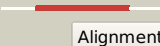

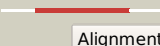

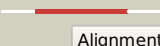


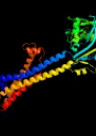


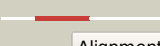



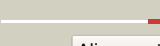
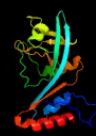



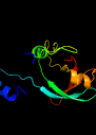


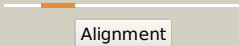


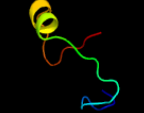

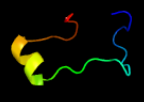
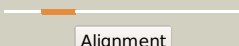

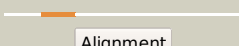

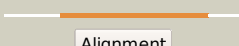

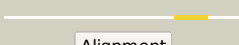
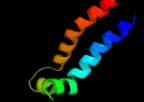
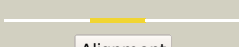

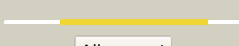



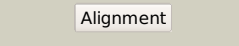

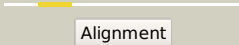
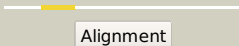




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0987_(-)_1102546_1105113
Date	Wed Jul 31 22:05:05 BST 2019
Unique Job ID	6e853b966a62dd9a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5ws4A_</a>	 Alignment		100.0	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
2	<a href="#">c5nikK_</a>	 Alignment		100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> K: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> structure of the macab-tolc abc-type tripartite multidrug efflux pump
3	<a href="#">c5xu1M_</a>	 Alignment		100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> M: <b>PDB Molecule:</b> abc transporter permeae; <b>PDBTitle:</b> structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
4	<a href="#">c5lj7B_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
5	<a href="#">c5udfB_</a>	 Alignment		99.4	14	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein-releasing system transmembrane protein lolc; <b>PDBTitle:</b> structure of the n-terminal domain of lipoprotein-releasing system2 transmembrane protein lolc from acinetobacter baumannii
6	<a href="#">c5naaB_</a>	 Alignment		99.4	18	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein-releasing system transmembrane protein lolc; <b>PDBTitle:</b> lipoprotein-releasing system transmembrane protein lolc
7	<a href="#">c3is6A_</a>	 Alignment		98.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative permease protein, abc transporter; <b>PDBTitle:</b> the crystal structure of a domain of a putative permease protein from2 porphyromonas gingivalis to 2a
8	<a href="#">c5f9qA_</a>	 Alignment		98.9	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein yknz; <b>PDBTitle:</b> crystal structure of the extracellular domain of noncanonic abc-type2 transporter yknz from gram-positive bacteria
9	<a href="#">c3ftjA_</a>	 Alignment		98.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein <b>PDBTitle:</b> crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans
10	<a href="#">c5c59F_</a>	 Alignment		98.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of the periplasmic region of macb from e. coli
11	<a href="#">c5c59G_</a>	 Alignment		96.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of the periplasmic region of macb from e. coli

12	<a href="#">d2jioa1</a>	 Alignment		83.3	13	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
13	<a href="#">c2a8vA</a>	 Alignment		81.8	23	<b>PDB header:</b> protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> rna binding domain of rho transcription <b>PDBTitle:</b> rho transcription termination factor/rna complex
14	<a href="#">d1a62a2</a>	 Alignment		81.1	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
15	<a href="#">d1vlfm1</a>	 Alignment		80.8	13	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
16	<a href="#">c2iv2X</a>	 Alignment		80.6	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> formate dehydrogenase h; <b>PDBTitle:</b> reinterpretation of reduced form of formate dehydrogenase h from e.2 coli
17	<a href="#">c4mt1A</a>	 Alignment		80.2	11	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> drug efflux protein; <b>PDBTitle:</b> crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
18	<a href="#">c5I75F</a>	 Alignment		78.3	18	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> fig000988: predicted permease; <b>PDBTitle:</b> a protein structure
19	<a href="#">c5gasN</a>	 Alignment		78.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> N: <b>PDB Molecule:</b> archaeal/vacuolar-type h+-atpase subunit i; <b>PDBTitle:</b> thermus thermophilus v/a-atpase, conformation 2
20	<a href="#">c2v50A</a>	 Alignment		77.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein mexb; <b>PDBTitle:</b> the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb
21	<a href="#">d1h0ha1</a>	 Alignment	not modelled	74.9	16	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
22	<a href="#">d2iv2x1</a>	 Alignment	not modelled	74.8	8	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
23	<a href="#">d1tmoa1</a>	 Alignment	not modelled	74.1	18	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
24	<a href="#">d1g8ka1</a>	 Alignment	not modelled	73.4	8	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
25	<a href="#">c5mkkB</a>	 Alignment	not modelled	72.8	21	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> multidrug resistance abc transporter atp-binding and <b>PDBTitle:</b> crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
26	<a href="#">d1ogya1</a>	 Alignment	not modelled	72.1	14	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
27	<a href="#">c5x5yF</a>	 Alignment	not modelled	71.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> a membrane protein complex
28	<a href="#">d1kqfa1</a>	 Alignment	not modelled	71.4	24	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain

29	<a href="#">c2fhdA</a>	Alignment	not modelled	70.4	11	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rhp9/crb2; <b>PDBTitle:</b> crystal structure of crb2 tandem tudor domains
30	<a href="#">c1ciiA</a>	Alignment	not modelled	69.9	16	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
31	<a href="#">c1eu1A</a>	Alignment	not modelled	69.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyl sulfoxide reductase; <b>PDBTitle:</b> the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
32	<a href="#">d1eu1a1</a>	Alignment	not modelled	68.8	16	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
33	<a href="#">c2mrnB</a>	Alignment	not modelled	68.8	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin maze; <b>PDBTitle:</b> structure of truncated ecmaze
34	<a href="#">d1y5ia1</a>	Alignment	not modelled	68.4	24	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
35	<a href="#">c6mjpF</a>	Alignment	not modelled	66.8	13	<b>PDB header:</b> lipid transport <b>Chain:</b> F: <b>PDB Molecule:</b> fig000988: predicted permease; <b>PDBTitle:</b> lptb(e163q)fgc from vibrio cholerae
36	<a href="#">c2v45A</a>	Alignment	not modelled	66.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
37	<a href="#">c1oy8A</a>	Alignment	not modelled	65.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sacriflavine resistance protein b; <b>PDBTitle:</b> structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
38	<a href="#">d1dmra1</a>	Alignment	not modelled	65.6	13	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
39	<a href="#">d1zq1a1</a>	Alignment	not modelled	65.2	21	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> GatD N-terminal domain-like <b>Family:</b> GatD N-terminal domain-like
40	<a href="#">c2nyaF</a>	Alignment	not modelled	65.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
41	<a href="#">c1h5nC</a>	Alignment	not modelled	64.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dmsO reductase; <b>PDBTitle:</b> dmsO reductase modified by the presence of dms and air
42	<a href="#">c1h0hA</a>	Alignment	not modelled	63.7	16	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase subunit alpha; <b>PDBTitle:</b> tungsten containing formate dehydrogenase from desulfovibrio gigas
43	<a href="#">c5I75G</a>	Alignment	not modelled	63.1	18	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> fig000906: predicted permease; <b>PDBTitle:</b> a protein structure
44	<a href="#">c6btmD</a>	Alignment	not modelled	62.0	12	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> alternative complex iii subunit d; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
45	<a href="#">c1tmoA</a>	Alignment	not modelled	60.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trimethylamine n-oxide reductase; <b>PDBTitle:</b> trimethylamine n-oxide reductase from shewanella massilia
46	<a href="#">c2pjhB</a>	Alignment	not modelled	60.5	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structural model of the p97 n domain- npl4 ubd complex
47	<a href="#">c6cz7C</a>	Alignment	not modelled	59.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> arra; <b>PDBTitle:</b> the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3
48	<a href="#">c1vlfQ</a>	Alignment	not modelled	59.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> pyrogallol hydroxytransferase large subunit; <b>PDBTitle:</b> crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici complexed with inhibitor 1,2,4,5-3 tetrahydroxy-benzene
49	<a href="#">c4aayE</a>	Alignment	not modelled	58.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> aroa; <b>PDBTitle:</b> crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
50	<a href="#">c1g8jC</a>	Alignment	not modelled	58.3	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> arsenite oxidase; <b>PDBTitle:</b> crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
51	<a href="#">c5t5iL</a>	Alignment	not modelled	58.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase subunit fwd; <b>PDBTitle:</b> tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
52	<a href="#">d1mvfd</a>	Alignment	not modelled	57.3	10	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> Kis/PemI addiction antidote
53	<a href="#">c1kqgA</a>	Alignment	not modelled	57.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, major subunit; <b>PDBTitle:</b> formate dehydrogenase n from e. coli

54	<a href="#">c2etnA</a>	Alignment	not modelled	56.1	24	<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
55	<a href="#">c5x5yG</a>	Alignment	not modelled	55.6	20	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> a membrane protein complex
56	<a href="#">c1ogyA</a>	Alignment	not modelled	55.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
57	<a href="#">c2ivfA</a>	Alignment	not modelled	53.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ethylbenzene dehydrogenase alpha-subunit; <b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum
58	<a href="#">c5ch7E</a>	Alignment	not modelled	53.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> dmsO reductase family type ii enzyme, molybdopterin <b>PDBTitle:</b> crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from azospira sullum ps
59	<a href="#">c2ki8A</a>	Alignment	not modelled	52.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase, <b>PDBTitle:</b> solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
60	<a href="#">c2p4vA</a>	Alignment	not modelled	52.3	12	<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
61	<a href="#">d1ylea1</a>	Alignment	not modelled	52.0	27	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> AstA-like
62	<a href="#">d1e32a1</a>	Alignment	not modelled	51.6	20	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
63	<a href="#">c2e7zA</a>	Alignment	not modelled	50.5	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylene hydratase ahy; <b>PDBTitle:</b> acetylene hydratase from pelobacter acetylenicus
64	<a href="#">c2vpyE</a>	Alignment	not modelled	49.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> thiosulfate reductase; <b>PDBTitle:</b> polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
65	<a href="#">d1ub4c</a>	Alignment	not modelled	47.8	13	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> Kis/PemI addiction antidote
66	<a href="#">c1y5iA</a>	Alignment	not modelled	47.4	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> respiratory nitrate reductase 1 alpha chain; <b>PDBTitle:</b> the crystal structure of the narghi mutant nari-k86a
67	<a href="#">c6ajjA</a>	Alignment	not modelled	46.6	15	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> drug exporters of the rnd superfamily-like protein, <b>PDBTitle:</b> crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
68	<a href="#">c6btmB</a>	Alignment	not modelled	43.2	26	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> alternative complex iii subunit b; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
69	<a href="#">d2vbu1</a>	Alignment	not modelled	42.6	16	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin kinase-like <b>Family:</b> CTP-dependent riboflavin kinase-like
70	<a href="#">c6mjpG</a>	Alignment	not modelled	41.1	9	<b>PDB header:</b> lipid transport <b>Chain:</b> G: <b>PDB Molecule:</b> lps export abc transporter permease lptg; <b>PDBTitle:</b> lptb(e163q)fgc from vibrio cholerae
71	<a href="#">c1wlfA</a>	Alignment	not modelled	41.1	28	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisome biogenesis factor 1; <b>PDBTitle:</b> structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain
72	<a href="#">c2fugC</a>	Alignment	not modelled	39.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> snadh-quinone oxidoreductase chain 3; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
73	<a href="#">c6owsB</a>	Alignment	not modelled	36.5	10	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> efflux pump membrane transporter; <b>PDBTitle:</b> cryo-em structure of an acinetobacter baumannii multidrug efflux pump
74	<a href="#">c2yujA</a>	Alignment	not modelled	36.1	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin fusion degradation 1-like; <b>PDBTitle:</b> solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
75	<a href="#">c3bmbB</a>	Alignment	not modelled	36.0	25	<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
76	<a href="#">c1zc1A</a>	Alignment	not modelled	35.8	15	<b>PDB header:</b> protein turnover <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin fusion degradation protein 1; <b>PDBTitle:</b> ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
77	<a href="#">d2f23a2</a>	Alignment	not modelled	35.5	22	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> GreA transcript cleavage factor, C-terminal domain
78	<a href="#">c6f0kB</a>	Alignment	not modelled	35.4	29	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> fe-s-cluster-containing hydrogenase; <b>PDBTitle:</b> alternative complex iii

79	<a href="#">c3l0oA</a>	Alignment	not modelled	34.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> transcription termination factor rho; <b>PDBTitle:</b> structure of rna-free rho transcription termination factor from2 thermotoga maritima
80	<a href="#">d2etna2</a>	Alignment	not modelled	32.6	22	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> GreA transcript cleavage factor, C-terminal domain
81	<a href="#">c2pn0D</a>	Alignment	not modelled	31.2	36	<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
82	<a href="#">c2l66B</a>	Alignment	not modelled	30.3	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcription regulator, abrb family; <b>PDBTitle:</b> the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
83	<a href="#">c4tqxA</a>	Alignment	not modelled	28.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sortase; <b>PDBTitle:</b> molecular basis of streptococcus mutans sortase a inhibition by2 chalcone.
84	<a href="#">c3l0oB</a>	Alignment	not modelled	25.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> transcription termination factor rho; <b>PDBTitle:</b> structure of rna-free rho transcription termination factor from2 thermotoga maritima
85	<a href="#">c5hu4A</a>	Alignment	not modelled	24.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine protease; <b>PDBTitle:</b> crystal structure of listeria monocytogenes sortase a
86	<a href="#">c2kw8A</a>	Alignment	not modelled	24.3	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> lpxtg-site transpeptidase family protein; <b>PDBTitle:</b> solution structure of bacillus anthracis sortase a (srta)2 transpeptidase
87	<a href="#">d1cz5a1</a>	Alignment	not modelled	24.0	15	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
88	<a href="#">d2d6fa1</a>	Alignment	not modelled	23.0	21	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> GatD N-terminal domain-like <b>Family:</b> GatD N-terminal domain-like
89	<a href="#">c1xpuB</a>	Alignment	not modelled	22.9	23	<b>PDB header:</b> transcription/rna <b>Chain:</b> B: <b>PDB Molecule:</b> rho transcription termination factor; <b>PDBTitle:</b> structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
90	<a href="#">c4ymuC</a>	Alignment	not modelled	22.5	10	<b>PDB header:</b> protein binding/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> abc-type amino acid transport system, permease component; <b>PDBTitle:</b> crystal structure of an amino acid abc transporter complex with2 arginines and atps
91	<a href="#">d2hyda2</a>	Alignment	not modelled	21.8	5	<b>Fold:</b> ABC transporter transmembrane region <b>Superfamily:</b> ABC transporter transmembrane region <b>Family:</b> ABC transporter transmembrane region
92	<a href="#">c3ltiA</a>	Alignment	not modelled	19.1	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta; <b>PDBTitle:</b> crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-beta4 domains
93	<a href="#">d1t2wa</a>	Alignment	not modelled	18.4	14	<b>Fold:</b> Sortase <b>Superfamily:</b> Sortase <b>Family:</b> Sortase
94	<a href="#">d1rqpa1</a>	Alignment	not modelled	18.3	17	<b>Fold:</b> Bacterial fluorinating enzyme, C-terminal domain <b>Superfamily:</b> Bacterial fluorinating enzyme, C-terminal domain <b>Family:</b> Bacterial fluorinating enzyme, C-terminal domain
95	<a href="#">c2w1tB</a>	Alignment	not modelled	17.9	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> stage v sporulation protein t; <b>PDBTitle:</b> crystal structure of b. subtilis spovt
96	<a href="#">d1dzfa2</a>	Alignment	not modelled	17.0	21	<b>Fold:</b> RPB5-like RNA polymerase subunit <b>Superfamily:</b> RPB5-like RNA polymerase subunit <b>Family:</b> RPB5
97	<a href="#">c4aa3A</a>	Alignment	not modelled	16.9	7	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 10, <b>PDBTitle:</b> structure of the human mitochondrial abc transporter,2 abcb10 (plate form)
98	<a href="#">d1udxa3</a>	Alignment	not modelled	16.4	13	<b>Fold:</b> Obg GTP-binding protein C-terminal domain <b>Superfamily:</b> Obg GTP-binding protein C-terminal domain <b>Family:</b> Obg GTP-binding protein C-terminal domain
99	<a href="#">c3l53F</a>	Alignment	not modelled	16.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative fumarylacetoacetate isomerase/hydrolase; <b>PDBTitle:</b> crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica