

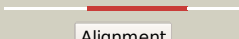
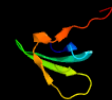
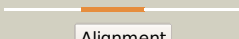
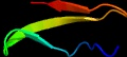





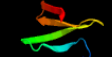
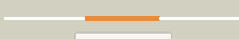

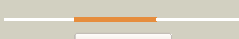

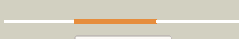
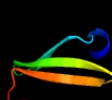
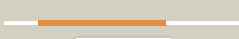





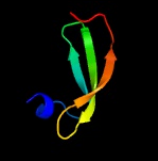
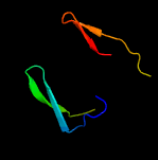

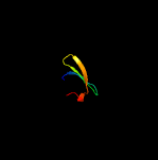


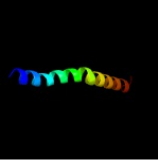


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2588c_(yajC)_2915856_2916203
 Date Wed Aug 7 12:50:22 BST 2019
 Unique Job ID ed961e0069352093

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rddB_	 Alignment		98.9	22	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
2	c4ytlB_	 Alignment		91.6	18	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
3	c2qf4A_	 Alignment		86.7	6	PDB header: structural protein Chain: A: PDB Molecule: cell shape determining protein mrec; PDBTitle: high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
4	c2j5uB_	 Alignment		86.7	26	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
5	c2vv5D_	 Alignment		86.1	19	PDB header: membrane protein Chain: D: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: the open structure of msccs
6	d2do3a1	 Alignment		84.7	19	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
7	d2vv5a1	 Alignment		83.5	19	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
8	d1pkma1	 Alignment		83.2	15	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
9	d2g50a1	 Alignment		83.0	15	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
10	c3t9nG_	 Alignment		81.0	17	PDB header: membrane protein Chain: G: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: crystal structure of a membrane protein
11	c2e6zA_	 Alignment		80.3	24	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: solution structure of the second kow motif of human2 transcription elongation factor spt5

12	c5t4oj_	Alignment		79.7	11	PDB header: hydrolase Chain: J; PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1
13	c4hw9E_	Alignment		79.0	18	PDB header: membrane protein Chain: E; PDB Molecule: mechanosensitive channel mscs; PDBTitle: crystal structure of helicobacter pylori mscs (closed state)
14	d1liua1	Alignment		75.9	15	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
15	c6bs8C_	Alignment		75.6	15	PDB header: hydrolase Chain: C; PDB Molecule: replicative dna helicase; PDBTitle: the class 3 dnab intein from mycobacterium smegmatis
16	d1e0ta1	Alignment		73.0	17	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
17	c2e70A_	Alignment		72.9	9	PDB header: transcription Chain: A; PDB Molecule: transcription elongation factor spt5; PDBTitle: solution structure of the fifth kow motif of human2 transcription elongation factor spt5
18	c6fkip_	Alignment		71.6	11	PDB header: membrane protein Chain: P; PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
19	c6fkib_	Alignment		69.0	6	PDB header: membrane protein Chain: B; PDB Molecule: atp synthase subunit beta, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
20	c4gn0D_	Alignment		57.3	10	PDB header: signaling protein Chain: D; PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
21	d1a3xa1	Alignment	not modelled	56.7	12	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
22	c5nbbA_	Alignment	not modelled	55.0	21	PDB header: chaperone Chain: A; PDB Molecule: rna chaperone proq; PDBTitle: structure of the c-terminal domain of the escherichia coli proq rna2 binding protein
23	c4l0jA_	Alignment	not modelled	54.2	18	PDB header: hydrolase Chain: A; PDB Molecule: dna helicase i; PDBTitle: structure of a translocation signal domain mediating conjugative2 transfer by type iv secretion systems
24	d1nxza1	Alignment	not modelled	53.3	19	Fold: PUA domain-like Superfamily: PUA domain-like Family: Yggj N-terminal domain-like
25	c2n2aA_	Alignment	not modelled	52.9	19	PDB header: membrane protein Chain: A; PDB Molecule: receptor tyrosine-protein kinase erb2-2; PDBTitle: spatial structure of her2/erb2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
26	c1rl2A_	Alignment	not modelled	52.3	17	PDB header: ribosomal protein Chain: A; PDB Molecule: protein (ribosomal protein l2); PDBTitle: ribosomal protein l2 rna-binding domain from bacillus2 stearothermophilus
27	c2lcIA_	Alignment	not modelled	51.8	22	PDB header: transcription Chain: A; PDB Molecule: transcriptional activator rfah; PDBTitle: solution structure of rfah carboxyterminal domain
28	c4gopX_	Alignment	not modelled	51.6	4	PDB header: dna binding protein/dna Chain: X; PDB Molecule: putative uncharacterized protein; PDBTitle: structure and conformational change of a replication protein a2 heterotrimer bound to ssdna PDB header: transcription/rna

29	c5xonW_	Alignment	not modelled	51.3	11	Chain: W: PDB Molecule: protein that forms a complex with spt4p; PDBTitle: rna polymerase ii elongation complex bound with spt4/5 and tfiis
30	d1vhka1	Alignment	not modelled	46.0	14	Fold: PUA domain-like Superfamily: PUA domain-like Family: YggJ N-terminal domain-like
31	d2j01d1	Alignment	not modelled	45.5	21	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
32	d1ib8a1	Alignment	not modelled	45.5	15	Fold: Sm-like fold Superfamily: YhbC-like, C-terminal domain Family: YhbC-like, C-terminal domain
33	c5lp5F_	Alignment	not modelled	45.1	31	PDB header: hydrolase/antibiotic Chain: F: PDB Molecule: rod shape-determining protein (mrec); PDBTitle: complex between penicillin-binding protein (pbp2) and mrec from2 helicobacter pylori
34	d2oara1	Alignment	not modelled	45.0	11	Fold: Gated mechanosensitive channel Superfamily: Gated mechanosensitive channel Family: Gated mechanosensitive channel
35	c2khiA_	Alignment	not modelled	44.4	21	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 4 of the e. coli ribosomal2 protein s1
36	d1nppa2	Alignment	not modelled	43.9	13	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
37	c2mfiA_	Alignment	not modelled	43.7	20	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: domain 1 of e. coli ribosomal protein s1
38	c6fc6A_	Alignment	not modelled	43.7	5	PDB header: cell cycle Chain: A: PDB Molecule: nuclear fusion protein bik1; PDBTitle: bik1 cap-gly domain with etf peptide from bim1
39	c5y4oA_	Alignment	not modelled	42.8	14	PDB header: membrane protein Chain: A: PDB Molecule: low conductance mechanosensitive channel ynai; PDBTitle: cryo-em structure of mscs channel, ynai
40	d3bzka4	Alignment	not modelled	41.6	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
41	c1dbgA_	Alignment	not modelled	41.0	17	PDB header: lyase Chain: A: PDB Molecule: chondroitinase b; PDBTitle: crystal structure of chondroitinase b
42	c3d5bD_	Alignment	not modelled	40.8	17	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l2; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
43	c4uc4A_	Alignment	not modelled	40.2	22	PDB header: replication Chain: A: PDB Molecule: lysine-specific demethylase 4b; PDBTitle: crystal structure of hybrid tudor domain of human lysine demethylase2 kdm4b
44	c5jefA_	Alignment	not modelled	39.9	5	PDB header: transferase Chain: A: PDB Molecule: nitrate/nitrite sensor protein narq; PDBTitle: fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
45	c2l8kA_	Alignment	not modelled	39.7	26	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 7; PDBTitle: nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
46	c2nbgA_	Alignment	not modelled	39.3	16	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: structure of the geobacillus stearotherophilus if2 g3-subdomain
47	d2qamc1	Alignment	not modelled	39.0	17	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
48	c5ohoB_	Alignment	not modelled	38.4	19	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: crystal structure of the kowx-kow4 domain of human dsif
49	c6ir9W_	Alignment	not modelled	38.2	15	PDB header: transcription/rna/dna Chain: W: PDB Molecule: spt5; PDBTitle: rna polymerase ii elongation complex bound with elf1 and spt4/5,2 stalled at shl(-1) of the nucleosome
50	c2khjA_	Alignment	not modelled	37.3	26	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
51	c2mi6A_	Alignment	not modelled	36.0	20	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusg; PDBTitle: solution structure of the carboxy terminal domain of nusg from2 mycobacterium tuberculosis
52	c2jvvA_	Alignment	not modelled	35.9	21	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of e. coli nusg carboxyterminal domain
53	c2kvqG_	Alignment	not modelled	35.9	21	PDB header: transcription Chain: G: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of nuse:nusg-ctd complex
54	d2cp6a1	Alignment	not modelled	35.5	18	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
						PDB header: gene regulation

55	c1d8lA_	Alignment	not modelled	34.3	10	Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
56	c1t5aB_	Alignment	not modelled	34.0	12	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase, m2 isozyme; PDBTitle: human pyruvate kinase m2
57	d1rl2a1	Alignment	not modelled	34.0	17	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
58	c3p8bB_	Alignment	not modelled	33.7	30	PDB header: transferase/transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
59	c1kqsA_	Alignment	not modelled	33.5	13	PDB header: ribosome Chain: A: PDB Molecule: ribosomal protein l2; PDBTitle: the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis
60	c6qh2A_	Alignment	not modelled	33.1	18	PDB header: signaling protein Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: solution nmr ensemble for a chimeric kh-s1 domain construct of2 exosomal polynucleotide phosphorylase at 298k compiled using the3 comand method
61	d1vqoa1	Alignment	not modelled	32.5	13	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
62	c4ytkA_	Alignment	not modelled	31.9	29	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow1-linker1 domain of transcription elongation2 factor spt5
63	d1bvsa3	Alignment	not modelled	31.9	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
64	c1a9fB_	Alignment	not modelled	31.8	15	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
65	c3qtgA_	Alignment	not modelled	31.3	14	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from pyrobaculum aerophilum
66	c2k8lA_	Alignment	not modelled	30.8	26	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: solution structure of e.coli slyd
67	c2oarA_	Alignment	not modelled	30.5	11	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)
68	d1ofla_	Alignment	not modelled	30.5	17	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Chondroitinase B
69	c1t3oA_	Alignment	not modelled	29.6	17	PDB header: rna binding protein Chain: A: PDB Molecule: carbon storage regulator; PDBTitle: solution structure of csra, a bacterial carbon storage2 regulatory protein
70	c5z1lL_	Alignment	not modelled	29.4	13	PDB header: protein fibril Chain: L: PDB Molecule: flagellin; PDBTitle: cryo-em structure of methanococcus maripaludis archaeillum
71	c4v19Y_	Alignment	not modelled	29.3	24	PDB header: ribosome Chain: Y: PDB Molecule: mitoribosomal protein ul24m, mrpl24; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
72	c5gkdA_	Alignment	not modelled	28.9	17	PDB header: lyase Chain: A: PDB Molecule: alycg; PDBTitle: structure of pl6 family alginate lyase alycg
73	c4kf9A_	Alignment	not modelled	28.7	24	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase protein; PDBTitle: crystal structure of a glutathione transferase family member from2 ralstonia solanacearum, target efi-501780, with bound gsh coordinated3 to a zinc ion, ordered active site
74	c2kfwA_	Alignment	not modelled	28.6	26	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase PDBTitle: solution structure of full-length slyd from e.coli
75	c3pr9A_	Alignment	not modelled	28.5	15	PDB header: chaperone Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase; PDBTitle: structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
76	d1a8pa1	Alignment	not modelled	28.3	17	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
77	c3f42A_	Alignment	not modelled	28.1	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hp0035; PDBTitle: crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
78	c1m1gB_	Alignment	not modelled	27.8	13	PDB header: transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
79	c3pifD_	Alignment	not modelled	27.4	23	PDB header: hydrolase Chain: D: PDB Molecule: 5'->3' exoribonuclease (xrn1); PDBTitle: crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
80	c1nnpA_	Alignment	not modelled	27.3	9	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1;

80	c9mka	Alignment	not modelled	27.3	9	PDBTitle: structural basis for targeting the ribosomal protein s1 of2 mycobacterium tuberculosis by pyrazinamide
81	d1j8ba	Alignment	not modelled	27.3	12	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
82	c3qia	Alignment	not modelled	27.2	26	PDB header: transcription regulator Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 2 of human phd finger protein 20
83	c4v19D	Alignment	not modelled	27.2	9	PDB header: ribosome Chain: D: PDB Molecule: mitoribosomal protein ul2m, mrpl2; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
84	c4q7jD	Alignment	not modelled	27.2	19	PDB header: translation/transferase Chain: D: PDB Molecule: 30s ribosomal protein s1; PDBTitle: complex structure of viral rna polymerase
85	c3ma8A	Alignment	not modelled	27.1	29	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
86	d1sroa	Alignment	not modelled	26.6	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
87	d1pkla1	Alignment	not modelled	26.5	12	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
88	d1ixra2	Alignment	not modelled	25.8	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
89	d1nz9a	Alignment	not modelled	25.6	20	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
90	c2dzca	Alignment	not modelled	25.6	16	PDB header: ligase Chain: A: PDB Molecule: biotin--[acetyl-coa-carboxylase] ligase; PDBTitle: crystal structure of biotin protein ligase from pyrococcus2 horikoshii, mutation r48a
91	d2if6a1	Alignment	not modelled	25.6	20	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Yiix-like
92	c5mmiv	Alignment	not modelled	24.6	24	PDB header: ribosome Chain: V: PDB Molecule: plastid ribosomal protein ul24c; PDBTitle: structure of the large subunit of the chloroplast ribosome
93	d1xnea	Alignment	not modelled	24.5	13	Fold: PUA domain-like Superfamily: PUA domain-like Family: ProFAR isomerase associated domain
94	c6du6D	Alignment	not modelled	24.5	22	PDB header: transferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of the pyruvate kinase (pk1) from the mosquito aedes2 aegypti
95	c2h5xA	Alignment	not modelled	24.4	14	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
96	c1vw4Q	Alignment	not modelled	23.5	31	PDB header: ribosome Chain: Q: PDB Molecule: 54s ribosomal protein l40, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
97	c6b8hb	Alignment	not modelled	23.0	16	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
98	c1vpzB	Alignment	not modelled	23.0	17	PDB header: rna binding protein Chain: B: PDB Molecule: carbon storage regulator homolog; PDBTitle: crystal structure of a putative carbon storage regulator protein2 (csra, pa0905) from pseudomonas aeruginosa at 2.05 a resolution
99	d1x5qa1	Alignment	not modelled	22.6	13	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
100	c3qglD	Alignment	not modelled	22.5	19	PDB header: protein binding Chain: D: PDB Molecule: sorting nexin-27; PDBTitle: crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the eseskv peptide corresponding to the c-terminal tail of girk3
101	d2zjrr1	Alignment	not modelled	22.3	21	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
102	c4ce4D	Alignment	not modelled	22.1	9	PDB header: ribosome Chain: D: PDB Molecule: mrpl2; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
103	c3iz5G	Alignment	not modelled	21.7	15	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l6 (l6e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
104	c2pqaB	Alignment	not modelled	21.6	15	PDB header: replication Chain: B: PDB Molecule: replication protein a 14 kda subunit; PDBTitle: crystal structure of full-length human rpa 14/32 heterodimer
105	c1ixrB	Alignment	not modelled	21.4	8	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
106	c1ybxA	Alignment	not modelled	21.3	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: conserved hypothetical protein cth-383 from clostridium

						thermocellum
107	c3nx6A_	Alignment	not modelled	21.3	7	PDB header: chaperone Chain: A: PDB Molecule: 10kda chaperonin; PDBTitle: crystal structure of co-chaperonin, groes (xoo4289) from xanthomonas2 oryzae pv. oryzae kacc10331
108	d2pi2e1	Alignment	not modelled	21.1	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
109	d1vpza_	Alignment	not modelled	21.1	17	Fold: CsrA-like Superfamily: CsrA-like Family: CsrA-like
110	c2y35A_	Alignment	not modelled	21.0	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: ld22664p; PDBTitle: crystal structure of xrn1-substrate complex
111	d1fdra1	Alignment	not modelled	21.0	25	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
112	c5dmbD_	Alignment	not modelled	20.9	31	PDB header: translation Chain: D: PDB Molecule: carbon storage regulator homolog; PDBTitle: crystal structure of a translational regulator bound to a flagellar2 assembly factor
113	c4xtrG_	Alignment	not modelled	20.8	30	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: pep12p; PDBTitle: structure of get3 bound to the transmembrane domain of pep12
114	d1cuka3	Alignment	not modelled	20.8	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
115	c2qqsB_	Alignment	not modelled	20.7	22	PDB header: oxidoreductase Chain: B: PDB Molecule: jmjc domain-containing histone demethylation PDBTitle: jmjd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide
116	c2he4A_	Alignment	not modelled	20.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: the crystal structure of the second pdz domain of human2 nherf-2 (slc9a3r2) interacting with a mode 1 pdz binding3 motif
117	c2ks1A_	Alignment	not modelled	20.5	26	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
118	c3mk7F_	Alignment	not modelled	20.5	12	PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
119	d2cp0a1	Alignment	not modelled	20.5	26	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
120	d2z0sa1	Alignment	not modelled	20.2	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like