













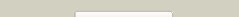
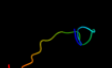



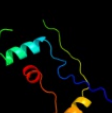

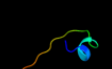
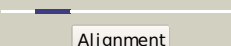
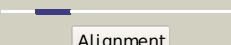
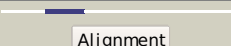
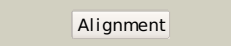
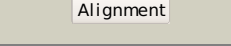
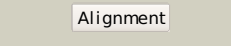

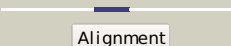

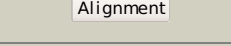
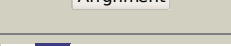
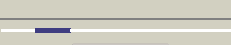


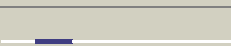

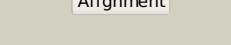
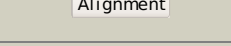
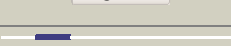




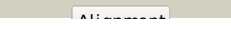



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kd8E_	 Alignment		32.5	18	PDB header: de novo protein Chain: E: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16v base-d12la16l
2	c3lg8B_	 Alignment		24.6	31	PDB header: hydrolase Chain: B: PDB Molecule: a-type atp synthase subunit e; PDBTitle: crystal structure of the c-terminal part of subunit e (e101-206) from2 methanocaldococcus jannaschii of a1ao atp synthase
3	c2f9jP_	 Alignment		24.3	50	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
4	d1gt0c1	 Alignment		16.0	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
5	d2qi2a1	 Alignment		15.3	25	Fold: Sm-like fold Superfamily: Dom34/Pelota N-terminal domain-like Family: Dom34/Pelota N-terminal domain-like
6	c3lydA_	 Alignment		13.6	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative uncharacterized protein from jonesia2 denitrificans
7	d1xl7a2	 Alignment		13.0	17	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
8	c1e2vB_	 Alignment		12.7	38	PDB header: electron transport proteins Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii
9	c2qi2A_	 Alignment		12.5	25	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein pelota related protein; PDBTitle: crystal structure of the thermoplasma acidophilum pelota2 protein
10	d1y1pa1	 Alignment		12.2	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
11	d1vf5c1	 Alignment		12.2	33	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain

12	c3mcaB_	Alignment		11.6	20	PDB header: translation regulation/hydrolase Chain: B: PDB Molecule: protein dom34; PDBTitle: structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
13	d1ci3m1	Alignment		11.1	40	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
14	d1e2wa1	Alignment		11.0	40	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
15	c2zkrx_	Alignment		10.5	67	PDB header: ribosomal protein/rna Chain: X: PDB Molecule: rna helices; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
16	c2fipA_	Alignment		10.4	30	PDB header: transcription Chain: A: PDB Molecule: late genes activator; PDBTitle: phage phi29 transcription regulator p4
17	d2vgna1	Alignment		10.4	31	Fold: Sm-like fold Superfamily: Dom34/Pelota N-terminal domain-like Family: Dom34/Pelota N-terminal domain-like
18	d1hcza1	Alignment		10.3	35	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
19	c3jywW_	Alignment		10.2	33	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l31(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
20	d1yu3a2	Alignment		10.1	40	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Mtd variable domain
21	c3agjD_	Alignment	not modelled	10.1	21	PDB header: translation/hydrolase Chain: D: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
22	c3agjB_	Alignment	not modelled	10.1	21	PDB header: translation/hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
23	d1em8b_	Alignment	not modelled	9.9	25	Fold: DNA polymerase III psi subunit Superfamily: DNA polymerase III psi subunit Family: DNA polymerase III psi subunit
24	d1whza_	Alignment	not modelled	9.9	25	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: YcfA-like
25	c2j376_	Alignment	not modelled	9.6	44	PDB header: ribosome Chain: 6: PDB Molecule: ribosomal protein l31; PDBTitle: model of mammalian srp bound to 80s rncs
26	c2h4tB_	Alignment	not modelled	9.5	21	PDB header: transferase Chain: B: PDB Molecule: carnitine o-palmitoyltransferase ii, PDBTitle: crystal structure of rat carnitine palmitoyltransferase ii
27	c3obyB_	Alignment	not modelled	9.5	21	PDB header: hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity PDB header: photosynthesis Chain: C: PDB Molecule: apocytochrome f; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
28	c2e75C_	Alignment	not modelled	9.4	33	PDB header: structural genomics, unknown function

29	c3kztB_	Alignment	not modelled	9.4	21	Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_812423.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
30	c3obwA_	Alignment	not modelled	9.2	19	PDB header: hydrolase Chain: A: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity
31	c3nauA_	Alignment	not modelled	9.2	13	PDB header: transcription Chain: A: PDB Molecule: zinc fingers and homeoboxes protein 2; PDBTitle: crystal structure of zhx2 hd2 (zinc-fingers and homeoboxes protein 2,2 homeodomain 2)
32	d1pufa_	Alignment	not modelled	9.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
33	c4a1eW_	Alignment	not modelled	9.2	44	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l31; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
34	c3m9vA_	Alignment	not modelled	9.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent oxidoreductase; PDBTitle: x-ray structure of a kjid3 in complex with dtdp
35	d1vqox1	Alignment	not modelled	8.9	56	Fold: Ribosomal protein L31e Superfamily: Ribosomal protein L31e Family: Ribosomal protein L31e
36	d1vkra_	Alignment	not modelled	8.8	22	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
37	c1vkrA_	Alignment	not modelled	8.8	22	PDB header: transferase Chain: A: PDB Molecule: mannitol-specific pts system enzyme iibc components; PDBTitle: structure of iib domain of the mannitol-specific permease enzyme ii
38	c2jxmB_	Alignment	not modelled	8.6	33	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
39	c3nbmA_	Alignment	not modelled	8.5	10	PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
40	d1yu0a2	Alignment	not modelled	8.4	40	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Mtd variable domain
41	c1t6fA_	Alignment	not modelled	8.4	19	PDB header: cell cycle Chain: A: PDB Molecule: geminin; PDBTitle: crystal structure of the coiled-coil dimerization motif of2 geminin
42	c1ctmA_	Alignment	not modelled	8.4	35	PDB header: electron transport(cytochrome) Chain: A: PDB Molecule: cytochrome f; PDBTitle: crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
43	d1w6ga2	Alignment	not modelled	8.4	13	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
44	d1pzra_	Alignment	not modelled	8.1	25	Fold: HLH-like Superfamily: Docking domain B of the erythromycin polyketide synthase (DEBS) Family: Docking domain B of the erythromycin polyketide synthase (DEBS)
45	d1nk3p_	Alignment	not modelled	8.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
46	c3phfX_	Alignment	not modelled	7.8	33	PDB header: viral protein Chain: X: PDB Molecule: envelope glycoprotein I; PDBTitle: crystal structure of the epstein-barr virus gh and gl complex
47	c1q90A_	Alignment	not modelled	7.8	38	PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastoquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
48	d9anta_	Alignment	not modelled	7.7	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
49	d1f43a_	Alignment	not modelled	7.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
50	c2pd0D_	Alignment	not modelled	7.2	29	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: protein cgd2_2020 from cryptosporidium parvum
51	d1tu2b1	Alignment	not modelled	7.2	33	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
52	d1mh3a1	Alignment	not modelled	7.1	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
53	c2zfdB_	Alignment	not modelled	7.1	14	PDB header: signaling protein/transferase Chain: B: PDB Molecule: putative uncharacterized protein t20115_90; PDBTitle: the crystal structure of plant specific calcium binding protein atcb122 in complex with the regulatory domain of atcpk14

54	c2e19A	 Alignment	not modelled	7.0	14	PDB header: transcription Chain: A: PDB Molecule: transcription factor 8; PDBTitle: solution structure of the homeobox domain from human nil-2-2 a zinc finger protein, transcription factor 8
55	c2da1A	 Alignment	not modelled	6.9	25	PDB header: transcription Chain: A: PDB Molecule: alpha-fetoprotein enhancer binding protein; PDBTitle: solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
56	c3hp7A	 Alignment	not modelled	6.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hemolysin, putative; PDBTitle: putative hemolysin from streptococcus thermophilus.
57	d1vnda	 Alignment	not modelled	6.6	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
58	d2k8ea2	 Alignment	not modelled	6.3	21	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
59	c1s1iW	 Alignment	not modelled	6.3	33	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l31; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
60	c1tu2B	 Alignment	not modelled	6.3	33	PDB header: electron transport Chain: B: PDB Molecule: apocytochrome f; PDBTitle: the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
61	d2k49a1	 Alignment	not modelled	6.2	21	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
62	d1le8a	 Alignment	not modelled	6.2	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
63	d1sana	 Alignment	not modelled	6.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
64	c1yfsB	 Alignment	not modelled	6.0	22	PDB header: ligase Chain: B: PDB Molecule: alanyl-trna synthetase; PDBTitle: the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
65	d1fj1b	 Alignment	not modelled	6.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
66	d1bw5a	 Alignment	not modelled	5.8	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
67	c2hl7A	 Alignment	not modelled	5.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
68	c3czcA	 Alignment	not modelled	5.6	33	PDB header: transferase Chain: A: PDB Molecule: rmpb; PDBTitle: the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
69	c2lkyA	 Alignment	not modelled	5.5	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msme1_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
70	d2elca1	 Alignment	not modelled	5.5	12	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
71	c3hxxA	 Alignment	not modelled	5.5	28	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
72	d1iqoa	 Alignment	not modelled	5.5	22	Fold: Hypothetical protein MTH1880 Superfamily: Hypothetical protein MTH1880 Family: Hypothetical protein MTH1880
73	d2fj6a1	 Alignment	not modelled	5.5	18	Fold: SAM domain-like Superfamily: YozE-like Family: YozE-like
74	c2iouC	 Alignment	not modelled	5.5	40	PDB header: viral protein/membrane protein Chain: C: PDB Molecule: major tropism determinant p1; PDBTitle: major tropism determinant p1 (mtd-p1) variant complexed with2 bordetella brochiseptica virulence factor pertactin extracellular3 domain (prn-e).
75	d1ztpa1	 Alignment	not modelled	5.4	18	Fold: eIF4e-like Superfamily: eIF4e-like Family: BLES03-like
76	d1x87a	 Alignment	not modelled	5.3	45	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
77	c3sxuB	 Alignment	not modelled	5.2	25	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit psi; PDBTitle: structure of the e. coli ssb-dna polymerase iii interface
78	c2vnmA	 Alignment	not modelled	5.0	42	PDB header: cell cycle Chain: A: PDB Molecule: dom34;

