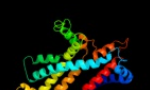
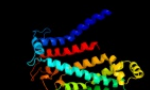
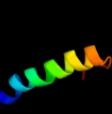
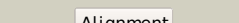
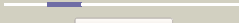
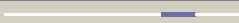


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r6gF_	 Alignment		100.0	100	PDB header: hydrolase/transport protein Chain: F: PDB Molecule: maltose transport system permease protein malf; PDBTitle: the crystal structure of the e. coli maltose transporter
2	c3fh6F_	 Alignment		100.0	85	PDB header: transport protein Chain: F: PDB Molecule: maltose transport system permease protein malf; PDBTitle: crystal structure of the resting state maltose transporter from e.2 coli
3	d2r6gf2	 Alignment		100.0	100	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
4	c2onkC_	 Alignment		100.0	16	PDB header: membrane protein Chain: C: PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
5	d2onkc1	 Alignment		100.0	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
6	c3d31D_	 Alignment		100.0	15	PDB header: transport protein Chain: D: PDB Molecule: sulfate/molybdate abc transporter, permease PDBTitle: modbc from methanosarcina acetivorans
7	d3d31c1	 Alignment		100.0	15	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	d2r6gg1	 Alignment		100.0	18	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
9	d3dhwa1	 Alignment		99.8	18	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	d2r6gf1	 Alignment		99.6	100	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
11	d1ntca_	 Alignment		53.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like

12	d1umqa_	 Alignment		50.2	3	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
13	c1umqA_	 Alignment		50.2	3	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
14	d1fipa_	 Alignment		42.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
15	d1etob_	 Alignment		37.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	d1etxa_	 Alignment		34.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
17	c3e7lD_	 Alignment		30.8	21	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
18	c2hx6A_	 Alignment		29.0	23	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
19	d2auwa1	 Alignment		24.8	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
20	d1g2ha_	 Alignment		23.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
21	c2jwaA_	 Alignment	not modelled	15.3	15	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
22	c2auwB_	 Alignment	not modelled	13.8	26	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
23	d1cf7a_	 Alignment	not modelled	11.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cell cycle transcription factor e2f-dp
24	c2cw1A_	 Alignment	not modelled	11.5	14	PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein
25	d1wdva_	 Alignment	not modelled	11.4	22	Fold: YbaK/ProRS associated domain Superfamily: YbaK/ProRS associated domain Family: YbaK/ProRS associated domain
26	c1pyuD_	 Alignment	not modelled	11.3	31	PDB header: lyase Chain: D: PDB Molecule: aspartate 1-decarboxylase alfa chain; PDBTitle: processed aspartate decarboxylase mutant with ser25 mutated to cys
27	d1v54g_	 Alignment	not modelled	11.3	18	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIa Family: Mitochondrial cytochrome c oxidase subunit VIa
28	c1lijA_	 Alignment	not modelled	10.9	26	PDB header: signaling protein Chain: A: PDB Molecule: erbb-2 receptor protein-tyrosine kinase; PDBTitle: solution structure of the neu/erbb-2 membrane spanning2 segment
						PDB header: hydrolase/dna

29	c2d7dB_	Alignment	not modelled	10.0	12	Chain: B: PDB Molecule: 40-mer from uvrabc system protein b; PDBTitle: structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
30	d1vz0a1	Alignment	not modelled	10.0	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
31	d2diiA1	Alignment	not modelled	9.7	22	Fold: BSD domain-like Superfamily: BSD domain-like Family: BSD domain
32	d2jdih2	Alignment	not modelled	9.4	11	Fold: Epsilon subunit of F1F0-ATP synthase N-terminal domain Superfamily: Epsilon subunit of F1F0-ATP synthase N-terminal domain Family: Epsilon subunit of F1F0-ATP synthase N-terminal domain
33	c2diiA_	Alignment	not modelled	9.0	22	PDB header: transcription Chain: A: PDB Molecule: tfiih basal transcription factor complex p62 PDBTitle: solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
34	c1ql1A_	Alignment	not modelled	8.8	19	PDB header: virus Chain: A: PDB Molecule: pf1 bacteriophage coat protein b; PDBTitle: inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
35	c2cx5B_	Alignment	not modelled	8.7	22	PDB header: translation Chain: B: PDB Molecule: a putative trans-editing enzyme; PDBTitle: crystal structure of a putative trans-editing enzyme for2 prolyl trna synthetase
36	c1vc3B_	Alignment	not modelled	8.6	23	PDB header: lyase Chain: B: PDB Molecule: l-aspartate-alpha-decarboxylase heavy chain; PDBTitle: crystal structure of l-aspartate-alpha-decarboxylase
37	d2ns0a1	Alignment	not modelled	8.3	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
38	c3hd7A_	Alignment	not modelled	8.2	17	PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
39	c3plxB_	Alignment	not modelled	8.1	31	PDB header: lyase Chain: B: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168
40	c2l2tA_	Alignment	not modelled	8.0	26	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-4; PDBTitle: solution nmr structure of the erbb4 dimeric membrane domain
41	c2voyG_	Alignment	not modelled	7.8	18	PDB header: hydrolase Chain: G: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
42	d3fapb_	Alignment	not modelled	7.5	32	Fold: Four-helical up-and-down bundle Superfamily: FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) Family: FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP)
43	c1twcF_	Alignment	not modelled	7.4	29	PDB header: transcription Chain: F: PDB Molecule: dna-directed rna polymerases i, ii, and iii 23 PDBTitle: rna polymerase ii complexed with gtp
44	d1twff_	Alignment	not modelled	7.4	29	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6
45	d1ppya_	Alignment	not modelled	7.2	31	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Pyruvoyl dependent aspartate decarboxylase, ADC
46	c2pmzW_	Alignment	not modelled	7.2	29	PDB header: translation, transferase Chain: W: PDB Molecule: dna-directed rna polymerase subunit k; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
47	c1ptlB_	Alignment	not modelled	7.2	31	PDB header: lyase Chain: B: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
48	d1st6a6	Alignment	not modelled	7.1	7	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
49	d1bl0a1	Alignment	not modelled	7.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
50	c1uheA_	Alignment	not modelled	7.0	23	PDB header: lyase Chain: A: PDB Molecule: aspartate 1-decarboxylase alpha chain; PDBTitle: crystal structure of aspartate decarboxylase, isoasparagine complex
51	c2k53A_	Alignment	not modelled	6.9	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a3dk08 protein; PDBTitle: nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
52	d2axtz1	Alignment	not modelled	6.9	15	Fold: Transmembrane helix hairpin Superfamily: PsbZ-like Family: PsbZ-like
53	c2k5eA_	Alignment	not modelled	6.6	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
						Fold: Putative DNA-binding domain

54	d1jicb2	Alignment	not modelled	6.5	9	Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
55	d1qkla	Alignment	not modelled	6.4	29	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6
56	d1ku7a	Alignment	not modelled	6.4	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
57	d1clia1	Alignment	not modelled	6.3	9	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
58	d1clib1	Alignment	not modelled	6.3	8	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
59	d1i3ja	Alignment	not modelled	6.2	9	Fold: DNA-binding domain of intron-encoded endonucleases Superfamily: DNA-binding domain of intron-encoded endonucleases Family: DNA-binding domain of intron-encoded endonucleases
60	c2i5gB	Alignment	not modelled	6.2	7	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from pseudomonas2 aeruginosa
61	c2c45F	Alignment	not modelled	6.1	31	PDB header: lyase Chain: F: PDB Molecule: aspartate 1-decarboxylase precursor; PDBTitle: native precursor of pyruvoyl dependent aspartate2 decarboxylase
62	c3t72o	Alignment	not modelled	6.1	11	PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
63	c1r71B	Alignment	not modelled	6.0	5	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in2 complex with the operator dna
64	c2g9jA	Alignment	not modelled	6.0	86	PDB header: structural protein Chain: A: PDB Molecule: tropomyosin 1 alpha chain/general control protein PDBTitle: complex of tm1a(1-14)zip with tm9a(251-284): a model for the2 polymerization domain ("overlap region") of tropomyosin,3 northeast structural genomics target or9
65	c1l0oC	Alignment	not modelled	6.0	12	PDB header: protein binding Chain: C: PDB Molecule: sigma factor; PDBTitle: crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
66	d1l0oc	Alignment	not modelled	6.0	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
67	c3mkuA	Alignment	not modelled	6.0	11	PDB header: transport protein Chain: A: PDB Molecule: multi antimicrobial extrusion protein (na(+)/drug PDBTitle: structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
68	d1coka	Alignment	not modelled	5.9	26	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
69	d1jhfa1	Alignment	not modelled	5.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
70	c3qkbB	Alignment	not modelled	5.9	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
71	c3h0gF	Alignment	not modelled	5.9	29	PDB header: transcription Chain: F: PDB Molecule: dna-directed rna polymerases i, ii, and iii PDBTitle: rna polymerase ii from schizosaccharomyces pombe
72	d1h6gb1	Alignment	not modelled	5.8	13	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
73	c3ougA	Alignment	not modelled	5.8	8	PDB header: lyase Chain: A: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis
74	c2kfsA	Alignment	not modelled	5.8	15	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
75	d1vr4a1	Alignment	not modelled	5.7	31	Fold: Dodecin subunit-like Superfamily: YbjQ-like Family: YbjQ-like
76	c3op6B	Alignment	not modelled	5.7	17	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an oligo-nucleotide binding protein (lpg1207)2 from legionella pneumophila subsp. pneumophila str. philadelphia 1 at3 2.00 a resolution
77	d1brwa3	Alignment	not modelled	5.7	38	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
78	c2latA	Alignment	not modelled	5.7	21	PDB header: membrane protein Chain: A: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: solution structure of a human minimembrane protein ost4

79	d3c9ua1	Alignment	not modelled	5.6	5	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
80	c2ka6B	Alignment	not modelled	5.6	31	PDB header: transcription regulator Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: nmr structure of the cbp-taz2/stat1-tad complex
81	d2oz6a1	Alignment	not modelled	5.5	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
82	clsneA	Alignment	not modelled	5.5	31	PDB header: de novo protein Chain: A: PDB Molecule: tetrameric beta-beta-alpha mini-protein; PDBTitle: an oligomeric domain-swapped beta-beta-alpha mini-protein
83	clsneB	Alignment	not modelled	5.5	31	PDB header: de novo protein Chain: B: PDB Molecule: tetrameric beta-beta-alpha mini-protein; PDBTitle: an oligomeric domain-swapped beta-beta-alpha mini-protein
84	d1p77a2	Alignment	not modelled	5.4	11	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
85	d2tpa3	Alignment	not modelled	5.4	31	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
86	d2hqva1	Alignment	not modelled	5.3	17	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: ChuX-like
87	c3rkoF	Alignment	not modelled	5.3	18	PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
88	d2phcb1	Alignment	not modelled	5.3	9	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
89	c1y2lC	Alignment	not modelled	5.3	23	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein s0862; PDBTitle: crystal structure of mcs9 target apc27401 from shigella2 flexneri
90	d1y2ia	Alignment	not modelled	5.3	23	Fold: Dodecin subunit-like Superfamily: YbjQ-like Family: YbjQ-like
91	c1y6uA	Alignment	not modelled	5.3	25	PDB header: dna binding protein Chain: A: PDB Molecule: excisionase from transposon tn916; PDBTitle: the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
92	d1i5za1	Alignment	not modelled	5.3	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
93	c2ph0A	Alignment	not modelled	5.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q6d2t7_erwct protein from erwinia2 carotovora. nesg target ewr41.
94	c2oviA	Alignment	not modelled	5.3	6	PDB header: ligand binding protein, metal transport Chain: A: PDB Molecule: hypothetical protein chux; PDBTitle: structure of the heme binding protein chux
95	d1ku2a1	Alignment	not modelled	5.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
96	c1rkcb	Alignment	not modelled	5.1	25	PDB header: cell adhesion, structural protein Chain: B: PDB Molecule: talín; PDBTitle: human vinculin head (1-258) in complex with talin's2 vinculin binding site 3 (residues 1944-1969)
97	c2r2vB	Alignment	not modelled	5.1	38	PDB header: de novo protein Chain: B: PDB Molecule: gcn4 leucine zipper; PDBTitle: sequence determinants of the topology of the lac repressor2 tetrameric coiled coil
98	d1ilga1	Alignment	not modelled	5.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
99	c1jb0X	Alignment	not modelled	5.0	33	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem i subunit psax; PDBTitle: crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria