








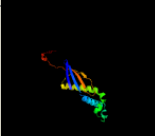







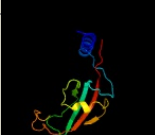

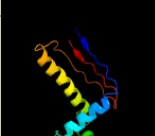


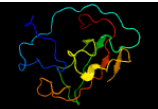
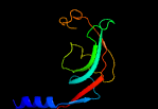









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2462c_(tig)_2763901_2765301
Date	Wed Aug 7 12:50:09 BST 2019
Unique Job ID	f5ae11b02439b6ec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w26B_	 Alignment		100.0	23	PDB header: chaperone Chain: B: PDB Molecule: trigger factor; PDBTitle: trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
2	c1t11A_	 Alignment		100.0	25	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: trigger factor
3	c3gtyX_	 Alignment		100.0	18	PDB header: chaperone/ribosomal protein Chain: X: PDB Molecule: trigger factor; PDBTitle: promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
4	d1t11a2	 Alignment		100.0	27	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain
5	d1w26a2	 Alignment		99.9	22	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain
6	d1w26a1	 Alignment		99.9	16	Fold: Triger factor/SurA peptide-binding domain-like Superfamily: Trigger factor/SurA peptide-binding domain-like Family: TF C-terminus
7	d1p9ya_	 Alignment		99.9	21	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain
8	c2nsaA_	 Alignment		99.9	15	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: structures of and interactions between domains of trigger factor from2 themotoga maritim
9	d1w26a3	 Alignment		99.8	34	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
10	c2d3o1_	 Alignment		99.8	32	PDB header: ribosome Chain: 1: PDB Molecule: trigger factor; PDBTitle: structure of ribosome binding domain of the trigger factor on the 50s2 ribosomal subunit from d. radiodurans
11	c2nscA_	 Alignment		99.8	19	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: structures of and interactions between domains of trigger factor from2 themotoga maritima

12	c5zr0A_	Alignment		99.8	30	PDB header: chaperone Chain: A: PDB Molecule: maltose-binding periplasmic protein,trigger factor; PDBTitle: solution structure of peptidyl-prolyl cis/trans isomerase domain of2 trigger factor in complex with mbp
13	d1t11a3	Alignment		99.8	36	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
14	d1l1pa_	Alignment		99.7	33	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
15	d1t11a1	Alignment		99.7	13	Fold: Triger factor/SurA peptide-binding domain-like Superfamily: Triger factor/SurA peptide-binding domain-like Family: TF C-terminus
16	c1hxvA_	Alignment		99.5	21	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: ppiase domain of the mycoplasma genitalium trigger factor
17	d1hxva_	Alignment		99.5	21	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
18	c3prdA_	Alignment		99.0	23	PDB header: chaperone, isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase; PDBTitle: structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
19	c4mspB_	Alignment		99.0	16	PDB header: isomerase Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp14; PDBTitle: crystal structure of human peptidyl-prolyl cis-trans isomerase fkbp222 (aka fkbp14) containing two ef-hand motifs
20	c3pr9A_	Alignment		98.6	28	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
21	c2kfwA_	Alignment	not modelled	98.6	33	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase PDBTitle: solution structure of full-length slyd from e.coli
22	c4odrB_	Alignment	not modelled	98.5	29	PDB header: isomerase, chaperone Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase slyd, peptidyl-prolyl PDBTitle: structure of slyd delta-if from thermus thermophilus in complex with2 fk506
23	c3cgnA_	Alignment	not modelled	98.5	37	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of thermophilic slyd
24	c2k8iA_	Alignment	not modelled	98.5	32	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: solution structure of e.coli slyd
25	c4dt4A_	Alignment	not modelled	98.4	25	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type 16 kda peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of the ppiase-chaperone slpa with the chaperone2 binding site occupied by the linker of the purification tag
26	c5i7pA_	Alignment	not modelled	98.3	22	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp1a,fkbp-type PDBTitle: crystal structure of fkbp12-if(slyd), a chimeric protein of human2 fkbp12 and the insert in flap domain of ecoli slyd
27	c2pbcd_	Alignment	not modelled	98.3	18	PDB header: isomerase Chain: D: PDB Molecule: fk506-binding protein 2; PDBTitle: fk506-binding protein 2
28	c4dipD_	Alignment	not modelled	98.2	17	PDB header: isomerase Chain: D: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp14; PDBTitle: crystal structure of human peptidyl-prolyl cis-trans isomerase fkbp14

29	d1ix5a_	Alignment	not modelled	98.1	38	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
30	c2kr7A_	Alignment	not modelled	98.1	25	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase slyd; PDBTitle: solution structure of helicobacter pylori slyd
31	c4g50A_	Alignment	not modelled	98.0	21	PDB header: isomerase, protein binding Chain: A: PDB Molecule: ubiquitin-like protein smt3, peptidyl-prolyl cis-trans PDBTitle: crystal structure of a smt fusion peptidyl-prolyl cis-trans isomerase2 with surface mutation d44g from burkholderia pseudomallei complexed3 with cj168
32	c4jysA_	Alignment	not modelled	98.0	13	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of fkbp25 from plasmodium vivax
33	c5hwbA_	Alignment	not modelled	98.0	22	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 1a; PDBTitle: aspergillus fumigatus fkbp12 apo protein in p212121 space group
34	c1q6uA_	Alignment	not modelled	98.0	20	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase fkpa; PDBTitle: crystal structure of fkpa from escherichia coli
35	c2vcdA_	Alignment	not modelled	97.9	15	PDB header: isomerase Chain: A: PDB Molecule: outer membrane protein mip; PDBTitle: solution structure of the fkbp-domain of legionella pneumophila mip in2 complex with rapamycin
36	c2lknA_	Alignment	not modelled	97.9	14	PDB header: protein binding Chain: A: PDB Molecule: ah receptor-interacting protein; PDBTitle: solution structure of the ppiase domain of human aryl-hydrocarbon2 receptor-interacting protein (aip)
37	d1c9ha_	Alignment	not modelled	97.9	10	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
38	d1q6ha_	Alignment	not modelled	97.9	15	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
39	c2jwxA_	Alignment	not modelled	97.8	21	PDB header: apoptosis, isomerase Chain: A: PDB Molecule: fk506-binding protein 8 variant; PDBTitle: solution structure of the n-terminal domain of human fkbp382 (fkbp38ntd)
40	c2mphA_	Alignment	not modelled	97.8	27	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp3; PDBTitle: solution structure of human fk506 binding protein 25
41	d1fd9a_	Alignment	not modelled	97.8	16	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
42	c2vn1A_	Alignment	not modelled	97.8	14	PDB header: isomerase Chain: A: PDB Molecule: 70 kda peptidylprolyl isomerase; PDBTitle: crystal structure of the fk506-binding domain of plasmodium2 falciparum fkbp35 in complex with fk506
43	d1kt0a2	Alignment	not modelled	97.8	15	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
44	d1jywa_	Alignment	not modelled	97.8	14	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
45	c1q1cA_	Alignment	not modelled	97.7	16	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 4; PDBTitle: crystal structure of n(1-260) of human fkbp52
46	d2ppna1	Alignment	not modelled	97.7	14	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
47	c2d9fA_	Alignment	not modelled	97.7	18	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 8 variant; PDBTitle: solution structure of ruh-047, an fkbp domain from human2 cdna
48	c6b4pB_	Alignment	not modelled	97.7	20	PDB header: isomerase Chain: B: PDB Molecule: peptidylprolyl isomerase; PDBTitle: crystal structure of peptidylprolyl isomerase from naegleria fowleri
49	c4bf8A_	Alignment	not modelled	97.7	24	PDB header: isomerase Chain: A: PDB Molecule: fpr4; PDBTitle: fpr4 ppi domain
50	d1kt0a3	Alignment	not modelled	97.7	19	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
51	d1yata_	Alignment	not modelled	97.6	21	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
52	c2lgoA_	Alignment	not modelled	97.6	18	PDB header: isomerase Chain: A: PDB Molecule: fkbp; PDBTitle: solution nmr structure of a fkbp-type peptidyl-prolyl cis-trans2 isomerase from giardia lamblia, seattle structural genomics center3 for infectious disease target gilaa.00840.a
53	c5u9jB_	Alignment	not modelled	97.6	14	PDB header: signaling protein Chain: B: PDB Molecule: aryl hydrocarbon receptor-interacting protein-like 1 PDBTitle: crystal structure of the fkbp domain of human aryl hydrocarbon2 receptor-interacting protein-like 1 (aip1) complexed with geranyl3 geranyl pyrophosphate
						Fold: FKBP-like

54	dlq1ca1	Alignment	not modelled	97.6	19	Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
55	c3o5dB_	Alignment	not modelled	97.6	20	PDB header: isomerase Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp5; PDBTitle: crystal structure of a fragment of fkbp51 comprising the fk1 and fk22 domains
56	c1qz2B_	Alignment	not modelled	97.6	13	PDB header: isomerase/chaperone Chain: B: PDB Molecule: fk506-binding protein 4; PDBTitle: crystal structure of fkbp52 c-terminal domain complex with2 the c-terminal peptide meevd of hsp90
57	c2ke0A_	Alignment	not modelled	97.6	19	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: solution structure of peptidyl-prolyl cis-trans isomerase from2 burkholderia pseudomallei
58	c1rouA_	Alignment	not modelled	97.6	20	PDB header: rotamase (isomerase) Chain: A: PDB Molecule: fkbp59-i; PDBTitle: structure of fkbp59-i, the n-terminal domain of a 59 kda2 fk506-binding protein, nmr, 22 structures
59	c3jxvA_	Alignment	not modelled	97.5	18	PDB header: isomerase Chain: A: PDB Molecule: 70 kda peptidyl-prolyl isomerase; PDBTitle: crystal structure of the 3 fkbp domains of wheat fkbp73
60	d1kt1a3	Alignment	not modelled	97.5	20	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
61	d1r9ha_	Alignment	not modelled	97.5	21	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
62	c3o5fA_	Alignment	not modelled	97.5	15	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp5; PDBTitle: fk1 domain of fkbp51, crystal form vii
63	c1zxB_	Alignment	not modelled	97.5	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein mg377 homolog; PDBTitle: crystal structure of the hypthetical mycoplasma protein, mpn555
64	c3jymA_	Alignment	not modelled	97.5	19	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein (fkbp) from wheat; PDBTitle: crystal structure of the 3 fkbp domains of wheat fkbp73
65	c5ompA_	Alignment	not modelled	97.4	15	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp5; PDBTitle: human fkbp5 protein
66	c5b8iC_	Alignment	not modelled	97.4	19	PDB header: hydrolase Chain: C: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of calcineurin a and calcineurin b in complex with2 fkbp12 and fk506 from coccidioides immitis rs
67	d1q1ca2	Alignment	not modelled	97.4	17	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
68	d1pbka_	Alignment	not modelled	97.4	27	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
69	c3oe2A_	Alignment	not modelled	97.4	9	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: 1.6 a crystal structure of peptidyl-prolyl cis-trans isomerase ppiase2 from pseudomonas syringae pv. tomato str. dc3000 (pspto dc3000)
70	c1kt0A_	Alignment	not modelled	97.3	17	PDB header: isomerase Chain: A: PDB Molecule: 51 kda fk506-binding protein; PDBTitle: structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
71	d1kt1a2	Alignment	not modelled	97.3	18	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
72	c6h3iB_	Alignment	not modelled	97.3	14	PDB header: protein transport Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: structural snapshots of the type 9 protein translocon
73	d1m5ya1	Alignment	not modelled	97.2	10	Fold: Triger factor/SurA peptide-binding domain-like Superfamily: Triger factor/SurA peptide-binding domain-like Family: Porin chaperone SurA, peptide-binding domain
74	c5mgxG_	Alignment	not modelled	97.2	17	PDB header: isomerase Chain: G: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp8; PDBTitle: the structure of fkbp38 in complex with the meevd tetratricopeptide2 binding-motif of hsp90
75	c3b7xA_	Alignment	not modelled	97.1	12	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 6; PDBTitle: crystal structure of human fk506-binding protein 6
76	c5i98A_	Alignment	not modelled	96.9	13	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 1; PDBTitle: structure of apo fkbp12(p104g) from c. albicans
77	c2f4eB_	Alignment	not modelled	96.7	13	PDB header: signaling protein Chain: B: PDB Molecule: atfkbp42; PDBTitle: n-terminal domain of fkbp42 from arabidopsis thaliana
78	d1u79a_	Alignment	not modelled	96.0	18	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
79	c1m5yB_	Alignment	not modelled	95.7	10	PDB header: isomerase, cell cycle Chain: B: PDB Molecule: survival protein sura; PDBTitle: crystallographic structure of sura, a molecular chaperone2 that facilitates outer membrane porin folding
80	c2if4A_	Alignment	not modelled	95.1	12	PDB header: signaling protein Chain: A: PDB Molecule: atfkbp42; PDBTitle: crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana

81	c4it4D_	Alignment	not modelled	94.8	9	PDB header: unknown function Chain: D: PDB Molecule: cg17282; PDBTitle: crystal structure of residues 1-211 of cg17282
82	c2pv3B_	Alignment	not modelled	89.2	13	PDB header: isomerase Chain: B: PDB Molecule: chaperone sura; PDBTitle: crystallographic structure of sura fragment lacking the second2 peptidyl-prolyl isomerase domain complexed with peptide nftlkfwdifrk
83	c2p4vA_	Alignment	not modelled	88.4	10	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
84	c3nrkA_	Alignment	not modelled	88.1	12	PDB header: unknown function Chain: A: PDB Molecule: lic12922; PDBTitle: the crystal structure of the leptospiral hypothetical protein lic12922
85	c3rgcB_	Alignment	not modelled	87.3	14	PDB header: chaperone Chain: B: PDB Molecule: possible periplasmic protein; PDBTitle: the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally related sura-like chaperones in the human pathogen3 campylobacter jejuni
86	c1grjA_	Alignment	not modelled	84.3	12	PDB header: transcription regulation Chain: A: PDB Molecule: grea protein; PDBTitle: grea transcript cleavage factor from escherichia coli
87	c3bmbB_	Alignment	not modelled	80.2	17	PDB header: rna binding protein Chain: B: PDB Molecule: regulator of nucleoside diphosphate kinase; PDBTitle: crystal structure of a new rna polymerase interacting2 protein
88	c5htfA_	Alignment	not modelled	79.4	17	PDB header: chaperone Chain: A: PDB Molecule: foldase protein prsa 1; PDBTitle: crystal structure of prsa1 from listeria monocytogenes
89	c4wo7A_	Alignment	not modelled	79.1	13	PDB header: isomerase Chain: A: PDB Molecule: foldase protein prsa; PDBTitle: crystal structure of prsa from bacillus subtilis
90	c4fukB_	Alignment	not modelled	67.6	26	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase; PDBTitle: aminopeptidase from trypanosoma brucei
91	c2pn0D_	Alignment	not modelled	63.2	17	PDB header: transcription Chain: D: PDB Molecule: prokaryotic transcription elongation factor PDBTitle: prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
92	c3s6bA_	Alignment	not modelled	59.7	26	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150
93	c2etnA_	Alignment	not modelled	56.9	17	PDB header: transcription Chain: A: PDB Molecule: anti-cleavage anti-grea transcription factor PDBTitle: crystal structure of thermus aquaticus gfh1
94	c5ez1B_	Alignment	not modelled	56.1	13	PDB header: isomerase Chain: B: PDB Molecule: putative peptidyl-prolyl cis-trans isomerase hp_0175; PDBTitle: crystal structure of cell binding factor 2 from helicobacter pylori in2 complex with i2ca
95	c3dinF_	Alignment	not modelled	49.0	27	PDB header: membrane protein, protein transport Chain: F: PDB Molecule: preprotein translocase subunit secy; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
96	c6n3qA_	Alignment	not modelled	46.3	19	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein sec61; PDBTitle: cryo-em structure of the yeast sec complex
97	c5eulY_	Alignment	not modelled	45.7	20	PDB header: protein transport Chain: Y: PDB Molecule: protein translocase subunit secy; PDBTitle: structure of the seca-secy complex with a translocating polypeptide2 substrate
98	c3j01A_	Alignment	not modelled	45.4	32	PDB header: ribosome/ribosomal protein Chain: A: PDB Molecule: preprotein translocase secy subunit; PDBTitle: structure of the ribosome-secy complex in the membrane environment
99	c3rfwA_	Alignment	not modelled	45.3	16	PDB header: chaperone Chain: A: PDB Molecule: cell-binding factor 2; PDBTitle: the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally-related sura-like chaperones in the human pathogen3 campylobacter jejuni
100	c3htxA_	Alignment	not modelled	44.4	20	PDB header: transferase/rna Chain: A: PDB Molecule: hen1; PDBTitle: crystal structure of small rna methyltransferase hen1
101	d2f23a2	Alignment	not modelled	44.2	8	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
102	d1jmx1	Alignment	not modelled	42.2	13	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
103	c1vx11_	Alignment	not modelled	41.2	22	PDB header: ribosome Chain: 1: PDB Molecule: sec61 alpha subunit; PDBTitle: structure of the translating mammalian ribosome-sec61 complex. this2 entry contains the large subunit ribosomal proteins.
104	d2etna2	Alignment	not modelled	39.9	14	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
105	c3mp7A_	Alignment	not modelled	39.4	38	PDB header: protein transport Chain: A: PDB Molecule: preprotein translocase subunit secy; PDBTitle: lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes Fold: Cytochrome c

106	d1pbya1	Alignment	not modelled	39.4	8	Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
107	c5tvA_	Alignment	not modelled	37.5	16	PDB header: isomerase Chain: A; PDB Molecule: foldase protein prsa; PDBTitle: crystal structure of foldase protein prsa from streptococcus2 pneumoniae str. canada mdr_19a
108	d1gria2	Alignment	not modelled	36.7	13	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
109	c1oqyA_	Alignment	not modelled	32.7	17	PDB header: replication Chain: A; PDB Molecule: uv excision repair protein rad23 homolog a; PDBTitle: structure of the dna repair protein hhr23a
110	c2zqpY_	Alignment	not modelled	32.7	24	PDB header: protein transport Chain: Y; PDB Molecule: preprotein translocase secy subunit; PDBTitle: crystal structure of secye translocon from thermus2 thermophilus
111	c3dl8H_	Alignment	not modelled	31.9	36	PDB header: protein transport Chain: H; PDB Molecule: preprotein translocase subunit secy; PDBTitle: structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
112	c4ipaC_	Alignment	not modelled	30.6	30	PDB header: hydrolase Chain: C; PDB Molecule: putative curved dna-binding protein; PDBTitle: structure of a thermophilic arx1
113	c1yw7A_	Alignment	not modelled	30.0	16	PDB header: hydrolase Chain: A; PDB Molecule: methionine aminopeptidase 2; PDBTitle: h-metap2 complexed with a444148
114	c2akiY_	Alignment	not modelled	29.8	32	PDB header: protein transport Chain: Y; PDB Molecule: preprotein translocase secy subunit; PDBTitle: normal mode-based flexible fitted coordinates of a translocating2 secyeg protein-conducting channel into the cryo-em map of a secyeg-3 nascent chain-70s ribosome complex from e. coli
115	c2q8kA_	Alignment	not modelled	29.7	28	PDB header: transcription Chain: A; PDB Molecule: proliferation-associated protein 2g4; PDBTitle: the crystal structure of ebp1
116	c2wwbA_	Alignment	not modelled	27.1	17	PDB header: ribosome Chain: A; PDB Molecule: protein transport protein sec61 subunit alpha isoform 1; PDBTitle: cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome
117	c1vw4E_	Alignment	not modelled	27.0	12	PDB header: ribosome Chain: E; PDB Molecule: 54s ribosomal protein l7, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
118	c2vcbA_	Alignment	not modelled	26.4	21	PDB header: hydrolase Chain: A; PDB Molecule: alpha-n-acetylglucosaminidase; PDBTitle: family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac
119	c2g6pA_	Alignment	not modelled	26.1	19	PDB header: hydrolase Chain: A; PDB Molecule: methionine aminopeptidase 1; PDBTitle: crystal structure of truncated (delta 1-89) human methionine2 aminopeptidase type 1 in complex with pyridyl pyrimidine derivative
120	c2gz5A_	Alignment	not modelled	26.1	19	PDB header: hydrolase Chain: A; PDB Molecule: methionine aminopeptidase 1; PDBTitle: human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang