







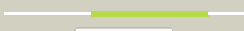






















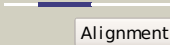
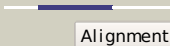


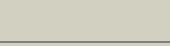
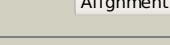
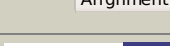
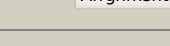
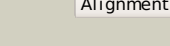



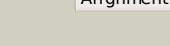



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	 Alignment		98.5	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	 Alignment		98.1	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
3	d1cxqa_	 Alignment		91.1	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
4	d1asua_	 Alignment		85.6	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	d1c0ma2	 Alignment		67.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
6	c1bg1A_	 Alignment		66.6	14	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
7	c3nf9A_	 Alignment		64.5	13	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
8	c1yv1B_	 Alignment		62.4	14	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
9	c3hefB_	 Alignment		51.6	15	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit
10	c1c0mA_	 Alignment		47.2	19	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
11	d1bcoa2	 Alignment		46.2	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain

12	d1hyva_	Alignment		40.9	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
13	c1bf5A_	Alignment		36.9	17	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: tyrosine phosphorylated stat-1/dna complex
14	c3f9kv_	Alignment		36.4	13	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
15	d1exqa_	Alignment		31.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
16	c1bcoA_	Alignment		30.9	16	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
17	d1k78a1	Alignment		30.8	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
18	c3nzqB_	Alignment		29.0	17	PDB header: lyase Chain: B: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
19	d6paxa1	Alignment		24.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
20	d1a9xa1	Alignment		21.6	12	Fold: Carbamoyl phosphate synthetase, large subunit connection domain Superfamily: Carbamoyl phosphate synthetase, large subunit connection domain Family: Carbamoyl phosphate synthetase, large subunit connection domain
21	c3n2oA_	Alignment	not modelled	20.4	32	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
22	c1k6yB_	Alignment	not modelled	19.7	15	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
23	d1c6va_	Alignment	not modelled	18.7	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
24	c3iwfA_	Alignment	not modelled	14.1	4	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
25	c2jg6A_	Alignment	not modelled	11.6	9	PDB header: hydrolase Chain: A: PDB Molecule: dna-3-methyladenine glycosidase; PDBTitle: crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
26	d1slma1	Alignment	not modelled	10.2	27	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
27	c3nzpA_	Alignment	not modelled	10.2	25	PDB header: lyase Chain: A: PDB Molecule: arginine decarboxylase; PDBTitle: crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
28	c2vkpA_	Alignment	not modelled	9.7	12	PDB header: protein-binding Chain: A: PDB Molecule: btb/poz domain-containing protein 6; PDBTitle: crystal structure of btb domain from btbd6

29	c3cwgA	 Alignment	not modelled	9.5	13	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
30	c1y1uA	 Alignment	not modelled	9.1	16	PDB header: signaling protein Chain: A: PDB Molecule: signal transducer and activator of transcription 5a; PDBTitle: structure of unphosphorylated stat5a
31	c3eusB	 Alignment	not modelled	8.9	16	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroiy
32	c2o3fC	 Alignment	not modelled	8.0	12	PDB header: transcription Chain: C: PDB Molecule: putative hth-type transcriptional regulator ybbh; PDBTitle: structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
33	d2o3fa1	 Alignment	not modelled	8.0	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: RpiR-like
34	d1nkua	 Alignment	not modelled	8.0	10	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase I (Tag)
35	c1ex4A	 Alignment	not modelled	7.7	17	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
36	d1a6qa1	 Alignment	not modelled	6.9	27	Fold: Another 3-helical bundle Superfamily: Protein serine/threonine phosphatase 2C, C-terminal domain Family: Protein serine/threonine phosphatase 2C, C-terminal domain
37	c2kvcA	 Alignment	not modelled	5.8	20	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
38	d1v77a	 Alignment	not modelled	5.8	7	Fold: 7-stranded beta/alpha barrel Superfamily: PHP domain-like Family: RNase P subunit p30
39	d1sbza	 Alignment	not modelled	5.5	19	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
40	c3hpgC	 Alignment	not modelled	5.3	13	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
41	c3g7pA	 Alignment	not modelled	5.2	15	PDB header: unknown function Chain: A: PDB Molecule: nitrogen fixation protein; PDBTitle: crystal structure of a nifx-associated protein of unknown function2 (afe_1514) from acidithiobacillus ferrooxidans atcc at 2.00 a3 resolution
42	c2lm4A	 Alignment	not modelled	5.1	14	PDB header: protein binding Chain: A: PDB Molecule: succinate dehydrogenase assembly factor 2, mitochondrial; PDBTitle: solution nmr structure of mitochondrial succinate dehydrogenase2 assembly factor 2 from saccharomyces cerevisiae, northeast structural3 genomics consortium target yt682a