodium-driven polar flagellar motor; PDBTitle: crystal structure of moty
53	c2jtmA_	Alignment	not modelled	27.9	24	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of sso6901 from sulfobolus solfataricus2 p2
54	d2hqsc1	Alignment	not modelled	27.8	12	Fold: Bacillus chorismate mutase-like Superfamily: OmpA-like Family: OmpA-like
						Fold: (Phosphotyrosine protein) phosphatases II

55	d2pt0a1	Alignment	not modelled	27.7	16	Superfamily: (Phosphotyrosine protein) phosphatases II Family: Myo-inositol hexaphosphate phosphohydrolase (phytase) Phya
56	c1u24A	Alignment	not modelled	23.2	16	PDB header: hydrolase Chain: A: PDB Molecule: myo-inositol hexaphosphate phosphohydrolase; PDBTitle: crystal structure of selenomonas ruminantium phytase
57	c2k1sA	Alignment	not modelled	21.9	7	PDB header: lipoprotein Chain: A: PDB Molecule: inner membrane lipoprotein yiad; PDBTitle: solution nmr structure of the folded c-terminal fragment of yiad from2 escherichia coli. northeast structural genomics consortium target3 er553.
58	d2aizp1	Alignment	not modelled	20.9	7	Fold: Bacillus chorismate mutase-like Superfamily: OmpA-like Family: OmpA-like
59	c3nngA	Alignment	not modelled	20.1	22	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
60	c2b9kA	Alignment	not modelled	19.8	26	PDB header: antibiotic Chain: A: PDB Molecule: antimicrobial peptide lci; PDBTitle: solution structure of lci, an amp from bacillus subtilis
61	c3g3sA	Alignment	not modelled	18.6	14	PDB header: transferase Chain: A: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: crystal structure of gcn5-related n-acetyltransferase-like protein2 (zp_00874857) (zp_00874857.1) from streptococcus suis 89/1591 at 1.803 a resolution
62	c3dcgF	Alignment	not modelled	18.4	25	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
63	c2kgwA	Alignment	not modelled	18.2	10	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein a; PDBTitle: solution structure of the carboxy-terminal domain of ompab, a pore2 forming protein from mycobacterium tuberculosis
64	c2l26A	Alignment	not modelled	17.9	9	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein rv0899/mt0922; PDBTitle: rv0899 from mycobacterium tuberculosis contains two separated domains
65	d1wwia1	Alignment	not modelled	17.8	9	Fold: Histone-fold Superfamily: Histone-fold Family: Bacterial histone-fold protein
66	c2pdoG	Alignment	not modelled	17.6	15	PDB header: transferase Chain: G: PDB Molecule: acetyltransferase ypea; PDBTitle: crystal structure of the putative acetyltransferase of gnat family2 from shigella flexneri
67	c3cjeA	Alignment	not modelled	17.2	3	PDB header: oxidoreductase Chain: A: PDB Molecule: osmc-like protein; PDBTitle: crystal structure of an osmc-like hydroperoxide resistance protein2 (jann_2040) from jannaschia sp. ccs1 at 1.70 a resolution
68	d1fgja	Alignment	not modelled	17.1	16	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
69	c1fgjA	Alignment	not modelled	17.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxylamine oxidoreductase; PDBTitle: x-ray structure of hydroxylamine oxidoreductase
70	c2f7tA	Alignment	not modelled	17.0	8	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
71	c2cntD	Alignment	not modelled	16.7	9	PDB header: transferase Chain: D: PDB Molecule: modification of 30s ribosomal subunit protein s18; PDBTitle: rimi - ribosomal s18 n-alpha-protein acetyltransferase in2 complex with coenzymeA.
72	d1ecfa1	Alignment	not modelled	16.3	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
73	c2yc2D	Alignment	not modelled	16.1	10	PDB header: transport protein Chain: D: PDB Molecule: small rab-related gtpase; PDBTitle: intraflagellar transport complex 25-27 from chlamydomonas
74	c2qiyC	Alignment	not modelled	15.9	50	PDB header: signaling protein/hydrolase Chain: C: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 3; PDBTitle: yeast deubiquitinase ubp3 and bre5 cofactor complex
75	c2jeuA	Alignment	not modelled	15.3	23	PDB header: transcription Chain: A: PDB Molecule: regulatory protein e2; PDBTitle: transcription activator structure reveals redox control of2 a replication initiation reaction
76	c3e0dA	Alignment	not modelled	14.9	22	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: insights into the replisome from the crystal structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
77	d1z3aa1	Alignment	not modelled	14.2	25	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
78	c3c5iD	Alignment	not modelled	14.1	13	PDB header: transferase Chain: D: PDB Molecule: choline kinase; PDBTitle: crystal structure of plasmodium knowlesi choline kinase, pkh_134520
79	c1trlB	Alignment	not modelled	14.0	22	PDB header: hydrolase (metalloprotease) Chain: B: PDB Molecule: thermolysin fragment 255 - 316; PDBTitle: nmr solution structure of the c-terminal fragment 255-

					3162 of thermolysin: a dimer formed by subunits having the3 native structure
80	c1tueG_	Alignment	not modelled	13.7	18 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
81	c1jr2A_	Alignment	not modelled	13.6	24 PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: structure of uroporphyrinogen iii synthase
82	d1jr2a_	Alignment	not modelled	13.6	24 Fold: HemD-like Superfamily: HemD-like Family: HemD-like
83	d1u09a_	Alignment	not modelled	13.5	11 Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
84	d1raja_	Alignment	not modelled	13.2	13 Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
85	c2dbqA_	Alignment	not modelled	13.0	10 PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
86	d1w79a1	Alignment	not modelled	12.9	16 Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
87	d1gph11	Alignment	not modelled	12.8	17 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
88	d1qqha_	Alignment	not modelled	12.8	18 Fold: E2 regulatory, transactivation domain Superfamily: E2 regulatory, transactivation domain Family: E2 regulatory, transactivation domain
89	c3f2rA_	Alignment	not modelled	12.7	14 PDB header: transferase Chain: A: PDB Molecule: choline kinase alpha; PDBTitle: crystal structure of human choline kinase alpha in complex2 with hemicholinium-3
90	c3td4D_	Alignment	not modelled	12.0	11 PDB header: membrane protein,peptide binding protein Chain: D: PDB Molecule: outer membrane protein omp38; PDBTitle: crystal structure of ompa-like domain from acinetobacter baumannii in2 complex with diaminopimelate
91	c2yt5A_	Alignment	not modelled	11.7	18 PDB header: transcription Chain: A: PDB Molecule: metal-response element-binding transcription PDBTitle: solution structure of the phd domain of metal-response2 element-binding transcription factor 2
92	c1lqlE_	Alignment	not modelled	11.5	3 PDB header: unknown function Chain: E: PDB Molecule: osmotical inducible protein c like family; PDBTitle: crystal structure of osmc like protein from mycoplasma2 pneumoniae
93	d1lqla_	Alignment	not modelled	11.5	3 Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
94	c21ezA_	Alignment	not modelled	11.3	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
95	d1ufra_	Alignment	not modelled	11.1	19 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
96	c1qqgA_	Alignment	not modelled	11.0	24 PDB header: signal transduction Chain: A: PDB Molecule: insulin receptor substrate 1; PDBTitle: crystal structure of the ph-ptb targeting region of irs-1
97	c2px2B_	Alignment	not modelled	10.7	21 PDB header: transferase Chain: B: PDB Molecule: genome polyprotein [contains: capsid protein c PDBTitle: crystal structure of the murray valley encephalitis virus2 ns5 2'-o methyltransferase domain in complex with sah3 (monoclinic form 1)
98	d2ffja1	Alignment	not modelled	10.7	15 Fold: AF1104-like Superfamily: AF1104-like Family: AF1104-like
99	d1ckqa_	Alignment	not modelled	10.6	22 Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease EcoRI