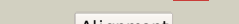
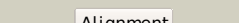
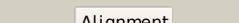
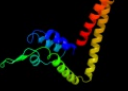
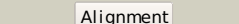
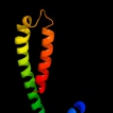
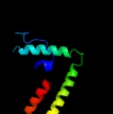
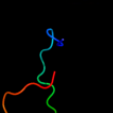
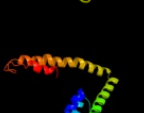


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlizma_	 Alignment		99.9	14	Fold: Ygfb-like Superfamily: Ygfb-like Family: Ygfb-like
2	c2i9wA_	 Alignment		99.6	52	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution
3	dl0zbi_	 Alignment		99.3	74	Fold: Sec-C motif Superfamily: Sec-C motif Family: Sec-C motif
4	c1ozbl_	 Alignment		99.3	74	PDB header: protein transport Chain: I: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of secb complexed with seca c-terminus
5	c1ozbj_	 Alignment		99.3	74	PDB header: protein transport Chain: J: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of secb complexed with seca c-terminus
6	d1tm6a_	 Alignment		99.3	89	Fold: Sec-C motif Superfamily: Sec-C motif Family: Sec-C motif
7	c1tm6A_	 Alignment		99.3	89	PDB header: protein transport Chain: A: PDB Molecule: preprotein translocase seca subunit; PDBTitle: nmr structure of the free zinc binding c-terminal domain of2 seca
8	d2i9wa3	 Alignment		97.7	58	Fold: Sec-C motif Superfamily: Sec-C motif Family: Sec-C motif
9	c2ipcB_	 Alignment		95.4	13	PDB header: transport protein Chain: B: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
10	c3dinB_	 Alignment		95.3	13	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: protein translocase subunit seca; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
11	d1tf5a2	 Alignment		95.0	15	Fold: Helical scaffold and wing domains of SecA Superfamily: Helical scaffold and wing domains of SecA Family: Helical scaffold and wing domains of SecA

12	dlnkta2	Alignment		93.5	12	Fold: Helical scaffold and wing domains of SecA Superfamily: Helical scaffold and wing domains of SecA Family: Helical scaffold and wing domains of SecA
13	c3juxA	Alignment		92.8	14	PDB header: protein transport Chain: A: PDB Molecule: protein translocase subunit seca; PDBTitle: structure of the translocation atpase seca from thermotoga2 maritima
14	c2vdaA	Alignment		88.9	15	PDB header: protein transport Chain: A: PDB Molecule: translocase subunit seca; PDBTitle: solution structure of the seca-signal peptide complex
15	c1tf2A	Alignment		88.6	14	PDB header: protein transport Chain: A: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of seca:adp in an open conformation from2 bacillus subtilis
16	c1nl3B	Alignment		86.4	14	PDB header: protein transport Chain: B: PDB Molecule: preprotein translocase seca 1 subunit; PDBTitle: crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
17	c3dl8B	Alignment		85.6	15	PDB header: protein transport Chain: B: PDB Molecule: protein translocase subunit seca; PDBTitle: structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
18	c1nniA	Alignment		84.5	9	PDB header: hydrolase Chain: A: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
19	d2baaa	Alignment		77.2	19	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Family 19 glycosidase
20	c2fsgA	Alignment		67.3	13	PDB header: protein transport Chain: A: PDB Molecule: preprotein translocase seca subunit; PDBTitle: complex seca:atp from escherichia coli
21	c1k82D	Alignment	not modelled	65.1	16	PDB header: hydrolase/dna Chain: D: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
22	d1o9ga	Alignment	not modelled	61.7	100	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase AviRa
23	d1nuia2	Alignment	not modelled	56.3	56	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
24	c2dkvA	Alignment	not modelled	56.1	19	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of class i chitinase from oryza sativa l.2 japonica
25	d1wgea1	Alignment	not modelled	54.2	71	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
26	d1ywsa1	Alignment	not modelled	51.3	71	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
27	c2z39A	Alignment	not modelled	47.5	38	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of brassica juncea chitinase catalytic2 module glu234ala mutant (bjchi3-e234a)
28	c3hbha	Alignment	not modelled	46.6	15	PDB header: hydrolase Chain: A: PDB Molecule: class iv chitinase chia4-pa2; PDBTitle: class iv chitinase structure from picea abies at 2.25a
						PDB header: dna binding protein

29	c1ee8A_	Alignment	not modelled	39.8	16	Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermophilus hb8
30	c2jr7A_	Alignment	not modelled	36.0	71	PDB header: metal binding protein Chain: A: PDB Molecule: dph3 homolog; PDBTitle: solution structure of human desr1
31	c1i6hA_	Alignment	not modelled	33.7	25	PDB header: transcription/dna-rna hybrid Chain: A: PDB Molecule: dna-directed rna polymerase ii largest subunit; PDBTitle: rna polymerase ii elongation complex
32	d1tdza3	Alignment	not modelled	33.4	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
33	c3khkA_	Alignment	not modelled	33.1	71	PDB header: dna binding protein Chain: A: PDB Molecule: type i restriction-modification system PDBTitle: crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosarchina mazel.
34	d1lgha_	Alignment	not modelled	31.7	45	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
35	c1dvvA_	Alignment	not modelled	28.7	36	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
36	d1twfa_	Alignment	not modelled	27.4	25	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta-prime
37	d1dxwa_	Alignment	not modelled	26.9	45	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
38	d1cu1a1	Alignment	not modelled	26.8	45	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
39	d1a1qa_	Alignment	not modelled	25.8	45	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
40	c1zmpD_	Alignment	not modelled	25.7	40	PDB header: antimicrobial protein Chain: D: PDB Molecule: defensin 5; PDBTitle: crystal structure of human defensin-5
41	d1h1oa1	Alignment	not modelled	25.5	14	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
42	d1dxja_	Alignment	not modelled	25.3	31	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Family 19 glycosidase
43	c2f9jp_	Alignment	not modelled	24.8	36	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
44	c2ee7A_	Alignment	not modelled	23.9	18	PDB header: structural protein Chain: A: PDB Molecule: sperm flagellar protein 1; PDBTitle: solution structure of the ch domain from human sperm2 flagellar protein 1
45	d1lr7a1	Alignment	not modelled	23.3	83	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: Follistatin (FS) module N-terminal domain, FS-N
46	c3a44D_	Alignment	not modelled	22.2	67	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
47	c3i5wB_	Alignment	not modelled	21.7	44	PDB header: antimicrobial protein Chain: B: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5 (mutant r13h)
48	c1zmpA_	Alignment	not modelled	21.4	44	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin 5; PDBTitle: crystal structure of human defensin-5
49	c1zmpB_	Alignment	not modelled	21.4	44	PDB header: antimicrobial protein Chain: B: PDB Molecule: defensin 5; PDBTitle: crystal structure of human defensin-5
50	c1zmpC_	Alignment	not modelled	21.4	44	PDB header: antimicrobial protein Chain: C: PDB Molecule: defensin 5; PDBTitle: crystal structure of human defensin-5
51	d1ug7a_	Alignment	not modelled	21.3	12	Fold: Four-helical up-and-down bundle Superfamily: Domain from hypothetical 2610208m17rik protein Family: Domain from hypothetical 2610208m17rik protein
52	c3s1sA_	Alignment	not modelled	20.7	71	PDB header: hydrolase, transferase Chain: A: PDB Molecule: restriction endonuclease bpusi; PDBTitle: characterization and crystal structure of the type iig restriction2 endonuclease bpusi
53	d5crxb2	Alignment	not modelled	20.2	10	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
54	c2ns5A_	Alignment	not modelled	20.0	42	PDB header: signaling protein Chain: A: PDB Molecule: partitioning-defective 3 homolog; PDBTitle: the conserved n-terminal domain of par-3 adopts a novel pb1-2 like structure required for par-3 oligomerization and3 apical membrane localization
						PDB header: toxin Chain: A: PDB Molecule: toxin

55	c2jtbA_	Alignment	not modelled	19.9	47	Chain: A: PDB Molecule: hainantoxin-3; PDBTitle: three dimensional solution structure of hainantoxin-iii by2 2d 1h-nmr
56	d1jmx1	Alignment	not modelled	19.8	15	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
57	c3h9gA_	Alignment	not modelled	19.3	42	PDB header: transferase/antibiotic Chain: A: PDB Molecule: mccb protein; PDBTitle: crystal structure of e. coli mccb + mcca-n7isoasn
58	c2f5qA_	Alignment	not modelled	19.1	9	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
59	d1jw2a_	Alignment	not modelled	18.8	31	Fold: Open three-helical up-and-down bundle Superfamily: Hemolysin expression modulating protein HHA Family: Hemolysin expression modulating protein HHA
60	c2wh9A_	Alignment	not modelled	17.5	100	PDB header: membrane protein inhibitor Chain: A: PDB Molecule: guangxitoxin-1egxb-1e; PDBTitle: solution structure of gxtb-1e
61	c2cnjD_	Alignment	not modelled	17.5	46	PDB header: receptor Chain: D: PDB Molecule: cation-independent mannose-6-phosphate receptor; PDBTitle: nmr studies on the interaction of insulin-growth factor ii (2 igf-ii) with igf2r domain 11
62	d1lkoa2	Alignment	not modelled	17.2	36	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
63	c1aqsA_	Alignment	not modelled	17.1	47	PDB header: metallothionein Chain: A: PDB Molecule: cu-metallothionein; PDBTitle: cu-metallothionein from saccharomyces cerevisiae, nmr, 102 structures
64	c1yuzB_	Alignment	not modelled	16.7	36	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
65	d1gp0a_	Alignment	not modelled	16.5	50	Fold: Mannose 6-phosphate receptor domain Superfamily: Mannose 6-phosphate receptor domain Family: Mannose 6-phosphate receptor domain
66	c1gp0A_	Alignment	not modelled	16.5	50	PDB header: receptor Chain: A: PDB Molecule: cation-independent mannose-6-phosphate receptor; PDBTitle: human igf2r domain 11
67	d1lpba2	Alignment	not modelled	16.2	67	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Colipase-like Family: Colipase-like
68	c2vsxA_	Alignment	not modelled	15.8	50	PDB header: translation/hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase eif4a; PDBTitle: crystal structure of a translation initiation complex
69	d2au5a1	Alignment	not modelled	15.6	18	Fold: EF2947-like Superfamily: EF2947-like Family: EF2947-like
70	d2aqaa1	Alignment	not modelled	15.5	14	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
71	c1gp3A_	Alignment	not modelled	15.1	50	PDB header: receptor Chain: A: PDB Molecule: cation-independent mannose-6-phosphate receptor; PDBTitle: human igf2r domain 11
72	d1sq1a_	Alignment	not modelled	14.8	67	Fold: Chorismate synthase, AroC Superfamily: Chorismate synthase, AroC Family: Chorismate synthase, AroC
73	d1z6ra3	Alignment	not modelled	14.3	27	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
74	d1tpna_	Alignment	not modelled	14.3	57	Fold: Fn1-like domain Superfamily: Fn1-like domain Family: Fibronectin type I module
75	c2rg8A_	Alignment	not modelled	13.8	19	PDB header: apoptosis, translation Chain: A: PDB Molecule: programmed cell death protein 4; PDBTitle: crystal structure of programmed for cell death 4 middle ma32 domain
76	c2fwrA_	Alignment	not modelled	13.7	83	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad25; PDBTitle: structure of archaeoglobus fulgidis xpb
77	c2apnA_	Alignment	not modelled	13.6	67	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hi1723; PDBTitle: hi1723 solution structure
78	c1k5kA_	Alignment	not modelled	13.6	67	PDB header: transcription Chain: A: PDB Molecule: tat protein; PDBTitle: homonuclear 1h nuclear magnetic resonance assignment and2 structural characterization of hiv-1 tat mal protein
79	c1hv8B_	Alignment	not modelled	13.3	67	PDB header: rna binding protein Chain: B: PDB Molecule: putative atp-dependent rna helicase mj0669; PDBTitle: crystal structure of a dead box protein from the2 hyperthermophile methanococcus jannaschii
80	c1zfnA_	Alignment	not modelled	12.5	63	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase thif; PDBTitle: structural analysis of escherichia coli thif
81	d3d4ub2	Alignment	not modelled	12.4	78	Fold: Defensin-like Superfamily: Defensin-like Family: Tick carboxypeptidase inhibitor-like

82	c1gqbB_	Alignment	not modelled	11.9	46	PDB header: receptor Chain: B: PDB Molecule: cation-independent mannose-6-phosphate receptor; PDBTitle: human mir-receptor, repeat 11
83	d1oywa2	Alignment	not modelled	11.7	67	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
84	c1imtA_	Alignment	not modelled	11.7	50	PDB header: toxin Chain: A: PDB Molecule: intestinal toxin 1; PDBTitle: mamba intestinal toxin 1, nmr, 39 structures
85	c3s8vX_	Alignment	not modelled	11.6	67	PDB header: signaling protein Chain: X: PDB Molecule: dickkopf-related protein 1; PDBTitle: crystal structure of lrp6-dkk1 complex
86	d1rifa_	Alignment	not modelled	11.6	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: DNA helicase UvsW
87	d1iqa2	Alignment	not modelled	11.6	67	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
88	d1pbya1	Alignment	not modelled	11.4	16	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
89	d1qypa_	Alignment	not modelled	11.4	40	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
90	c3fhtA_	Alignment	not modelled	11.2	50	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: crystal structure of human dbp5 in complex with amppnp and rna
91	c1aq5C_	Alignment	not modelled	11.0	64	PDB header: coiled-coil Chain: C: PDB Molecule: cartilage matrix protein; PDBTitle: high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
92	c2gajA_	Alignment	not modelled	11.0	25	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase i; PDBTitle: structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
93	c2elrA_	Alignment	not modelled	11.0	100	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 15th c2h2 zinc finger of human2 zinc finger protein 406
94	d1uhwa_	Alignment	not modelled	10.9	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
95	c2j04C_	Alignment	not modelled	10.9	15	PDB header: transcription Chain: C: PDB Molecule: hypothetical protein ypl007c; PDBTitle: the tau60-tau91 subcomplex of yeast transcription factor2 iiic
96	c2bx9J_	Alignment	not modelled	10.9	75	PDB header: transcription regulation Chain: J: PDB Molecule: tryptophan rna-binding attenuator protein-inhibitory PDBTitle: crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
97	d1khda1	Alignment	not modelled	10.9	14	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
98	c3i5yA_	Alignment	not modelled	10.9	50	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase mss116; PDBTitle: structure of mss116p bound to ssrna containing a single 5-bru and amp-2 pnp
99	d1gkub1	Alignment	not modelled	10.7	67	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase