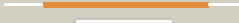
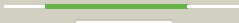
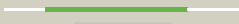
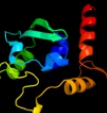
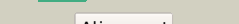
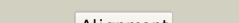
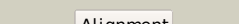
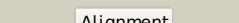
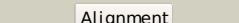
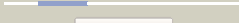


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nkhB_	 Alignment		100.0	25	PDB header: recombination Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of integrase from mrsa strain staphylococcus aureus
2	d1a0pa2	 Alignment		100.0	20	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
3	d1aiha_	 Alignment		99.9	18	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
4	d1f44a2	 Alignment		99.9	13	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
5	d1ae9a_	 Alignment		99.9	14	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
6	c1z1bA_	 Alignment		99.9	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of a lambda integrase dimer bound to a2 coc' core site
7	c1a0pA_	 Alignment		99.9	19	PDB header: dna recombination Chain: A: PDB Molecule: site-specific recombinase xerd; PDBTitle: site-specific recombinase, xerd
8	d1p7da_	 Alignment		99.9	13	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
9	c1ma7A_	 Alignment		99.8	15	PDB header: hydrolase, ligase/dna Chain: A: PDB Molecule: cre recombinase; PDBTitle: crystal structure of cre site-specific recombinase2 complexed with a mutant dna substrate, loxp-a8/t27
10	c1crxA_	 Alignment		99.8	12	PDB header: replication/dna Chain: A: PDB Molecule: cre recombinase; PDBTitle: cre recombinase/dna complex reaction intermediate i
11	d5crxb2	 Alignment		99.8	15	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core

12	c2a3vA	 Alignment		99.8	28	PDB header: recombination Chain: A: PDB Molecule: site-specific recombinase inti4; PDBTitle: structural basis for broad dna-specificity in integron2 recombination
13	c2v6eB	 Alignment		97.6	13	PDB header: hydrolase Chain: B: PDB Molecule: protelemorase; PDBTitle: protelomerase telk complexed with substrate dna
14	c2f4gA	 Alignment		95.0	15	PDB header: isomerase Chain: A: PDB Molecule: type i topoisomerase, putative; PDBTitle: crystal structure of deinococcus radiodurans topoisomerase ib
15	c2h7fX	 Alignment		89.4	20	PDB header: isomerase/dna Chain: X: PDB Molecule: dna topoisomerase 1; PDBTitle: structure of variola topoisomerase covalently bound to dna
16	d1rr8c1	 Alignment		53.4	19	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Eukaryotic DNA topoisomerase I, catalytic core
17	c2b9sA	 Alignment		52.0	14	PDB header: isomerase/dna Chain: A: PDB Molecule: topoisomerase i-like protein; PDBTitle: crystal structure of heterodimeric I. donovani2 topoisomerase i-vanadate-dna complex
18	d1khda1	 Alignment		49.2	24	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
19	d1k4ta2	 Alignment		44.2	15	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Eukaryotic DNA topoisomerase I, catalytic core
20	d1uoua1	 Alignment		42.0	16	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
21	d2tpa1	 Alignment	not modelled	41.9	12	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
22	d1v8ga1	 Alignment	not modelled	40.7	20	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
23	d2cgra1	 Alignment	not modelled	32.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
24	d1brwa1	 Alignment	not modelled	29.4	20	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
25	d1a41a	 Alignment	not modelled	29.2	20	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Eukaryotic DNA topoisomerase I, catalytic core
26	d1f43a	 Alignment	not modelled	28.4	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
27	c2j0fC	 Alignment	not modelled	24.8	16	PDB header: transferase Chain: C: PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
28	c2k0A	 Alignment	not modelled	23.4	11	PDB header: transcription regulation Chain: A: PDB Molecule: homeobox protein nanog;

28	c2kwa_	Alignment	not modelled	23.4	11	PDBTitle: solution structure of human stem cell transcription factor nanog2 homeodomain fragment PDB header: transferase
29	c3h5qa_	Alignment	not modelled	22.6	14	Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
30	c2dsja_	Alignment	not modelled	20.7	12	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
31	c1otpa_	Alignment	not modelled	20.5	16	PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
32	d1o17a1	Alignment	not modelled	20.3	24	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
33	d1vnda_	Alignment	not modelled	20.1	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
34	c1brwB_	Alignment	not modelled	18.1	18	PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
35	d1pufa_	Alignment	not modelled	17.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
36	c2dmsA_	Alignment	not modelled	17.2	8	PDB header: dna binding protein Chain: A: PDB Molecule: homeobox protein otx2; PDBTitle: solution structure of the homeobox domain of homeobox2 protein otx2
37	c2bpgB_	Alignment	not modelled	17.1	14	PDB header: transferase Chain: B: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
38	d1trra_	Alignment	not modelled	16.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
39	d1hdpa_	Alignment	not modelled	15.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
40	c1a31A_	Alignment	not modelled	15.7	18	PDB header: isomerase/dna Chain: A: PDB Molecule: protein (topoisomerase i); PDBTitle: human reconstituted dna topoisomerase i in covalent complex2 with a 22 base pair dna duplex
41	c2l9ra_	Alignment	not modelled	15.3	7	PDB header: transcription Chain: A: PDB Molecule: homeobox protein nkx-3.1; PDBTitle: solution nmr structure of homeobox domain of homeobox protein nkx-3.12 from homo sapiens, northeast structural genomics consortium target3 hr6470a
42	c1vquB_	Alignment	not modelled	14.9	16	PDB header: transferase Chain: B: PDB Molecule: anthranilate phosphoribosyltransferase 2; PDBTitle: crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
43	d1jhga_	Alignment	not modelled	14.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
44	d1xc5a1	Alignment	not modelled	14.6	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
45	c2djna_	Alignment	not modelled	14.5	13	PDB header: transcription Chain: A: PDB Molecule: homeobox protein dlx-5; PDBTitle: the solution structure of the homeobox domain of human2 homeobox protein dlx-5
46	d1fjlb_	Alignment	not modelled	13.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
47	c2dmuA_	Alignment	not modelled	13.3	13	PDB header: dna binding protein Chain: A: PDB Molecule: homeobox protein gooseoid; PDBTitle: solution structure of the homeobox domain of homeobox2 protein gooseoid
48	c1khdD_	Alignment	not modelled	12.9	23	PDB header: transferase Chain: D: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.93 resolution (current name, pectobacterium carotovorum)
49	d1ocpa_	Alignment	not modelled	12.5	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
50	c2dmtA_	Alignment	not modelled	12.4	18	PDB header: dna binding protein Chain: A: PDB Molecule: homeobox protein barh-like 1; PDBTitle: solution structure of the homeobox domain of homeobox2 protein barh-like 1
51	c1v8gB_	Alignment	not modelled	12.3	20	PDB header: transferase Chain: B: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
52	c2da3A_	Alignment	not modelled	11.6	19	PDB header: transcription Chain: A: PDB Molecule: alpha-fetoprotein enhancer binding protein;

						PDBTitle: solution structure of the third homeobox domain of at-2 binding transcription factor 1 (atbf1)
53	dlig7a_	Alignment	not modelled	10.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
54	dlcc5a_	Alignment	not modelled	10.1	8	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
55	dlztra1	Alignment	not modelled	9.9	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
56	dlfjla_	Alignment	not modelled	9.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
57	d2elca1	Alignment	not modelled	9.8	22	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
58	dlgt0c1	Alignment	not modelled	9.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
59	c3mzyA_	Alignment	not modelled	9.3	13	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
60	d2e1oa1	Alignment	not modelled	9.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
61	c2f9jp_	Alignment	not modelled	9.2	14	PDB header: rna binding protein Chain: P: PDB Molecule: splicing factor 3b subunit 1; PDBTitle: 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
62	c1o17A_	Alignment	not modelled	9.0	25	PDB header: transferase Chain: A: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyl-transferase (trpd)
63	dlgefa_	Alignment	not modelled	9.0	13	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
64	dlbw5a_	Alignment	not modelled	8.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
65	c2wj0B_	Alignment	not modelled	8.5	25	PDB header: hydrolase/dna Chain: B: PDB Molecule: archaeal hjc; PDBTitle: crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate
66	c2juhA_	Alignment	not modelled	8.5	11	PDB header: nuclear protein Chain: A: PDB Molecule: telomere binding protein tbp1; PDBTitle: solution structure of dna binding domain of ngtrf1
67	c2kq6A_	Alignment	not modelled	8.4	17	PDB header: transport protein Chain: A: PDB Molecule: polycystin-2; PDBTitle: the structure of the ef-hand domain of polycystin-2 suggests a2 mechanism for ca2+-dependent regulation of polycystin-2 channel3 activity
68	c2dmqA_	Alignment	not modelled	8.4	10	PDB header: dna binding protein Chain: A: PDB Molecule: lim/homeobox protein lhx9; PDBTitle: solution structure of the homeobox domain of lim/homeobox2 protein lhx9
69	c2da2A_	Alignment	not modelled	8.1	10	PDB header: transcription Chain: A: PDB Molecule: alpha-fetoprotein enhancer binding protein; PDBTitle: solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)
70	c3hugA_	Alignment	not modelled	8.1	11	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
71	dlahdp_	Alignment	not modelled	7.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
72	dlsf9a_	Alignment	not modelled	7.8	10	Fold: SH3-like barrel Superfamily: Hypothetical protein YfhH Family: Hypothetical protein YfhH
73	c3hxxA_	Alignment	not modelled	7.4	26	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
74	dl0ctc1	Alignment	not modelled	7.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
75	c3a01A_	Alignment	not modelled	7.1	15	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeodomain-containing protein; PDBTitle: crystal structure of aristaless and clawless homeodomains bound to dna
76	dljhfa1	Alignment	not modelled	7.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
77	dlyz8p1	Alignment	not modelled	6.9	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
						Fold: Cytochrome c Superfamily: Cytochrome c

78	d1h9xa1	Alignment	not modelled	6.8	11	Supersfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
79	d2ecba1	Alignment	not modelled	6.7	14	Fold: DNA/RNA-binding 3-helical bundle Supersfamily: Homeodomain-like Family: Homeodomain
80	d1a56a	Alignment	not modelled	6.7	8	Fold: Cytochrome c Supersfamily: Cytochrome c Family: monodomain cytochrome c
81	d1b8ia	Alignment	not modelled	6.6	13	Fold: DNA/RNA-binding 3-helical bundle Supersfamily: Homeodomain-like Family: Homeodomain
82	c2x48B	Alignment	not modelled	6.4	33	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfolobus islandicus rudivirus 1
83	d1kx7a	Alignment	not modelled	6.4	8	Fold: Cytochrome c Supersfamily: Cytochrome c Family: monodomain cytochrome c
84	c3sohB	Alignment	not modelled	6.4	10	PDB header: motor protein Chain: B: PDB Molecule: flagellar motor switch protein flig; PDBTitle: architecture of the flagellar rotor
85	d2hddb	Alignment	not modelled	6.2	14	Fold: DNA/RNA-binding 3-helical bundle Supersfamily: Homeodomain-like Family: Homeodomain
86	d2cuea1	Alignment	not modelled	6.1	18	Fold: DNA/RNA-binding 3-helical bundle Supersfamily: Homeodomain-like Family: Homeodomain
87	c2kleA	Alignment	not modelled	6.0	19	PDB header: membrane protein Chain: A: PDB Molecule: polycystin-2; PDBTitle: isic refined solution structure of the calcium binding2 domain of the c-terminal cytosolic domain of polycystin-2
88	d1zq3p1	Alignment	not modelled	5.9	18	Fold: DNA/RNA-binding 3-helical bundle Supersfamily: Homeodomain-like Family: Homeodomain
89	c2l4dA	Alignment	not modelled	5.9	20	PDB header: electron transport Chain: A: PDB Molecule: sco1/senc family protein/cytochrome c; PDBTitle: cytochrome c domain of pp3183 protein from pseudomonas putida
90	c2o8xA	Alignment	not modelled	5.9	8	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
91	c3h0gE	Alignment	not modelled	5.9	16	PDB header: transcription Chain: E: PDB Molecule: dna-directed rna polymerases i, ii, and iii PDBTitle: rna polymerase ii from schizosaccharomyces pombe
92	c2zonG	Alignment	not modelled	5.8	0	PDB header: oxidoreductase/electron transport Chain: G: PDB Molecule: cytochrome c551; PDBTitle: crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c
93	c2d0sA	Alignment	not modelled	5.5	15	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
94	d1au7a1	Alignment	not modelled	5.5	7	Fold: DNA/RNA-binding 3-helical bundle Supersfamily: Homeodomain-like Family: Homeodomain
95	c3hefB	Alignment	not modelled	5.5	13	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit
96	d1litya	Alignment	not modelled	5.4	22	Fold: DNA/RNA-binding 3-helical bundle Supersfamily: Homeodomain-like Family: DNA-binding domain of telomeric protein
97	d1ob8a	Alignment	not modelled	5.3	13	Fold: Restriction endonuclease-like Supersfamily: Restriction endonuclease-like Family: Hjc-like
98	d1fcdc1	Alignment	not modelled	5.1	8	Fold: Cytochrome c Supersfamily: Cytochrome c Family: Two-domain cytochrome c
99	d2craa1	Alignment	not modelled	5.1	11	Fold: DNA/RNA-binding 3-helical bundle Supersfamily: Homeodomain-like Family: Homeodomain