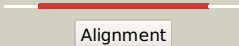



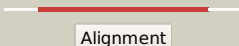

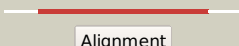

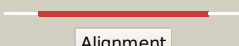

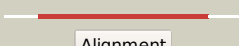

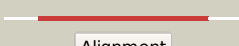















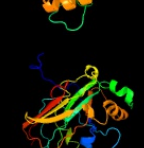

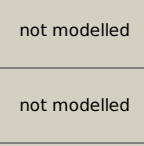


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2993c_(-)_3350284_3351003
Date	Thu Aug 8 16:20:16 BST 2019
Unique Job ID	17af2dede0e704fb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4dbhA_</a>	 Alignment		100.0	55	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; <b>PDBTitle:</b> crystal structure of cg1458 with inhibitor
2	<a href="#">c6iyxB_</a>	 Alignment		100.0	46	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase; <b>PDBTitle:</b> fumarylacetoacetate hydrolase (eafah) from psychrophilic2 exiguobacterium antarcticum
3	<a href="#">c2dfuB_</a>	 Alignment		100.0	39	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; <b>PDBTitle:</b> crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
4	<a href="#">c3qdfA_</a>	 Alignment		100.0	95	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; <b>PDBTitle:</b> crystal structure of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from mycobacterium marinum
5	<a href="#">c3r6oA_</a>	 Alignment		100.0	36	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; <b>PDBTitle:</b> crystal structure of a probable 2-hydroxyhepta-2,4-diene-1,7-2 dioate isomerase from mycobacterium abscessus
6	<a href="#">c1wzoC_</a>	 Alignment		100.0	43	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> hpce; <b>PDBTitle:</b> crystal structure of the hpce from thermus thermophilus hb8
7	<a href="#">c1i7oC_</a>	 Alignment		100.0	36	<b>PDB header:</b> isomerase, lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxyphenylacetate degradation bifunctional <b>PDBTitle:</b> crystal structure of hpce
8	<a href="#">c3lzkC_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> fumarylacetoacetate hydrolase family protein; <b>PDBTitle:</b> the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
9	<a href="#">c3s52A_</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative fumarylacetoacetate hydrolase family protein; <b>PDBTitle:</b> crystal structure of a putative fumarylacetoacetate hydrolase family2 protein from yersinia pestis co92
10	<a href="#">c4maqB_</a>	 Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative fumarylpyruvate hydrolase; <b>PDBTitle:</b> crystal structure of a putative fumarylpyruvate hydrolase from2 burkholderia cenocepacia
11	<a href="#">c2q1dX_</a>	 Alignment		100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> X: <b>PDB Molecule:</b> 2-keto-3-deoxy-d-arabinonate dehydratase; <b>PDBTitle:</b> 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and2 2,5-dioxopentanoate

12	<a href="#">d1gtta2</a>	Alignment		100.0	36	<b>Fold:</b> FAH <b>Superfamily:</b> FAH <b>Family:</b> FAH
13	<a href="#">c6jvwA</a>	Alignment		100.0	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maleylpyruvate hydrolase; <b>PDBTitle:</b> crystal structure of maleylpyruvate hydrolase from sphingobium sp.2 syk-6 in complex with manganese (ii) ion and pyruvate
14	<a href="#">c3l53F</a>	Alignment		100.0	34	<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
15	<a href="#">d1gtta1</a>	Alignment		100.0	31	<b>Fold:</b> FAH <b>Superfamily:</b> FAH <b>Family:</b> FAH
16	<a href="#">d1nr9a</a>	Alignment		100.0	37	<b>Fold:</b> FAH <b>Superfamily:</b> FAH <b>Family:</b> FAH
17	<a href="#">d1sawa</a>	Alignment		100.0	43	<b>Fold:</b> FAH <b>Superfamily:</b> FAH <b>Family:</b> FAH
18	<a href="#">d1nkqa</a>	Alignment		100.0	34	<b>Fold:</b> FAH <b>Superfamily:</b> FAH <b>Family:</b> FAH
19	<a href="#">c4qkuC</a>	Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> crystal structure of a putative hydrolase from burkholderia2 cenocepacia
20	<a href="#">c1hyoB</a>	Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fumarylacetoacetate hydrolase; <b>PDBTitle:</b> crystal structure of fumarylacetoacetate hydrolase2 complexed with 4-(hydroxymethylphosphinoyl)-3-oxo-butanoic3 acid
21	<a href="#">d1hyoa2</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> FAH <b>Superfamily:</b> FAH <b>Family:</b> FAH
22	<a href="#">d1sv6a</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> FAH <b>Superfamily:</b> FAH <b>Family:</b> FAH
23	<a href="#">c5d2hA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-oxalocrotonate decarboxylase nahk; <b>PDBTitle:</b> 4-oxalocrotonate decarboxylase from pseudomonas putida g7 - complexed2 with magnesium and alpha-ketoglutarate
24	<a href="#">c2eb5D</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-oxo-hept-3-ene-1,7-dioate hydratase; <b>PDBTitle:</b> crystal structure of hpcg complexed with oxalate
25	<a href="#">d2cu3a1</a>	Alignment	not modelled	62.4	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> ThiS
26	<a href="#">c2ki0A</a>	Alignment	not modelled	57.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiamin biosynthesis this; <b>PDBTitle:</b> solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
27	<a href="#">c6b4aB</a>	Alignment	not modelled	51.9	18	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> doublecortin; <b>PDBTitle:</b> crystal structure of the c-terminal domain of doublecortin (tgdcx)2 from toxoplasma gondii me49
28	<a href="#">d2evra2</a>	Alignment	not modelled	47.8	32	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> NlpC/P60 <b>PDB header:</b> biosynthetic protein

29	<a href="#">c3cwiA_</a>	Alignment	not modelled	45.2	16	<b>Chain:</b> A: <b>PDB Molecule:</b> thiamine-biosynthesis protein this; <b>PDBTitle:</b> crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
30	<a href="#">d1zud21</a>	Alignment	not modelled	44.3	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/This <b>Family:</b> This
31	<a href="#">d2f4la1</a>	Alignment	not modelled	40.0	33	<b>Fold:</b> CUB-like <b>Superfamily:</b> Acetamidase/Formamidase-like <b>Family:</b> Acetamidase/Formamidase-like
32	<a href="#">c1tygG_</a>	Alignment	not modelled	32.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> G: <b>PDB Molecule:</b> yjbs; <b>PDBTitle:</b> structure of the thiazole synthase/this complex
33	<a href="#">d1tygb_</a>	Alignment	not modelled	29.9	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/This <b>Family:</b> This
34	<a href="#">c4ejqB_</a>	Alignment	not modelled	24.9	38	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinesin-like protein kif1a; <b>PDBTitle:</b> crystal structure of kif1a c-c1-fha
35	<a href="#">d2g1la1</a>	Alignment	not modelled	21.3	39	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
36	<a href="#">c2n84A_</a>	Alignment	not modelled	20.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of the fha domain of tbpar42
37	<a href="#">d2vbua1</a>	Alignment	not modelled	19.9	46	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin kinase-like <b>Family:</b> CTP-dependent riboflavin kinase-like
38	<a href="#">d1t8sa_</a>	Alignment	not modelled	19.9	19	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
39	<a href="#">c2dnfA_</a>	Alignment	not modelled	19.3	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> doublecortin domain-containing protein 2; <b>PDBTitle:</b> solution structure of rsgi ruh-062, a dcx domain from human
40	<a href="#">d1pk6c_</a>	Alignment	not modelled	18.6	13	<b>Fold:</b> TNF-like <b>Superfamily:</b> TNF-like <b>Family:</b> TNF-like
41	<a href="#">c5fwhA_</a>	Alignment	not modelled	18.5	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> essc; <b>PDBTitle:</b> n-terminal fha domain from essc a component of the2 bacterial type vii secretion apparatus
42	<a href="#">d2ba0a2</a>	Alignment	not modelled	17.9	39	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Ribosomal L27 protein-like <b>Family:</b> ECR1 N-terminal domain-like
43	<a href="#">c3pbiA_</a>	Alignment	not modelled	17.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> invasion protein; <b>PDBTitle:</b> structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
44	<a href="#">c3mjJD_</a>	Alignment	not modelled	17.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> predicted acetamidase/formamidase; <b>PDBTitle:</b> crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
45	<a href="#">c6ccdA_</a>	Alignment	not modelled	17.3	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding/permease protein rv1747; <b>PDBTitle:</b> the crystal structure of mycobacterium tuberculosis rv1747 fha-1
46	<a href="#">c1qr3A_</a>	Alignment	not modelled	16.5	8	<b>PDB header:</b> collagen <b>Chain:</b> A: <b>PDB Molecule:</b> collagen x; <b>PDBTitle:</b> structure of the human collagen x nc1 trimer
47	<a href="#">d1qr3a_</a>	Alignment	not modelled	16.5	8	<b>Fold:</b> TNF-like <b>Superfamily:</b> TNF-like <b>Family:</b> TNF-like
48	<a href="#">c4nv4A_</a>	Alignment	not modelled	16.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> signal peptidase i; <b>PDBTitle:</b> 1.8 angstrom crystal structure of signal peptidase i from bacillus2 anthracis.
49	<a href="#">c3h41A_</a>	Alignment	not modelled	16.1	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nlp/p60 family protein; <b>PDBTitle:</b> crystal structure of a nlp/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
50	<a href="#">c6ar2B_</a>	Alignment	not modelled	14.6	31	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> sarcolemmal membrane-associated protein; <b>PDBTitle:</b> structure of human slmap fha domain in complex with pmst2
51	<a href="#">d1ybfa_</a>	Alignment	not modelled	14.6	21	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
52	<a href="#">c3kw0D_</a>	Alignment	not modelled	14.4	33	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cysteine peptidase; <b>PDBTitle:</b> crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
53	<a href="#">c2xivA_</a>	Alignment	not modelled	14.3	21	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical invasion protein; <b>PDBTitle:</b> structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis
54	<a href="#">c3fm8A_</a>	Alignment	not modelled	14.3	42	<b>PDB header:</b> transport protein/hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif13b; <b>PDBTitle:</b> crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)

55	<a href="#">c5b6IA</a>	Alignment	not modelled	13.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine protease hhoa; <b>PDBTitle:</b> structure of deg protease hhoa from synechocystis sp. pcc 6803
56	<a href="#">c3qt2A</a>	Alignment	not modelled	13.5	45	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c
57	<a href="#">c3qo6B</a>	Alignment	not modelled	13.1	29	<b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 1, chloroplastic; <b>PDBTitle:</b> crystal structure analysis of the plant protease deg1
58	<a href="#">c4wviA</a>	Alignment	not modelled	13.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,signal peptidase lb; <b>PDBTitle:</b> crystal structure of the type-i signal peptidase from staphylococcus2 aureus (spsb) in complex with a substrate peptide (pep2).
59	<a href="#">c2eh0A</a>	Alignment	not modelled	12.7	35	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif1b; <b>PDBTitle:</b> solution structure of the fha domain from human kinesin-2 like protein kif1b
60	<a href="#">c3m9bK</a>	Alignment	not modelled	12.6	15	<b>PDB header:</b> chaperone <b>Chain:</b> K: <b>PDB Molecule:</b> proteasome-associated atpase; <b>PDBTitle:</b> crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
61	<a href="#">c5svbD</a>	Alignment	not modelled	12.0	15	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> acetone carboxylase alpha subunit; <b>PDBTitle:</b> mechanism of atp-dependent acetone carboxylation, acetone carboxylase2 amp bound structure
62	<a href="#">c5kc5A</a>	Alignment	not modelled	11.9	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cerebellin-1; <b>PDBTitle:</b> crystal structure of the cbln1 c1q domain trimer
63	<a href="#">c6b8cA</a>	Alignment	not modelled	11.8	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nlp/p60; <b>PDBTitle:</b> crystal structure of nlp/p60 domain of peptidoglycan hydrolase saga
64	<a href="#">c4eqxA</a>	Alignment	not modelled	11.7	38	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif1a; <b>PDBTitle:</b> crystal structure of kif1a cc1-fha tandem
65	<a href="#">d2je6i2</a>	Alignment	not modelled	11.5	21	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Ribosomal L27 protein-like <b>Family:</b> ECR1 N-terminal domain-like
66	<a href="#">c1rl2A</a>	Alignment	not modelled	11.2	25	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (ribosomal protein l2); <b>PDBTitle:</b> ribosomal protein l2 rna-binding domain from bacillus2 stearothermophilus
67	<a href="#">c5n76C</a>	Alignment	not modelled	11.0	32	<b>PDB header:</b> nickel-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> coot; <b>PDBTitle:</b> crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
68	<a href="#">c1kqsA</a>	Alignment	not modelled	10.9	22	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal protein l2; <b>PDBTitle:</b> the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis
69	<a href="#">c3ccdD</a>	Alignment	not modelled	10.8	19	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> prophage muso2, 43 kda tail protein; <b>PDBTitle:</b> crystal structure of prophage muso2, 43 kda tail protein from2 shewanella oneidensis
70	<a href="#">c4jonA</a>	Alignment	not modelled	10.8	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> centrosomal protein of 170 kda; <b>PDBTitle:</b> crystal structure of a centrosomal protein 170kda, transcript variant2 beta (cep170) from homo sapiens at 2.15 a resolution (psi community3 target, sundstrom)
71	<a href="#">d1yvca1</a>	Alignment	not modelled	10.7	44	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> TRAM domain
72	<a href="#">c5l9wA</a>	Alignment	not modelled	10.5	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetophenone carboxylase delta subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
73	<a href="#">d2gp4a1</a>	Alignment	not modelled	10.2	21	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IlvD-like <b>Family:</b> IlvD/EDD C-terminal domain-like
74	<a href="#">c5ze4A</a>	Alignment	not modelled	10.2	36	<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
75	<a href="#">c2pkpA</a>	Alignment	not modelled	10.1	37	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> homoaconitase small subunit; <b>PDBTitle:</b> crystal structure of 3-isopropylmalate dehydratase (leud)2 from methanocaldococcus jannaschii dsm2661 (mj1271)
76	<a href="#">c6a8wA</a>	Alignment	not modelled	10.1	38	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 64; <b>PDBTitle:</b> crystal structure of the fha domain of far9
77	<a href="#">c5oynB</a>	Alignment	not modelled	9.6	33	<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
78	<a href="#">c3frnA</a>	Alignment	not modelled	9.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein flga; <b>PDBTitle:</b> crystal structure of flagellar protein flga from thermotoga maritima2 msb8
79	<a href="#">c4v19D</a>	Alignment	not modelled	9.4	26	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> mitoribosomal protein ul2m, mrpl2; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
						<b>Fold:</b> SMAD/FHA domain

80	<a href="#">d1gxca_</a>	Alignment	not modelled	9.3	15	<b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
81	<a href="#">c1gxca_</a>	Alignment	not modelled	9.3	15	<b>PDB header:</b> phosphoprotein-binding domain <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase chk2; <b>PDBTitle:</b> fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
82	<a href="#">c3j21B_</a>	Alignment	not modelled	9.3	33	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> 50s ribosomal protein l2p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
83	<a href="#">d1ds1a_</a>	Alignment	not modelled	9.1	24	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminatase synthase-like <b>Family:</b> Clavaminatase synthase
84	<a href="#">d2qamc2</a>	Alignment	not modelled	9.0	42	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
85	<a href="#">d2q8oa1</a>	Alignment	not modelled	8.9	22	<b>Fold:</b> TNF-like <b>Superfamily:</b> TNF-like <b>Family:</b> TNF-like
86	<a href="#">c4ce4D_</a>	Alignment	not modelled	8.8	26	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> mrpl2; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
87	<a href="#">c4d7yA_</a>	Alignment	not modelled	8.8	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> c1q-related factor; <b>PDBTitle:</b> crystal structure of mouse c1q1 globular domain
88	<a href="#">d1rl2a2</a>	Alignment	not modelled	8.8	33	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
89	<a href="#">d1c3ha_</a>	Alignment	not modelled	8.7	13	<b>Fold:</b> TNF-like <b>Superfamily:</b> TNF-like <b>Family:</b> TNF-like
90	<a href="#">c1o91B_</a>	Alignment	not modelled	8.7	13	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha 1(viii) chain; <b>PDBTitle:</b> crystal structure of a collagen viii nc1 domain trimer
91	<a href="#">d1o91a_</a>	Alignment	not modelled	8.7	13	<b>Fold:</b> TNF-like <b>Superfamily:</b> TNF-like <b>Family:</b> TNF-like
92	<a href="#">d1hmja_</a>	Alignment	not modelled	8.6	15	<b>Fold:</b> RPB5-like RNA polymerase subunit <b>Superfamily:</b> RPB5-like RNA polymerase subunit <b>Family:</b> RPB5
93	<a href="#">c3elsA_</a>	Alignment	not modelled	8.6	29	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna leakage protein 1; <b>PDBTitle:</b> crystal structure of yeast pml1p, residues 51-204
94	<a href="#">c2z9iB_</a>	Alignment	not modelled	8.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable serine protease pepd; <b>PDBTitle:</b> crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
95	<a href="#">c6biqA_</a>	Alignment	not modelled	8.5	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> clan ca, family c40, nlpc/p60 superfamily cysteine <b>PDBTitle:</b> structure of nlpc2 from trichomonas vaginalis
96	<a href="#">c3hx1B_</a>	Alignment	not modelled	8.3	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> slr1951 protein; <b>PDBTitle:</b> crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
97	<a href="#">d1j99a_</a>	Alignment	not modelled	8.3	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
98	<a href="#">c2jkdB_</a>	Alignment	not modelled	8.1	31	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> pre-mrna leakage protein 1; <b>PDBTitle:</b> structure of the yeast pml1 splicing factor and its2 integration into the res complex
99	<a href="#">c1lcyA_</a>	Alignment	not modelled	8.1	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> htra2 serine protease; <b>PDBTitle:</b> crystal structure of the mitochondrial serine protease htra2