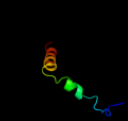
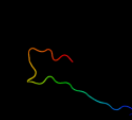
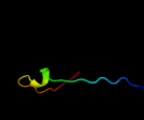
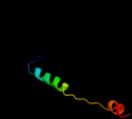
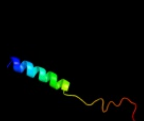
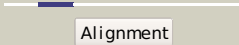
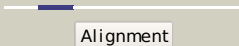
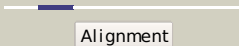
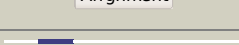
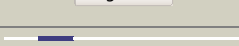
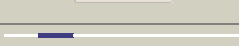
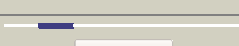
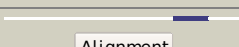
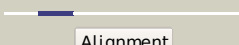
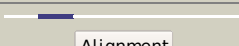
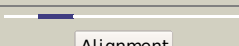
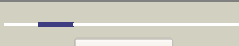
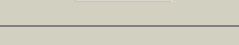
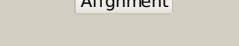
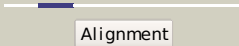
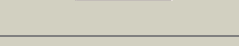
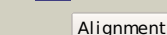
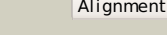
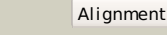
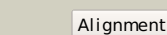
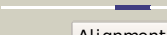
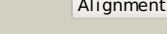
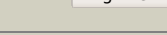
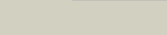
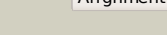
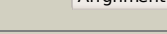


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qnqD_	 Alignment		100.0	12	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the 2 n,n'-diacetylchitobiose-specific phosphotransferase system
2	c3ipjB_	 Alignment		99.9	27	PDB header: transferase Chain: B: PDB Molecule: pts system, iiabc component; PDBTitle: the crystal structure of one domain of the pts system, iiabc component2 from clostridium difficile
3	c1ibaA_	 Alignment		99.8	22	PDB header: phosphotransferase Chain: A: PDB Molecule: glucose permease; PDBTitle: glucose permease (domain iib), nmr, 11 structures
4	d3bp8c1	 Alignment		99.8	21	Fold: Homing endonuclease-like Superfamily: Glucose permease domain IIB Family: Glucose permease domain IIB
5	c2voyB_	 Alignment		48.2	18	PDB header: hydrolase Chain: B: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: cryoem model of copa, the copper transporting atpase from 2 archaeoglobus fulgidus
6	c3sy6A_	 Alignment		44.2	21	PDB header: cell adhesion Chain: A: PDB Molecule: fimbrial protein bf1861; PDBTitle: crystal structure of a fimbrial protein bf1861 [bacteroides fragilis2 nctc 9343] (bf1861) from bacteroides fragilis nctc 9343 at 1.90 a3 resolution
7	c3t2IA_	 Alignment		39.2	16	PDB header: cell adhesion Chain: A: PDB Molecule: putative cell adhesion protein; PDBTitle: crystal structure of a putative cell adhesion protein (bf1858) from 2 bacteroides fragilis nctc 9343 at 2.33 a resolution
8	c2janD_	 Alignment		29.3	24	PDB header: ligase Chain: D: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from mycobacterium tuberculosis in 2 unliganded state
9	c2kncB_	 Alignment		25.7	14	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfa iib-beta3 transmembrane-cytoplasmic2 heterocomplex
10	c2kncA_	 Alignment		25.4	6	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfa iib-beta3 transmembrane-cytoplasmic2 heterocomplex
11	d1ffgb_	 Alignment		23.5	10	Fold: Ferredoxin-like Superfamily: CheY-binding domain of CheA Family: CheY-binding domain of CheA

12	c1a0oH_	Alignment		22.6	10	PDB header: chemotaxis Chain: H: PDB Molecule: chea; PDBTitle: chey-binding domain of chea in complex with chey
13	c2pmuD_	Alignment		19.4	15	PDB header: transcription regulation Chain: D: PDB Molecule: response regulator phop; PDBTitle: crystal structure of the dna-binding domain of phop
14	c2hqnA_	Alignment		18.8	12	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
15	c1m6yA_	Alignment		17.3	11	PDB header: transferase Chain: A: PDB Molecule: s-adenosyl-methyltransferase mraw; PDBTitle: crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah
16	d1pu6a_	Alignment		17.0	4	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
17	d2bgwa1	Alignment		16.8	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
18	d1vgga_	Alignment		16.4	22	Fold: Ta1353-like Superfamily: Ta1353-like Family: Ta1353-like
19	d1kgsa1	Alignment		16.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
20	d1vr6a1	Alignment		15.2	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
21	d1ciya1	Alignment	not modelled	15.2	26	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: delta-Endotoxin, C-terminal domain
22	d2cyya2	Alignment	not modelled	15.0	11	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
23	d1gxqa_	Alignment	not modelled	14.9	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
24	d2gola1	Alignment	not modelled	14.6	8	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: Immunodeficiency virus matrix proteins
25	c3zqsB_	Alignment	not modelled	14.6	11	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase fancI; PDBTitle: human fancI central domain
26	c1oy8A_	Alignment	not modelled	14.6	17	PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
27	c2wshC_	Alignment	not modelled	14.5	10	PDB header: hydrolase Chain: C: PDB Molecule: endonuclease ii; PDBTitle: structure of bacteriophage t4 endoii e118a mutant
28	d1ji6a1	Alignment	not modelled	12.9	26	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: delta-Endotoxin, C-terminal domain
29	c3k8hA_	Alignment	not modelled	12.5	25	PDB header: membrane protein Chain: A: PDB Molecule: 30kIp;

					PDBTitle: structure of crystal form i of tp0453
30	d2cfua2	Alignment	not modelled	12.3	21 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like
31	c1vbka	Alignment	not modelled	11.8	9 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
32	c3ufia	Alignment	not modelled	10.9	17 PDB header: cell adhesion Chain: A: PDB Molecule: hypothetical protein bacova_04980; PDBTitle: crystal structure of a hypothetical protein2 bacova_04980(zp_02067969.1) from bacteroides ovatus atcc 8483 at 2.183 a resolution
33	c2cfua	Alignment	not modelled	10.8	21 PDB header: hydrolase Chain: A: PDB Molecule: sdsa1; PDBTitle: crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
34	d1qu3a1	Alignment	not modelled	10.7	10 Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
35	d2a5la1	Alignment	not modelled	10.2	11 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
36	d1wlqc	Alignment	not modelled	10.1	15 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DNA replication factor Cdt1
37	d1mwza	Alignment	not modelled	10.1	12 Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
38	c3ibwa	Alignment	not modelled	10.0	8 PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
39	c2jnhA	Alignment	not modelled	10.0	7 PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase cbl-b; PDBTitle: solution structure of the uba domain from cbl-b
40	c2ekmC	Alignment	not modelled	9.8	30 PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein st1511; PDBTitle: structure of st1219 protein from sulfolobus tokodaii
41	d2r7da2	Alignment	not modelled	9.8	14 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RNB domain-like
42	c2ql0A	Alignment	not modelled	9.6	33 PDB header: transferase Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: structure of pae2307 in complex with adenosine
43	d1fzda	Alignment	not modelled	9.6	22 Fold: Fibrinogen C-terminal domain-like Superfamily: Fibrinogen C-terminal domain-like Family: Fibrinogen C-terminal domain-like
44	d1l6na1	Alignment	not modelled	9.4	8 Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: Immunodeficiency virus matrix proteins
45	c2j61B	Alignment	not modelled	9.0	26 PDB header: lectin Chain: B: PDB Molecule: ficolin-2; PDBTitle: I-ficolin complexed to n-acetylglucosamine (forme c)
46	d1l1ga2	Alignment	not modelled	8.4	10 Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
47	d2prra1	Alignment	not modelled	8.3	24 Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
48	c2jzyA	Alignment	not modelled	8.2	19 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein pcor; PDBTitle: solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
49	c2bbjB	Alignment	not modelled	8.2	13 PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
50	d1tama	Alignment	not modelled	8.1	8 Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: Immunodeficiency virus matrix proteins
51	c2k5eA	Alignment	not modelled	8.1	13 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
52	d1od5a2	Alignment	not modelled	7.9	22 Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
53	d1lwub1	Alignment	not modelled	7.7	13 Fold: Fibrinogen C-terminal domain-like Superfamily: Fibrinogen C-terminal domain-like Family: Fibrinogen C-terminal domain-like
54	d1hiwa	Alignment	not modelled	7.7	4 Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: Immunodeficiency virus matrix proteins

55	c2xv4S	 Alignment	not modelled	7.6	15	PDB header: transcription Chain: S: PDB Molecule: dna-directed rna polymerase iii subunit rpc3; PDBTitle: structure of human rpc62 (partial)
56	c2do6A	 Alignment	not modelled	7.6	7	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase cbl-b; PDBTitle: solution structure of rsgi ruh-065, a uba domain from human2 cdna
57	d1m1jc1	 Alignment	not modelled	7.3	26	Fold: Fibrinogen C-terminal domain-like Superfamily: Fibrinogen C-terminal domain-like Family: Fibrinogen C-terminal domain-like
58	d1ffya1	 Alignment	not modelled	7.3	12	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
59	d1rrqa1	 Alignment	not modelled	7.3	11	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
60	c2aj1A	 Alignment	not modelled	7.3	13	PDB header: hydrolase Chain: A: PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada
61	d1x0pa1	 Alignment	not modelled	7.2	24	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: BLUF domain
62	d2a1jb1	 Alignment	not modelled	7.2	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
63	d1ngka	 Alignment	not modelled	7.2	15	Fold: Globin-like Superfamily: Globin-like Family: Truncated hemoglobin
64	c2d9sA	 Alignment	not modelled	7.2	7	PDB header: ligase Chain: A: PDB Molecule: cbl e3 ubiquitin protein ligase; PDBTitle: solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
65	d1j9ia	 Alignment	not modelled	7.1	8	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
66	d1x2ia1	 Alignment	not modelled	7.0	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
67	d1orna	 Alignment	not modelled	7.0	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
68	d1j4na	 Alignment	not modelled	7.0	14	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
69	d1dlca1	 Alignment	not modelled	7.0	39	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: delta-Endotoxin, C-terminal domain
70	c2ksaA	 Alignment	not modelled	6.9	25	PDB header: unknown function Chain: A: PDB Molecule: cyanoglobin; PDBTitle: solution structure of synechococcus sp. pcc 7002 hemoglobin
71	c1dlcA	 Alignment	not modelled	6.9	32	PDB header: toxin Chain: A: PDB Molecule: delta-endotoxin cryiiaa; PDBTitle: crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution
72	d1fida	 Alignment	not modelled	6.9	30	Fold: Fibrinogen C-terminal domain-like Superfamily: Fibrinogen C-terminal domain-like Family: Fibrinogen C-terminal domain-like
73	c2e1cA	 Alignment	not modelled	6.9	10	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
74	c1p68A	 Alignment	not modelled	6.7	29	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein s-824; PDBTitle: solution structure of s-824, a de novo designed four helix2 bundle
75	d1fftb2	 Alignment	not modelled	6.6	12	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
76	c2zbcH	 Alignment	not modelled	6.6	13	PDB header: transcription Chain: H: PDB Molecule: 83aa long hypothetical transcriptional regulator asnc; PDBTitle: crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
77	c2r7fA	 Alignment	not modelled	6.6	14	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease ii family protein; PDBTitle: crystal structure of ribonuclease ii family protein from deinococcus2 radiodurans, hexagonal crystal form. northeast structural genomics3 target drr63
78	d1m1ha2	 Alignment	not modelled	6.5	13	Fold: Ferredoxin-like Superfamily: N-utilization substance G protein NusG, N-terminal domain Family: N-utilization substance G protein NusG, N-terminal domain
79	c3aq8A	 Alignment	not modelled	6.5	17	PDB header: oxygen binding Chain: A: PDB Molecule: group 1 truncated hemoglobin; PDBTitle: crystal structure of truncated hemoglobin from tetrahymena pyriformis, 2 q46e mutant, fe(iii) form

80	c2djwF_	 Alignment	not modelled	6.4	25	PDB header: unknown function Chain: F: PDB Molecule: probable transcriptional regulator, asnc family; PDBTitle: crystal structure of ttha0845 from thermus thermophilus hb8
81	c3pcoD_	 Alignment	not modelled	6.4	15	PDB header: ligase Chain: D: PDB Molecule: phenylalanyl-trna synthetase, beta chain; PDBTitle: crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
82	c2w1oA_	 Alignment	not modelled	6.4	25	PDB header: translation Chain: A: PDB Molecule: 60s acidic ribosomal protein p2; PDBTitle: nmr structure of dimerization domain of human ribosomal2 protein p2
83	c2jsxA_	 Alignment	not modelled	6.4	8	PDB header: chaperone Chain: A: PDB Molecule: protein napd; PDBTitle: solution structure of the e. coli tat proofreading2 chaperone protein napd
84	d1s69a_	 Alignment	not modelled	6.3	25	Fold: Globin-like Superfamily: Globin-like Family: Truncated hemoglobin
85	d2csba3	 Alignment	not modelled	6.2	17	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
86	d1ilea1	 Alignment	not modelled	6.2	15	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
87	c2hfnJ_	 Alignment	not modelled	6.2	24	PDB header: electron transport Chain: J: PDB Molecule: synechocystis photoreceptor (slr1694); PDBTitle: crystal structures of the synechocystis photoreceptor slr1694 reveal2 distinct structural states related to signaling
88	d2vv5a3	 Alignment	not modelled	6.2	10	Fold: Mechanosensitive channel protein MscS (YggB), transmembrane region Superfamily: Mechanosensitive channel protein MscS (YggB), transmembrane region Family: Mechanosensitive channel protein MscS (YggB), transmembrane region
89	c3bvhc_	 Alignment	not modelled	6.1	30	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
90	d1jida_	 Alignment	not modelled	6.1	40	Fold: SRP19 Superfamily: SRP19 Family: SRP19
91	d1vpba_	 Alignment	not modelled	6.0	13	Fold: Putative modulator of DNA gyrase, PmbA/TldD Superfamily: Putative modulator of DNA gyrase, PmbA/TldD Family: Putative modulator of DNA gyrase, PmbA/TldD
92	d1rzsa_	 Alignment	not modelled	6.0	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
93	c1jb7A_	 Alignment	not modelled	6.0	14	PDB header: dna-binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: dna g-quartets in a 1.86 a resolution structure of an oxytricha nova2 telomeric protein-dna complex
94	c1ph4A_	 Alignment	not modelled	6.0	14	PDB header: dna binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: crystal structure of the oxytricha nova telomere end-binding protein2 complexed with noncognate ssdna ggggtttggcg
95	d1f7ua3	 Alignment	not modelled	6.0	12	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain Family: Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
96	c2jvaA_	 Alignment	not modelled	6.0	23	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase domain protein; PDBTitle: nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211
97	d2cfxa2	 Alignment	not modelled	6.0	25	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
98	d1re3b1	 Alignment	not modelled	5.9	17	Fold: Fibrinogen C-terminal domain-like Superfamily: Fibrinogen C-terminal domain-like Family: Fibrinogen C-terminal domain-like
99	c2kddB_	 Alignment	not modelled	5.8	31	PDB header: cell cycle Chain: B: PDB Molecule: borealin; PDBTitle: solution structure of the conserved c-terminal dimerization2 domain of borealin