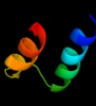
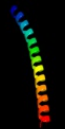
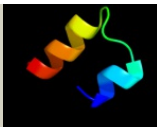
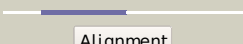
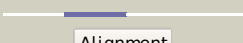
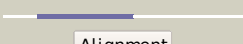
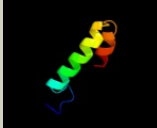
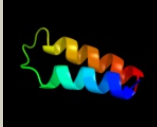
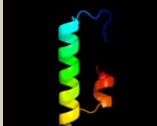
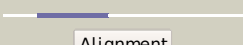
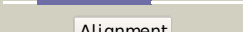


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlvp7b_	 Alignment		99.8	43	Fold: Spectrin repeat-like Superfamily: XseB-like Family: XseB-like
2	dlvp7a_	 Alignment		99.8	47	Fold: Spectrin repeat-like Superfamily: XseB-like Family: XseB-like
3	c1vp7D_	 Alignment		99.7	50	PDB header: hydrolase Chain: D: PDB Molecule: exodeoxyribonuclease vii small subunit; PDBTitle: crystal structure of exodeoxyribonuclease vii small subunit2 (np_881400.1) from bordetella pertussis at 2.40 a resolution
4	c3he4A_	 Alignment		75.7	30	PDB header: de novo protein Chain: A: PDB Molecule: synzip6; PDBTitle: heterospecific coiled-coil pair synzip5:synzip6
5	c1ic2B_	 Alignment		32.7	22	PDB header: contractile protein Chain: B: PDB Molecule: tropomyosin alpha chain, skeletal muscle; PDBTitle: deciphering the design of the tropomyosin molecule
6	c3hxxA_	 Alignment		30.1	23	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
7	c2y0sQ_	 Alignment		29.8	28	PDB header: transferase Chain: Q: PDB Molecule: rna polymerase subunit 13; PDBTitle: crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
8	c2y0sJ_	 Alignment		29.8	28	PDB header: transferase Chain: J: PDB Molecule: rna polymerase subunit 13; PDBTitle: crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
9	d2o3la1	 Alignment		25.8	18	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
10	c3hkzY_	 Alignment		23.4	34	PDB header: transferase Chain: Y: PDB Molecule: dna-directed rna polymerase subunit 13; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
11	c3u1aC_	 Alignment		21.0	19	PDB header: contractile protein Chain: C: PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha

12	c2wb1Q_	 Alignment		19.5	32	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
13	c3k2tA_	 Alignment		19.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2511 protein; PDBTitle: crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
14	c3hkzZ_	 Alignment		19.1	34	PDB header: transferase Chain: Z: PDB Molecule: dna-directed rna polymerase subunit 13; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
15	c2wb1J_	 Alignment		18.8	32	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
16	c2jzvA_	 Alignment		18.0	13	PDB header: isomerase Chain: A: PDB Molecule: foldase protein prsa; PDBTitle: solution structure of s. aureus prsa-ppiase
17	d1wtya_	 Alignment		17.8	25	Fold: Four-helical up-and-down bundle Superfamily: Nucleotidyltransferase substrate binding subunit/domain Family: Family 1 bi-partite nucleotidyltransferase subunit
18	c3ctwB_	 Alignment		17.3	35	PDB header: protein binding Chain: B: PDB Molecule: rcda; PDBTitle: crystal structure of rcda from caulobacter crescentus cb15
19	d1pina2	 Alignment		16.8	19	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
20	c2waqQ_	 Alignment		16.6	32	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
21	c3iv1F_	 Alignment	not modelled	16.4	22	PDB header: hydrolase Chain: F: PDB Molecule: tumor susceptibility gene 101 protein; PDBTitle: coiled-coil domain of tumor susceptibility gene 101
22	c3pu2G_	 Alignment	not modelled	16.1	29	PDB header: structure genomics, unknown function Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q3j4m4_rhos4 protein from rhodobacter2 sphaeroides. northeast structural genomics consortium target rhr263.
23	c2dl1A_	 Alignment	not modelled	13.1	25	PDB header: protein transport Chain: A: PDB Molecule: spartin; PDBTitle: solution structure of the mit domain from human spartin
24	c2v6xA_	 Alignment	not modelled	12.6	11	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4; PDBTitle: structural insight into the interaction between escrt-iii2 and vps4
25	c2xa6B_	 Alignment	not modelled	12.4	25	PDB header: transcription Chain: B: PDB Molecule: kh domain-containing\,rna-binding\,signal PDBTitle: structural basis for homodimerization of the src-associated2 during mitosis, 68 kd protein (sam68) qua1 domain
26	c2krxA_	 Alignment	not modelled	12.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: asl3597 protein; PDBTitle: solution nmr structure of asl3597 from nostoc sp. pcc7120. northeast2 structural genomics consortium target id nsr244.
27	c2ehwD_	 Alignment	not modelled	11.7	33	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein tthb059; PDBTitle: conserved hypothetical protein (tthb059) from thermo thermophilus hb8
28	d2ig9a1	 Alignment	not modelled	10.7	18	Fold: Spectrin repeat-like Superfamily: MIT domain

						Family: MIT domain
29	c3l32B_	Alignment	not modelled	10.7	50	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the dimerisation domain of the rabies virus2 phosphoprotein
30	c1u2uA_	Alignment	not modelled	10.3	31	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: nmr solution structure of a designed heterodimeric leucine2 zipper
31	c1eqfA_	Alignment	not modelled	10.3	10	PDB header: transcription Chain: A: PDB Molecule: rna polymerase ii transcription initiation PDBTitle: crystal structure of the double bromodomain module from2 human tafii250
32	c2r5xA_	Alignment	not modelled	10.1	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein yugn from2 geobacillus kaustophilus hta426
33	d1x79a_	Alignment	not modelled	9.8	20	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
34	c1yfsB_	Alignment	not modelled	9.5	6	PDB header: ligase Chain: B: PDB Molecule: alanyl-trna synthetase; PDBTitle: the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
35	d1pgya_	Alignment	not modelled	9.4	41	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
36	c1f8aB_	Alignment	not modelled	9.2	19	PDB header: isomerase Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase nima- PDBTitle: structural basis for the phosphoserine-proline recognition2 by group iv ww domains
37	d1riqa1	Alignment	not modelled	9.0	13	Fold: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) Superfamily: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) Family: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
38	c2eqbC_	Alignment	not modelled	8.1	15	PDB header: endocytosis/exocytosis Chain: C: PDB Molecule: rab guanine nucleotide exchange factor sec2; PDBTitle: crystal structure of the rab gtpase sec4p, the sec2p gef2 domain, and phosphate complex
39	c3cd0B_	Alignment	not modelled	8.1	33	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxy-3-methylglutaryl-coenzyme a reductase; PDBTitle: thermodynamic and structure guided design of statin hmg-coa2 reductase inhibitors
40	d1dqa4_	Alignment	not modelled	7.8	33	Fold: Substrate-binding domain of HMG-CoA reductase Superfamily: Substrate-binding domain of HMG-CoA reductase Family: Substrate-binding domain of HMG-CoA reductase
41	c3mstA_	Alignment	not modelled	7.5	19	PDB header: transport protein Chain: A: PDB Molecule: putative nitrate transport protein; PDBTitle: crystal structure of a putative nitrate transport protein (tn0104)2 from thermoplasma volcanium at 1.35 a resolution
42	c3o3xA_	Alignment	not modelled	7.5	22	PDB header: viral protein Chain: A: PDB Molecule: gp41-5; PDBTitle: crystal structure of gp41-5, a single-chain 5-helix-bundle based on2 hiv gp41
43	c3epyA_	Alignment	not modelled	7.4	10	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coa-binding domain-containing protein 7; PDBTitle: crystal structure of human acyl-coa binding domain 72 complexed with palmitoyl-coa
44	d1wr0a1	Alignment	not modelled	7.2	21	Fold: Spectrin repeat-like Superfamily: MIT domain Family: MIT domain
45	c1ty4D_	Alignment	not modelled	7.2	29	PDB header: apoptosis Chain: D: PDB Molecule: egg laying defective egl-1, programmed cell death PDBTitle: crystal structure of a ced-9/egl-1 complex
46	c3iabB_	Alignment	not modelled	6.8	12	PDB header: hydrolase/rna Chain: B: PDB Molecule: ribonucleases p/mrp protein subunit pop7; PDBTitle: crystal structure of rnase p /rnase mrp proteins pop6, pop72 in a complex with the p3 domain of rnase mrp rna
47	c2xt6B_	Alignment	not modelled	6.8	29	PDB header: lyase Chain: B: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
48	d1orja_	Alignment	not modelled	6.7	13	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone FlIS Family: Flagellar export chaperone FlIS
49	d2cpta1	Alignment	not modelled	6.5	25	Fold: Spectrin repeat-like Superfamily: MIT domain Family: MIT domain
50	d1j3ma_	Alignment	not modelled	6.4	14	Fold: TBP-like Superfamily: TT1751-like Family: TT1751-like
51	d2ftsa2	Alignment	not modelled	6.4	15	Fold: MoeA N-terminal region -like Superfamily: MoeA N-terminal region -like Family: MoeA N-terminal region -like
52	c3ck4K_	Alignment	not modelled	6.3	28	PDB header: protein binding Chain: K: PDB Molecule: gcn4 leucine zipper; PDBTitle: a heterospecific leucine zipper tetramer
53	d1m5ya3	Alignment	not modelled	6.2	33	Fold: FKBP-like Superfamily: FKBP-like

					Family: FKBP immunophilin/proline isomerase
54	c2cxaA_	Alignment	not modelled	5.4	35 PDB header: transferase Chain: A: PDB Molecule: leucyl/phenylalanyl-trna-protein transferase; PDBTitle: crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
55	d2cxaa1	Alignment	not modelled	5.4	35 Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: LFTR-like
56	d1uz5a2	Alignment	not modelled	5.4	25 Fold: MoeA N-terminal region -like Superfamily: MoeA N-terminal region -like Family: MoeA N-terminal region -like
57	d2hh6a1	Alignment	not modelled	5.4	31 Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
58	c2qr4B_	Alignment	not modelled	5.3	13 PDB header: hydrolase Chain: B: PDB Molecule: peptidase m3b, oligoendopeptidase f; PDBTitle: crystal structure of oligoendopeptidase-f from enterococcus faecium
59	c2gl2B_	Alignment	not modelled	5.3	15 PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
60	c1junB_	Alignment	not modelled	5.3	23 PDB header: transcription regulation Chain: B: PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer