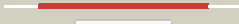



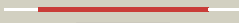






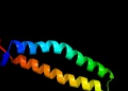












# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1080c\_greA\_1205309\_1205803  
 Date Wed Jul 31 22:05:15 BST 2019  
 Unique Job ID 8ff0fbc2b787557c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2p4vA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor greb; <b>PDBTitle:</b> crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
2	<a href="#">c1grjA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> greA protein; <b>PDBTitle:</b> grea transcript cleavage factor from escherichia coli
3	<a href="#">c2etnA_</a>	 Alignment		100.0	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> anti-cleavage anti-grea transcription factor <b>PDBTitle:</b> crystal structure of thermus aquaticus gfh1
4	<a href="#">c3bmbB_</a>	 Alignment		99.9	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> regulator of nucleoside diphosphate kinase; <b>PDBTitle:</b> crystal structure of a new rna polymerase interacting2 protein
5	<a href="#">c2pn0D_</a>	 Alignment		99.9	24	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> prokaryotic transcription elongation factor <b>PDBTitle:</b> prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
6	<a href="#">d1grja1</a>	 Alignment		99.9	47	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> GreA transcript cleavage protein, N-terminal domain <b>Family:</b> GreA transcript cleavage protein, N-terminal domain
7	<a href="#">d2f23a1</a>	 Alignment		99.9	28	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> GreA transcript cleavage protein, N-terminal domain <b>Family:</b> GreA transcript cleavage protein, N-terminal domain
8	<a href="#">d2f23a2</a>	 Alignment		99.8	25	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> GreA transcript cleavage factor, C-terminal domain
9	<a href="#">d2etna2</a>	 Alignment		99.7	23	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> GreA transcript cleavage factor, C-terminal domain
10	<a href="#">d1grja2</a>	 Alignment		99.7	18	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> GreA transcript cleavage factor, C-terminal domain
11	<a href="#">c3gtyX_</a>	 Alignment		95.3	15	<b>PDB header:</b> chaperone/ribosomal protein <b>Chain:</b> X: <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone

12	<a href="#">c1w26B_</a>	Alignment		92.4	16	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
13	<a href="#">d1t11a3</a>	Alignment		91.1	14	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
14	<a href="#">d1w26a3</a>	Alignment		89.8	14	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
15	<a href="#">c1t11A_</a>	Alignment		88.2	13	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> trigger factor
16	<a href="#">d1krha1</a>	Alignment		78.6	23	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
17	<a href="#">d1l1pa_</a>	Alignment		74.7	25	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
18	<a href="#">c5zr0A_</a>	Alignment		72.4	24	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,trigger factor; <b>PDBTitle:</b> solution structure of peptidyl-prolyl cis/trans isomerase domain of2 trigger factor in complex with mbp
19	<a href="#">c2dq0A_</a>	Alignment		67.1	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
20	<a href="#">d1q1ca1</a>	Alignment		64.5	24	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
21	<a href="#">c2kfwA_</a>	Alignment	not modelled	62.6	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase <b>PDBTitle:</b> solution structure of full-length slyd from e.coli
22	<a href="#">d1fdra1</a>	Alignment	not modelled	61.9	16	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
23	<a href="#">c3lssA_</a>	Alignment	not modelled	61.7	4	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> trypanosoma brucei seryl-trna synthetase in complex with atp
24	<a href="#">d1seta1</a>	Alignment	not modelled	59.6	18	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> tRNA-binding arm <b>Family:</b> Seryl-tRNA synthetase (SerRS)
25	<a href="#">c5i7pA_</a>	Alignment	not modelled	55.4	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase fkbp1a,fkbp-type <b>PDBTitle:</b> crystal structure of fkbp12-if(slyd), a chimeric protein of human2 fkbp12 and the insert in flap domain of ecoli slyd
26	<a href="#">c3h0gE_</a>	Alignment	not modelled	53.8	18	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii subunit rpabc1; <b>PDBTitle:</b> rna polymerase ii from schizosaccharomyces pombe
27	<a href="#">c3j20G_</a>	Alignment	not modelled	53.5	13	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 30s ribosomal protein s6e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
28	<a href="#">c2k8iA_</a>	Alignment	not modelled	53.3	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> solution structure of e.coli slyd

29	<a href="#">c3cgnA</a>	Alignment	not modelled	51.7	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> crystal structure of thermophilic slyd
30	<a href="#">c4ijjA</a>	Alignment	not modelled	51.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative c4-type zinc finger protein, dksa/trar family; <b>PDBTitle:</b> structure of transcription factor dksa2 from pseudomonas aeruginosa
31	<a href="#">c1zeqX</a>	Alignment	not modelled	50.9	11	<b>PDB header:</b> metal binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> cation efflux system protein cusf; <b>PDBTitle:</b> 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
32	<a href="#">d1eika</a>	Alignment	not modelled	50.3	23	<b>Fold:</b> RPB5-like RNA polymerase subunit <b>Superfamily:</b> RPB5-like RNA polymerase subunit <b>Family:</b> RPB5
33	<a href="#">c2I55A</a>	Alignment	not modelled	49.5	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> silb,silver efflux protein, mfp component of the three <b>PDBTitle:</b> solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
34	<a href="#">c6girA</a>	Alignment	not modelled	48.0	10	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> serine--trna ligase, cytoplasmic; <b>PDBTitle:</b> arabidopsis thaliana cytosolic seryl-trna synthetase
35	<a href="#">d1e32a3</a>	Alignment	not modelled	47.6	16	<b>Fold:</b> Cdc48 domain 2-like <b>Superfamily:</b> Cdc48 domain 2-like <b>Family:</b> Cdc48 domain 2-like
36	<a href="#">c6o38H</a>	Alignment	not modelled	46.8	30	<b>PDB header:</b> sugar binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> type ii secretion chaperone cpab; <b>PDBTitle:</b> structure of a chaperone-substrate complex
37	<a href="#">c2pjhB</a>	Alignment	not modelled	46.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> strctural model of the p97 n domain- npl4 ubd complex
38	<a href="#">c1cz5A</a>	Alignment	not modelled	45.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> vcp-like atpase; <b>PDBTitle:</b> nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
39	<a href="#">c2xznY</a>	Alignment	not modelled	45.5	12	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> rps6e; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
40	<a href="#">c2kr7A</a>	Alignment	not modelled	44.8	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase slyd; <b>PDBTitle:</b> solution structure of helicobacter pylori slyd
41	<a href="#">c4he5A</a>	Alignment	not modelled	44.7	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase family u32; <b>PDBTitle:</b> crystal structure of the selenomethionine variant of the c-terminal2 domain of geobacillus thermoleovorans putative u32 peptidase
42	<a href="#">c3u5cG</a>	Alignment	not modelled	44.5	10	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 40s ribosomal protein s6-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
43	<a href="#">d1dzfa2</a>	Alignment	not modelled	43.7	19	<b>Fold:</b> RPB5-like RNA polymerase subunit <b>Superfamily:</b> RPB5-like RNA polymerase subunit <b>Family:</b> RPB5
44	<a href="#">c4qiwh</a>	Alignment	not modelled	43.0	23	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> dna-directed rna polymerase subunit h; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
45	<a href="#">c3j38G</a>	Alignment	not modelled	42.3	5	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 40s ribosomal protein s6; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins
46	<a href="#">d1gvha2</a>	Alignment	not modelled	41.0	16	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
47	<a href="#">c4y66D</a>	Alignment	not modelled	38.8	12	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> putative tbpip family protein; <b>PDBTitle:</b> crystal structure of giardia lamblia hop2-mnd1 complex
48	<a href="#">d1s04a</a>	Alignment	not modelled	37.8	28	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> ProFAR isomerase associated domain
49	<a href="#">d1hxva</a>	Alignment	not modelled	37.5	21	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
50	<a href="#">c1hxvA</a>	Alignment	not modelled	37.5	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> ppiase domain of the mycoplasma genitalium trigger factor
51	<a href="#">c1wleB</a>	Alignment	not modelled	37.4	9	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
52	<a href="#">d1tvca1</a>	Alignment	not modelled	36.8	21	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
53	<a href="#">d1a8pa1</a>	Alignment	not modelled	36.3	19	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
54	<a href="#">c6b0vA</a>	Alignment	not modelled	35.9	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> serine--trna ligase;

54	<a href="#">c0lzA_</a>	Alignment	not modelled	33.9	11	<b>PDBTitle:</b> klebsiella pneumoniae seryl-trna synthetase in complex with the2 intermediate analog 5'-o-(n-(l-seryl)-sulfamoyl)adenosine
55	<a href="#">c4lhzE_</a>	Alignment	not modelled	35.8	20	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> rab-3a-interacting protein; <b>PDBTitle:</b> crystal structure of gtp-bound rab8:rabin8
56	<a href="#">c5hwbA_</a>	Alignment	not modelled	35.6	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fk506-binding protein 1a; <b>PDBTitle:</b> aspergillus fumigatus fkbp12 apo protein in p212121 space group
57	<a href="#">c5flmE_</a>	Alignment	not modelled	35.0	18	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii subunit rpabc1; <b>PDBTitle:</b> structure of transcribing mammalian rna polymerase ii
58	<a href="#">c2gpiA_</a>	Alignment	not modelled	34.2	16	<b>PDB header:</b> fad-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> siderophore-interacting protein; <b>PDBTitle:</b> crystal structure of a siderophore-interacting protein (sputc32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
59	<a href="#">c3btpA_</a>	Alignment	not modelled	33.8	28	<b>PDB header:</b> dna binding protein, chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> single-strand dna-binding protein; <b>PDBTitle:</b> crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
60	<a href="#">c5xxuG_</a>	Alignment	not modelled	32.9	5	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> ribosomal protein es6; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
61	<a href="#">c5udfB_</a>	Alignment	not modelled	32.6	8	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein-releasing system transmembrane protein lole; <b>PDBTitle:</b> structure of the n-terminal domain of lipoprotein-releasing system2 transmembrane protein lole from acinetobacter baumannii
62	<a href="#">c3pr9A_</a>	Alignment	not modelled	32.3	35	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
63	<a href="#">d2piaa1</a>	Alignment	not modelled	31.0	11	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
64	<a href="#">c2pbcD_</a>	Alignment	not modelled	30.2	20	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> fk506-binding protein 2; <b>PDBTitle:</b> fk506-binding protein 2
65	<a href="#">c4picA_</a>	Alignment	not modelled	29.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> arginine phosphatase ywle; <b>PDBTitle:</b> ywle arginine phosphatase from geobacillus stearothermophilus
66	<a href="#">d1ep3b1</a>	Alignment	not modelled	29.4	11	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
67	<a href="#">c3zey3_</a>	Alignment	not modelled	29.2	16	<b>PDB header:</b> ribosome <b>Chain:</b> 3: <b>PDB Molecule:</b> 40s ribosomal protein s6; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
68	<a href="#">c3o5fA_</a>	Alignment	not modelled	28.8	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase fkbp5; <b>PDBTitle:</b> fk1 domain of fkbp51, crystal form vii
69	<a href="#">d2cnda1</a>	Alignment	not modelled	28.7	13	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
70	<a href="#">c4mspB_</a>	Alignment	not modelled	28.4	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase fkbp14; <b>PDBTitle:</b> crystal structure of human peptidyl-prolyl cis-trans isomerase fkbp222 (aka fkbp14) containing two ef-hand motifs
71	<a href="#">c2pmzV_</a>	Alignment	not modelled	27.8	33	<b>PDB header:</b> translation, transferase <b>Chain:</b> V: <b>PDB Molecule:</b> dna-directed rna polymerase subunit h; <b>PDBTitle:</b> archaeal rna polymerase from sulfolobus solfataricus
72	<a href="#">d1c9ha_</a>	Alignment	not modelled	26.7	10	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
73	<a href="#">c2l66B_</a>	Alignment	not modelled	26.2	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, abrb family; <b>PDBTitle:</b> the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
74	<a href="#">d1d2ea1</a>	Alignment	not modelled	25.8	15	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
75	<a href="#">c3prdA_</a>	Alignment	not modelled	25.7	37	<b>PDB header:</b> chaperone, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
76	<a href="#">c3gpkA_</a>	Alignment	not modelled	25.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ppic-type peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution.
77	<a href="#">c3tnuA_</a>	Alignment	not modelled	24.2	14	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> keratin, type i cytoskeletal 14; <b>PDBTitle:</b> heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
78	<a href="#">c6mv2A_</a>	Alignment	not modelled	23.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome b5 reductase 4; <b>PDBTitle:</b> 2.05a resolution structure of the cs-b5r domains of human ncb5or2 (nadp+ form)
						<b>PDB header:</b> hydrolase

79	<a href="#">c5hu4A_</a>	Alignment	not modelled	23.5	15	<b>Chain:</b> A: <b>PDB Molecule:</b> cysteine protease; <b>PDBTitle:</b> crystal structure of listeria monocytogenes sortase a
80	<a href="#">c2mrnB_</a>	Alignment	not modelled	23.1	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin maze; <b>PDBTitle:</b> structure of truncated ecmaze
81	<a href="#">c2lgoA_</a>	Alignment	not modelled	23.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp; <b>PDBTitle:</b> 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
82	<a href="#">c1rouA_</a>	Alignment	not modelled	22.8	19	<b>PDB header:</b> rotamase (isomerase) <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp59-i; <b>PDBTitle:</b> structure of fkbp59-i, the n-terminal domain of a 59 kda2 fk506-binding protein, nmr, 22 structures
83	<a href="#">c5oynB_</a>	Alignment	not modelled	22.7	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dehydratase, ilvd/edd family; <b>PDBTitle:</b> crystal structure of d-xylonate dehydratase in holo-form
84	<a href="#">d1ix5a_</a>	Alignment	not modelled	22.3	26	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
85	<a href="#">c2jv2A_</a>	Alignment	not modelled	22.3	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph1500; <b>PDBTitle:</b> solution structure of the n-terminal domain of ph1500
86	<a href="#">d2gp4a1</a>	Alignment	not modelled	22.2	17	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IvD-like <b>Family:</b> IvD/EDD C-terminal domain-like
87	<a href="#">c1krhA_</a>	Alignment	not modelled	21.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> benzoate 1,2-dioxygenase reductase; <b>PDBTitle:</b> x-ray structure of benzoate dioxygenase reductase
88	<a href="#">d1gawa1</a>	Alignment	not modelled	21.9	19	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
89	<a href="#">c2pv3B_</a>	Alignment	not modelled	20.1	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> chaperone sura; <b>PDBTitle:</b> crystallographic structure of sura fragment lacking the second2 peptidyl-prolyl isomerase domain complexed with peptide nftlkfwdifrk
90	<a href="#">d2d9ra1</a>	Alignment	not modelled	19.5	19	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AF2212/PG0164-like <b>Family:</b> PG0164-like
91	<a href="#">c1vpzB_</a>	Alignment	not modelled	19.5	38	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> carbon storage regulator homolog; <b>PDBTitle:</b> crystal structure of a putative carbon storage regulator protein2 (csra, pa0905) from pseudomonas aeruginosa at 2.05 a resolution
92	<a href="#">c2ln7A_</a>	Alignment	not modelled	19.4	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> lpxtg-site transpeptidase family protein; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for the catalytic2 domain of b. anthracis srtD
93	<a href="#">d1vhka1</a>	Alignment	not modelled	19.1	15	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> YggJ N-terminal domain-like
94	<a href="#">d2csba1</a>	Alignment	not modelled	19.0	31	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Topoisomerase V repeat domain
95	<a href="#">c5j84A_</a>	Alignment	not modelled	19.0	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase; <b>PDBTitle:</b> crystal structure of l-arabinonate dehydratase in holo-form
96	<a href="#">c5ze4A_</a>	Alignment	not modelled	18.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase, chloroplastic; <b>PDBTitle:</b> the structure of holo- structure of dhad complex with [2fe-2s] cluster
97	<a href="#">c5ym0A_</a>	Alignment	not modelled	18.8	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase, chloroplastic; <b>PDBTitle:</b> the crystal structure of dhad
98	<a href="#">c5uttD_</a>	Alignment	not modelled	18.8	7	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sortase; <b>PDBTitle:</b> srtA sortase from actinomyces oris
99	<a href="#">d1pina2</a>	Alignment	not modelled	18.6	20	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase