



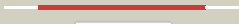

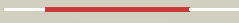

















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0771 (-) _864143_864577
Date	Fri Jul 26 01:50:35 BST 2019
Unique Job ID	5269c47f163f77eb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2af7a1</a>	 Alignment		100.0	23	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> CMD-like
2	<a href="#">c4g9qA</a>	 Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-carboxymuconolactone decarboxylase; <b>PDBTitle:</b> crystal structure of a 4-carboxymuconolactone decarboxylase
3	<a href="#">d2q0ta1</a>	 Alignment		99.9	20	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> AhpD
4	<a href="#">c3d7iB</a>	 Alignment		99.7	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxymuconolactone decarboxylase family protein; <b>PDBTitle:</b> crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
5	<a href="#">d2cwqa1</a>	 Alignment		99.7	12	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> TTHA0727-like
6	<a href="#">d1vkeb</a>	 Alignment		99.6	12	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> CMD-like
7	<a href="#">c5dipB</a>	 Alignment		99.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxide reductase ahpd; <b>PDBTitle:</b> crystal structure of lpg0406 in reduced form from legionella2 pneumophila
8	<a href="#">c3beyC</a>	 Alignment		99.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> conserved protein o27018; <b>PDBTitle:</b> crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
9	<a href="#">c1p8cD</a>	 Alignment		99.5	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of tm1620 (apc4843) from thermotoga2 maritima
10	<a href="#">c2qeua</a>	 Alignment		99.5	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxymuconolactone decarboxylase; <b>PDBTitle:</b> crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
11	<a href="#">d1vkea</a>	 Alignment		99.4	10	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> CMD-like

12	<a href="#">d1knca_</a>	Alignment		99.3	16	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> AhpD
13	<a href="#">d2ouwa1</a>	Alignment		98.6	14	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> TTHA0727-like
14	<a href="#">c3lvyB_</a>	Alignment		96.9	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxymuconolactone decarboxylase family; <b>PDBTitle:</b> crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
15	<a href="#">c6ohiA_</a>	Alignment		95.7	8	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> debrominase bmp8; <b>PDBTitle:</b> crystal structure of the debrominase bmp8 (apo)
16	<a href="#">d2gmya1</a>	Alignment		95.0	15	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> Atu0492-like
17	<a href="#">d2o4da1</a>	Alignment		94.3	14	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> Atu0492-like
18	<a href="#">d2prra1</a>	Alignment		94.3	14	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> Atu0492-like
19	<a href="#">d2oyoal</a>	Alignment		93.9	13	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> Atu0492-like
20	<a href="#">d2pfxa1</a>	Alignment		93.6	10	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> Atu0492-like
21	<a href="#">c4d9jl_</a>	Alignment	not modelled	93.2	16	<b>PDB header:</b> de novo protein <b>Chain:</b> I: <b>PDB Molecule:</b> designed 16nm tetrahedral protein cage containing non-haem <b>PDBTitle:</b> structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains
22	<a href="#">c3c1B_</a>	Alignment	not modelled	92.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative antioxidant defense protein mlr4105; <b>PDBTitle:</b> crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
23	<a href="#">c5dj4D_</a>	Alignment	not modelled	77.6	21	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> sestrin-2; <b>PDBTitle:</b> leucine-bound sestrin2 from homo sapiens
24	<a href="#">c5gzxD_</a>	Alignment	not modelled	64.7	8	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> (r)-2-haloacid dehalogenase; <b>PDBTitle:</b> the complex structure of d-2-haloacid dehalogenase mutant with d-2-cpa
25	<a href="#">c5twaA_</a>	Alignment	not modelled	45.4	34	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-x homologous protein, bhp2; <b>PDBTitle:</b> crystal structure of geodia cydonium bhp2 in complex with lubomirskia2 baicalensis bak-2
26	<a href="#">c5tmxA_</a>	Alignment	not modelled	32.5	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> protein sini; <b>PDBTitle:</b> solution structure of sini, antagonist to the master biofilm-regulator2 sinr in bacillus subtilis
27	<a href="#">c3pybB_</a>	Alignment	not modelled	28.5	27	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ent-copalyl diphosphate synthase, chloroplastic; <b>PDBTitle:</b> crystal structure of ent-copalyl diphosphate synthase from arabidopsis2 thaliana in complex with 13-aza-13,14-dihydrocopalyl diphosphate

28	<a href="#">c3s9vD_</a>	Alignment	not modelled	27.0	22	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> abietadiene synthase, chloroplastic; <b>PDBTitle:</b> abietadiene synthase from abies grandis
29	<a href="#">c4wpxB_</a>	Alignment	not modelled	22.5	19	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> putative sac3 family protein; <b>PDBTitle:</b> chaetomium thermophilum trex2 cid domain complex
30	<a href="#">c5aonB_</a>	Alignment	not modelled	19.9	27	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxin 14; <b>PDBTitle:</b> crystal structure of the conserved n-terminal domain of2 pex14 from trypanosoma brucei
31	<a href="#">c5iooA_</a>	Alignment	not modelled	19.1	28	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> avpa; <b>PDBTitle:</b> accommodation of massive sequence variation in nanoarchaeota by the c-2 type lectin fold
32	<a href="#">c3ff5B_</a>	Alignment	not modelled	18.4	27	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal biogenesis factor 14; <b>PDBTitle:</b> crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
33	<a href="#">c3p5rB_</a>	Alignment	not modelled	17.6	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> taxadiene synthase; <b>PDBTitle:</b> crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
34	<a href="#">c5i87A_</a>	Alignment	not modelled	17.4	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peroxin 14; <b>PDBTitle:</b> targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis.
35	<a href="#">c2w85A_</a>	Alignment	not modelled	15.7	27	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal membrane anchor protein pex14; <b>PDBTitle:</b> structure of pex14 in complex with pex19
36	<a href="#">d1dwka1</a>	Alignment	not modelled	15.5	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Cyanase N-terminal domain
37	<a href="#">c5oynB_</a>	Alignment	not modelled	14.1	15	<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
38	<a href="#">d1b0na1</a>	Alignment	not modelled	13.9	17	<b>Fold:</b> Dimerisation interlock <b>Superfamily:</b> SinR repressor dimerisation domain-like <b>Family:</b> SinR repressor dimerisation domain-like
39	<a href="#">d1mpga1</a>	Alignment	not modelled	13.0	12	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> DNA repair glycosylase, 2 C-terminal domains
40	<a href="#">c3s6iA_</a>	Alignment	not modelled	12.5	13	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna-3-methyladenine glycosylase 1; <b>PDBTitle:</b> schizosaccharomyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
41	<a href="#">d1qaxa2</a>	Alignment	not modelled	12.1	14	<b>Fold:</b> Substrate-binding domain of HMG-CoA reductase <b>Superfamily:</b> Substrate-binding domain of HMG-CoA reductase <b>Family:</b> Substrate-binding domain of HMG-CoA reductase
42	<a href="#">d1sqwa2</a>	Alignment	not modelled	11.8	39	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Pre-PUA domain <b>Family:</b> Nip7p homolog, N-terminal domain
43	<a href="#">c5ze4A_</a>	Alignment	not modelled	11.8	7	<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
44	<a href="#">d1r5ta_</a>	Alignment	not modelled	11.7	22	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
45	<a href="#">d2g39a2</a>	Alignment	not modelled	11.7	25	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase alpha subunit-like
46	<a href="#">c3saeA_</a>	Alignment	not modelled	11.5	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-bisabolene synthase; <b>PDBTitle:</b> structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production
47	<a href="#">c6ckqA_</a>	Alignment	not modelled	10.5	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusB; <b>PDBTitle:</b> solution structure of the burkholderia thailandensis transcription2 antitermination protein nusB (bth_i1529) - seattle structural3 genomics center for infectious disease target butha.17903.a
48	<a href="#">c5tn2B_</a>	Alignment	not modelled	10.4	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator sinr; <b>PDBTitle:</b> solution structure of the c-terminal multimerization domain of the2 master biofilm-regulator sinr from bacillus subtilis
49	<a href="#">c4b24A_</a>	Alignment	not modelled	10.4	11	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> probable dna-3-methyladenine glycosylase 2; <b>PDBTitle:</b> unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2
50	<a href="#">c1qaxA_</a>	Alignment	not modelled	10.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (3-hydroxy-3-methylglutaryl-coenzyme a reductase); <b>PDBTitle:</b> ternary complex of pseudomonas mevalonii hmg-coa reductase with hmg-2 coa and nad+
51	<a href="#">d1adta1</a>	Alignment	not modelled	10.2	11	<b>Fold:</b> Domain of early E2A DNA-binding protein, ADDBP <b>Superfamily:</b> Domain of early E2A DNA-binding protein, ADDBP <b>Family:</b> Domain of early E2A DNA-binding protein, ADDBP
52	<a href="#">c2mn4A_</a>	Alignment	not modelled	9.0	32	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> computational designed protein based on structure template <b>PDBTitle:</b> nmr solution structure of a computational designed protein based on2 structure template 1cy5 <b>PDB header:</b> lyase

53	<a href="#">c5j84A_</a>	Alignment	not modelled	9.0	15	<b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase; <b>PDBTitle:</b> crystal structure of l-arabinonate dehydratase in holo-form
54	<a href="#">c5a2tG_</a>	Alignment	not modelled	8.5	3	<b>PDB header:</b> viral protein <b>Chain:</b> G: <b>PDB Molecule:</b> coat protein; <b>PDBTitle:</b> the molecular basis for flexibility in the flexible2 filamentous plant viruses
55	<a href="#">c2rohA_</a>	Alignment	not modelled	8.5	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> telomere binding protein-1; <b>PDBTitle:</b> the dna binding domain of rtbp1
56	<a href="#">c6nmiD_</a>	Alignment	not modelled	8.2	10	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> general transcription factor iih subunit 4, p52; <b>PDBTitle:</b> cryo-em structure of the human tfiih core complex
57	<a href="#">c4dbgB_</a>	Alignment	not modelled	7.9	8	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ring finger protein 31; <b>PDBTitle:</b> crystal structure of hoil-1-ubl complexed with a hoip-uba derivative
58	<a href="#">c3s19H_</a>	Alignment	not modelled	7.3	20	<b>PDB header:</b> signaling protein, protein binding <b>Chain:</b> H: <b>PDB Molecule:</b> b-cell cl/lymphoma 9 protein; <b>PDBTitle:</b> x-ray structure of beta catenin in complex with bcl9
59	<a href="#">d1ey1a_</a>	Alignment	not modelled	6.9	10	<b>Fold:</b> NusB-like <b>Superfamily:</b> NusB-like <b>Family:</b> Antitermination factor NusB
60	<a href="#">c2yg8B_</a>	Alignment	not modelled	6.8	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna-3-methyladenine glycosidase ii, putative; <b>PDBTitle:</b> structure of an unusual 3-methyladenine dna glycosylase ii (alka) from2 deinococcus radiodurans
61	<a href="#">c4wuiA_</a>	Alignment	not modelled	6.6	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> n-(5'-phosphoribosyl)anthranilate isomerase; <b>PDBTitle:</b> crystal structure of trpf from jonesia denitrificans
62	<a href="#">c4kt3B_</a>	Alignment	not modelled	6.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> structure of a type vi secretion system effector-immunity complex from2 pseudomonas protegens
63	<a href="#">d1sqaq1</a>	Alignment	not modelled	6.5	10	<b>Fold:</b> NusB-like <b>Superfamily:</b> NusB-like <b>Family:</b> RmsB N-terminal domain-like
64	<a href="#">c2dvwB_</a>	Alignment	not modelled	6.5	6	<b>PDB header:</b> cell cycle/protein-binding <b>Chain:</b> B: <b>PDB Molecule:</b> 26s protease regulatory subunit 6b; <b>PDBTitle:</b> structure of the oncoprotein gankyrin in complex with s62 atpase of the 26s proteasome
65	<a href="#">c3qauA_</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxy-3-methylglutaryl-coenzyme a reductase; <b>PDBTitle:</b> 3-hydroxy-3-methylglutaryl-coenzyme a reductase from streptococcus2 pneumoniae
66	<a href="#">c1sqwA_</a>	Alignment	not modelled	6.4	39	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> saccharomyces cerevisiae nip7p homolog; <b>PDBTitle:</b> crystal structure of kd93, a novel protein expressed in the2 human pro
67	<a href="#">d1r1ra1</a>	Alignment	not modelled	5.7	7	<b>Fold:</b> R1 subunit of ribonucleotide reductase, N-terminal domain <b>Superfamily:</b> R1 subunit of ribonucleotide reductase, N-terminal domain <b>Family:</b> R1 subunit of ribonucleotide reductase, N-terminal domain
68	<a href="#">c1yvrA_</a>	Alignment	not modelled	5.6	8	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 60-kda ss-a/ro ribonucleoprotein; <b>PDBTitle:</b> ro autoantigen
69	<a href="#">c3u5cN_</a>	Alignment	not modelled	5.6	25	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 40s ribosomal protein s13; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
70	<a href="#">c5i4aC_</a>	Alignment	not modelled	5.5	29	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> argonaute protein; <b>PDBTitle:</b> x-ray crystal structure of marinitoga piezophila argonaute in complex2 with 5' oh guide rna
71	<a href="#">c1zaxX_</a>	Alignment	not modelled	5.4	40	<b>PDB header:</b> structural protein <b>Chain:</b> X: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
72	<a href="#">c1zavX_</a>	Alignment	not modelled	5.4	40	<b>PDB header:</b> structural protein <b>Chain:</b> X: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
73	<a href="#">c1zavY_</a>	Alignment	not modelled	5.4	40	<b>PDB header:</b> structural protein <b>Chain:</b> Y: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
74	<a href="#">c1zaxY_</a>	Alignment	not modelled	5.4	40	<b>PDB header:</b> structural protein <b>Chain:</b> Y: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
75	<a href="#">c1zaxV_</a>	Alignment	not modelled	5.4	40	<b>PDB header:</b> structural protein <b>Chain:</b> V: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
76	<a href="#">c1zavV_</a>	Alignment	not modelled	5.4	40	<b>PDB header:</b> structural protein <b>Chain:</b> V: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
77	<a href="#">c1zavW_</a>	Alignment	not modelled	5.4	40	<b>PDB header:</b> structural protein <b>Chain:</b> W: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
78	<a href="#">c1zaxW_</a>	Alignment	not modelled	5.4	40	<b>PDB header:</b> structural protein <b>Chain:</b> W: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b

79	<a href="#">c1zaxU_</a>	Alignment	not modelled	5.4	40	<b>PDB header:</b> structural protein <b>Chain:</b> U: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
80	<a href="#">d1zavu1</a>	Alignment	not modelled	5.4	40	<b>Fold:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Superfamily:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Family:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain
81	<a href="#">c1zavU_</a>	Alignment	not modelled	5.4	40	<b>PDB header:</b> structural protein <b>Chain:</b> U: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
82	<a href="#">d1a9xa1</a>	Alignment	not modelled	5.3	16	<b>Fold:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Superfamily:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Family:</b> Carbamoyl phosphate synthetase, large subunit connection domain
83	<a href="#">c4huqS_</a>	Alignment	not modelled	5.3	31	<b>PDB header:</b> hydrolase <b>Chain:</b> S: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a transporter
84	<a href="#">c5odvB_</a>	Alignment	not modelled	5.2	12	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> coat protein; <b>PDBTitle:</b> structure of watermelon mosaic virus potyvirus.
85	<a href="#">c4aajA_</a>	Alignment	not modelled	5.2	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> n-(5'-phosphoribosyl)anthranilate isomerase; <b>PDBTitle:</b> structure of n-(5'-phosphoribosyl)anthranilate isomerase from <i>2 pyrococcus furiosus</i>
86	<a href="#">c2v07A_</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c6; <b>PDBTitle:</b> structure of the arabidopsis thaliana cytochrome c6a v52q variant
87	<a href="#">c3p5nA_</a>	Alignment	not modelled	5.2	29	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin uptake protein; <b>PDBTitle:</b> structure and mechanism of the s component of a bacterial ecf2 transporter
88	<a href="#">c3sl9F_</a>	Alignment	not modelled	5.1	20	<b>PDB header:</b> signaling protein, protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> b-cell cl/lymphoma 9 protein; <b>PDBTitle:</b> x-ray structure of beta catenin in complex with bcl9
89	<a href="#">c3sl9C_</a>	Alignment	not modelled	5.1	20	<b>PDB header:</b> signaling protein, protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> b-cell cl/lymphoma 9 protein; <b>PDBTitle:</b> x-ray structure of beta catenin in complex with bcl9
90	<a href="#">c4nvsB_</a>	Alignment	not modelled	5.0	21	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative enzyme, glyoxalase family; <b>PDBTitle:</b> crystal structure of the q18cp6_clod6 protein from glyoxalase family.2 northeast structural genomics consortium target cfr3
91	<a href="#">c2gl7C_</a>	Alignment	not modelled	5.0	20	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> b-cell lymphoma 9 protein; <b>PDBTitle:</b> crystal structure of a beta-catenin/bcl9/tcf4 complex