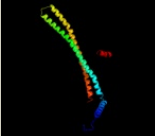
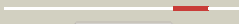
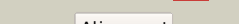
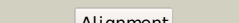
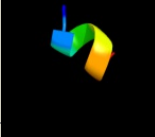
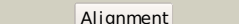
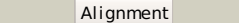
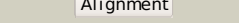
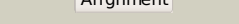
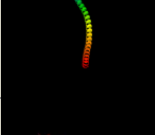
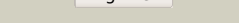
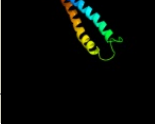
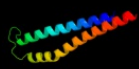
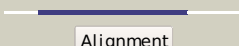
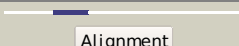
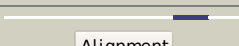
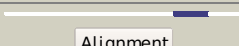
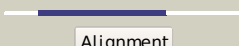
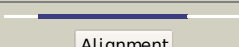
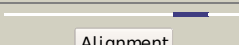
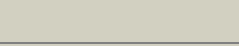
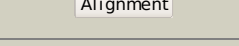
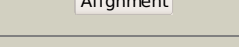
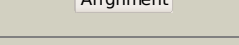
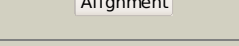
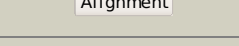
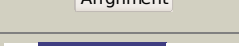
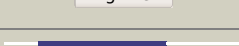
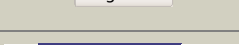
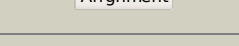


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kmiZ_	 Alignment		100.0	100	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
2	c2pl9D_	 Alignment		97.1	100	PDB header: signaling protien Chain: D: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
3	c2pl9E_	 Alignment		95.9	100	PDB header: signaling protien Chain: E: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
4	c2pl9F_	 Alignment		95.9	100	PDB header: signaling protien Chain: F: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
5	c2damA_	 Alignment		43.1	75	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: etea protein; PDBTitle: solution structure of the novel identified uba-like domain2 in the n-terminal of human etea protein
6	c1zvzA_	 Alignment		35.4	14	PDB header: protein binding Chain: A: PDB Molecule: vinculin; PDBTitle: vinculin head (0-258) in complex with the talin rod residue2 820-844
7	d1szia_	 Alignment		34.5	15	Fold: Four-helical up-and-down bundle Superfamily: Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain Family: Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
8	d2a2pa1	 Alignment		32.2	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
9	d1rqba1	 Alignment		30.8	20	Fold: RuvA C-terminal domain-like Superfamily: post-HMGL domain-like Family: Conserved carboxylase domain
10	c2wpqA_	 Alignment		27.6	7	PDB header: membrane protein Chain: A: PDB Molecule: trimeric autotransporter adhesin fragment; PDBTitle: salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion)
11	c2vs0B_	 Alignment		21.7	9	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa

12	c3gvmA_	Alignment		18.2	13	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
13	c1rr2A_	Alignment		18.1	20	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
14	d1wa8a1	Alignment		15.4	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
15	c3hkzZ_	Alignment		14.5	33	PDB header: transferase Chain: Z: PDB Molecule: dna-directed rna polymerase subunit 13; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
16	c3ayhA_	Alignment		14.3	13	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase iii subunit rpc9; PDBTitle: crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
17	c3hkzY_	Alignment		13.8	32	PDB header: transferase Chain: Y: PDB Molecule: dna-directed rna polymerase subunit 13; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
18	c2waqQ_	Alignment		13.6	28	PDB header: transcription Chain: Q: PDB Molecule: dna-directed rna polymerase rpo13 subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
19	d2e1fa1	Alignment		12.5	10	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
20	c2y0sj_	Alignment		12.0	30	PDB header: transferase Chain: J: PDB Molecule: rna polymerase subunit 13; PDBTitle: crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
21	c2y0sQ_	Alignment	not modelled	12.0	30	PDB header: transferase Chain: Q: PDB Molecule: rna polymerase subunit 13; PDBTitle: crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
22	c2nx9B_	Alignment	not modelled	11.7	20	PDB header: lyase Chain: B: PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
23	d1wa8b1	Alignment	not modelled	11.3	12	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
24	d1we1a_	Alignment	not modelled	10.9	22	Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: Eukaryotic type heme oxygenase
25	c2wb1Q_	Alignment	not modelled	10.3	30	PDB header: transcription Chain: Q: PDB Molecule: dna-directed rna polymerase rpo13 subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
26	c2dnxA_	Alignment	not modelled	10.1	13	PDB header: transport protein Chain: A: PDB Molecule: syntaxin-12; PDBTitle: solution structure of rsgi ruh-063, an n-terminal domain of2 syntaxin 12 from human cdna
27	c2wb1J_	Alignment	not modelled	9.7	30	PDB header: transcription Chain: J: PDB Molecule: dna-directed rna polymerase rpo13 subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
28	d2fyma2	Alignment	not modelled	9.6	20	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like

29	c3g67A	 Alignment	not modelled	9.4	12	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
30	d1ei1a	 Alignment	not modelled	9.3	50	Fold: RuvA C-terminal domain-like Superfamily: Double-stranded DNA-binding domain Family: Double-stranded DNA-binding domain
31	c2vzdD	 Alignment	not modelled	9.2	50	PDB header: cell adhesion Chain: D: PDB Molecule: paxillin; PDBTitle: crystal structure of the c-terminal calponin homology2 domain of alpha parvin in complex with paxillin ld1 motif
32	c2krcA	 Alignment	not modelled	9.1	13	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit delta; PDBTitle: solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase
33	c2pmzF	 Alignment	not modelled	9.1	16	PDB header: translation, transferase Chain: F: PDB Molecule: dna-directed rna polymerase subunit f; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
34	c2vzdC	 Alignment	not modelled	9.0	50	PDB header: cell adhesion Chain: C: PDB Molecule: paxillin; PDBTitle: crystal structure of the c-terminal calponin homology2 domain of alpha parvin in complex with paxillin ld1 motif
35	d2dnaa1	 Alignment	not modelled	8.4	31	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
36	d1dd5a	 Alignment	not modelled	8.2	14	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
37	d2akza2	 Alignment	not modelled	7.6	33	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
38	d1ug7a	 Alignment	not modelled	7.4	19	Fold: Four-helical up-and-down bundle Superfamily: Domain from hypothetical 2610208m17rik protein Family: Domain from hypothetical 2610208m17rik protein
39	d2al1a2	 Alignment	not modelled	7.3	53	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
40	d1pdza2	 Alignment	not modelled	7.1	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
41	c3k8wA	 Alignment	not modelled	7.0	17	PDB header: structural protein Chain: A: PDB Molecule: flagellin homolog; PDBTitle: crystal structure of a bacterial cell-surface flagellin n20c45
42	c3s90B	 Alignment	not modelled	6.7	14	PDB header: cell adhesion Chain: B: PDB Molecule: vinculin; PDBTitle: human vinculin head domain vh1 (residues 1-252) in complex with murine2 talin (vbs33; residues 1512-1546)
43	d2dsma1	 Alignment	not modelled	6.6	40	Fold: Yqal-like Superfamily: Yqal-like Family: Yqal-like
44	c2drnC	 Alignment	not modelled	6.6	36	PDB header: transferase Chain: C: PDB Molecule: 24-residues peptide from an a-kinase anchoring PDBTitle: docking and dimerization domain (d/d) of the type ii-alpha2 regulatory subunit of protein kinase a (pka) in complex3 with a peptide from an a-kinase anchoring protein
45	d1jjcb2	 Alignment	not modelled	6.2	22	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
46	d1st6a5	 Alignment	not modelled	6.1	15	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
47	c2a93B	 Alignment	not modelled	6.0	57	PDB header: leucine zippers Chain: B: PDB Molecule: c-myc-max heterodimeric leucine zipper; PDBTitle: nmr solution structure of the c-myc-max heterodimeric2 leucine zipper, 40 structures
48	d1qf9a	 Alignment	not modelled	5.9	38	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
49	d1u2ma	 Alignment	not modelled	5.7	40	Fold: OmpH-like Superfamily: OmpH-like Family: OmpH-like
50	c2k5cA	 Alignment	not modelled	5.7	27	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
51	d1s94a	 Alignment	not modelled	5.5	14	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
52	c1s94A	 Alignment	not modelled	5.5	14	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: s-syntaxin; PDBTitle: crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
53	c3cdhB	 Alignment	not modelled	5.4	19	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3
54	c2ch7A	 Alignment	not modelled	5.2	14	PDB header: chemotaxis Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima

55	c3tj5A_	Alignment	not modelled	5.1	17	PDB header: protein binding/toxin Chain: A: PDB Molecule: vinculin; PDBTitle: human vinculin head domain (vh1, residues 1-258) in complex with the2 vinculin binding site of the surface cell antigen 4 (sca4-vbs-n;3 residues 412-434) from rickettsia rickettsii
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