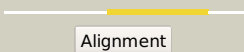
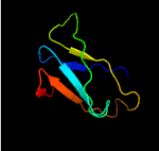
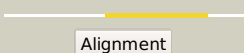

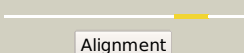
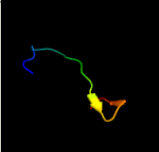
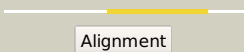

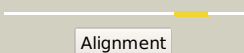
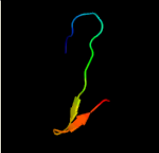
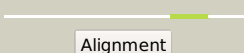
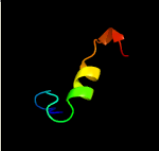



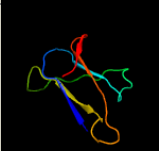

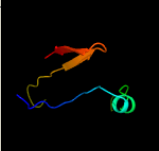
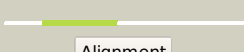

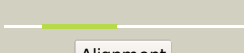

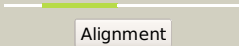
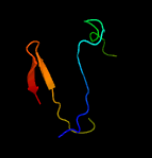
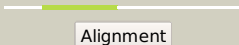
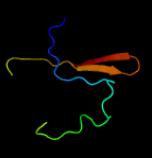
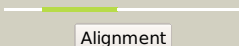
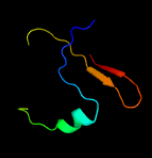
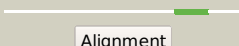
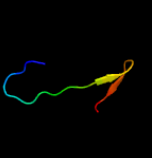
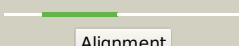
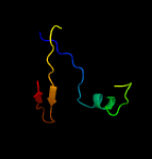
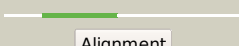
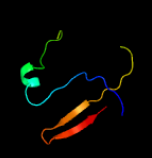
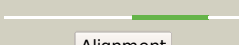

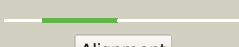
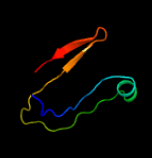


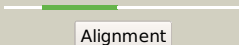
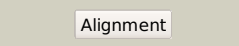
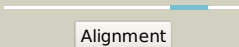
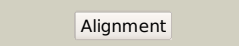



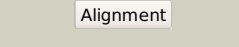


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1778c_(-)_2012088_2012537
Date	Fri Aug 2 13:30:38 BST 2019
Unique Job ID	bbafefabae854fb7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1z0na1</a>	 Alignment		77.1	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> AMPK-beta glycogen binding domain-like
2	<a href="#">d2f15a1</a>	 Alignment		76.1	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> AMPK-beta glycogen binding domain-like
3	<a href="#">d1z0mb1</a>	 Alignment		75.6	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> AMPK-beta glycogen binding domain-like
4	<a href="#">c4cffb_</a>	 Alignment		72.3	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5'-amp-activated protein kinase subunit beta-1; <b>PDBTitle:</b> structure of full length human ampk in complex with a small molecule2 activator, a thienopyridone derivative (a-769662)
5	<a href="#">d2qvlv1</a>	 Alignment		70.9	29	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> AMPK-beta glycogen binding domain-like
6	<a href="#">c1jsuC_</a>	 Alignment		68.9	42	<b>PDB header:</b> complex (transferase/cyclin/inhibitor) <b>Chain:</b> C: <b>PDB Molecule:</b> p27; <b>PDBTitle:</b> p27(kip1)/cyclin a/cdk2 complex
7	<a href="#">c3a0oB_</a>	 Alignment		66.4	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oligo alginate lyase; <b>PDBTitle:</b> crystal structure of alginate lyase from agrobacterium tumefaciens c58
8	<a href="#">c2qvlvB_</a>	 Alignment		65.7	18	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> protein sip2; <b>PDBTitle:</b> crystal structure of the heterotrimer core of the s. cerevisiae ampk2 homolog snf1
9	<a href="#">d1m1jb1</a>	 Alignment		63.5	22	<b>Fold:</b> Fibrinogen C-terminal domain-like <b>Superfamily:</b> Fibrinogen C-terminal domain-like <b>Family:</b> Fibrinogen C-terminal domain-like
10	<a href="#">c1ei3E_</a>	 Alignment		62.4	24	<b>PDB header:</b> blood clotting <b>Chain:</b> E: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
11	<a href="#">c4m7fB_</a>	 Alignment		62.0	24	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> fibrinogen c domain-containing protein 1; <b>PDBTitle:</b> crystal structure of tetrameric fibrinogen-like recognition domain of2 fibcd1 with bound mannac

12	<a href="#">c1jc9A_</a>	 Alignment		61.7	17	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> techylectin-5a; <b>PDBTitle:</b> tachylectin 5a from tachypleus tridentatus (japanese horseshoe crab)
13	<a href="#">d1jc9a_</a>	 Alignment		61.7	17	<b>Fold:</b> Fibrinogen C-terminal domain-like <b>Superfamily:</b> Fibrinogen C-terminal domain-like <b>Family:</b> Fibrinogen C-terminal domain-like
14	<a href="#">c4epuB_</a>	 Alignment		61.4	29	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> angiopoietin-1; <b>PDBTitle:</b> ang1 fibrinogen-related domain (fred)
15	<a href="#">c3nmeA_</a>	 Alignment		59.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sex4 glucan phosphatase; <b>PDBTitle:</b> structure of a plant phosphatase
16	<a href="#">c3ghgl_</a>	 Alignment		59.0	27	<b>PDB header:</b> blood clotting <b>Chain:</b> I: <b>PDB Molecule:</b> fibrinogen gamma chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
17	<a href="#">c6euaA_</a>	 Alignment		58.6	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> angiopoietin-related protein 3; <b>PDBTitle:</b> the fibrinogen-like domain of human angptl3
18	<a href="#">c5kpeA_</a>	 Alignment		55.2	24	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo beta sheet design protein or664; <b>PDBTitle:</b> solution nmr structure of denovo beta sheet design protein, northeast2 structural genomics consortium (nesh) target or664
19	<a href="#">c2j61B_</a>	 Alignment		54.8	22	<b>PDB header:</b> lectin <b>Chain:</b> B: <b>PDB Molecule:</b> ficolin-2; <b>PDBTitle:</b> l-ficolin complexed to n-acetylglucosamine (forme c)
20	<a href="#">c1degO_</a>	 Alignment		52.6	24	<b>PDB header:</b> blood clotting <b>Chain:</b> O: <b>PDB Molecule:</b> fibrinogen (beta chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
21	<a href="#">c2hpcF_</a>	 Alignment	not modelled	51.6	24	<b>PDB header:</b> blood clotting <b>Chain:</b> F: <b>PDB Molecule:</b> fibrinogen, gamma polypeptide; <b>PDBTitle:</b> crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
22	<a href="#">d2npta1</a>	 Alignment	not modelled	43.9	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
23	<a href="#">c3vn3B_</a>	 Alignment	not modelled	38.1	32	<b>PDB header:</b> antifreeze protein <b>Chain:</b> B: <b>PDB Molecule:</b> antifreeze protein; <b>PDBTitle:</b> fungal antifreeze protein exerts hyperactivity by constructing an2 inequable beta-helix
24	<a href="#">c4nu3A_</a>	 Alignment	not modelled	35.3	28	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> ice-binding protein; <b>PDBTitle:</b> crystal structure of mffibp, a capping head region swapped mutant of2 ice-binding protein
25	<a href="#">c2w87B_</a>	 Alignment	not modelled	34.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase d; <b>PDBTitle:</b> xyl-cbm35 in complex with glucuronic acid containing2 disaccharide.
26	<a href="#">c6gszA_</a>	 Alignment	not modelled	32.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-l-rhamnosidase; <b>PDBTitle:</b> crystal structure of native alfa-l-rhamnosidase from aspergillus2 terreus
27	<a href="#">c2yrlA_</a>	 Alignment	not modelled	32.2	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa1837 protein; <b>PDBTitle:</b> solution structure of the pkd domain from kiaa 1837 protein
28	<a href="#">c6i60B_</a>	 Alignment	not modelled	30.6	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-rhamnosidase; <b>PDBTitle:</b> structure of alpha-l-rhamnosidase from dictyoglumus thermophilum
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c5n1tM</a>	Alignment	not modelled	29.6	14	<b>Chain:</b> M: <b>PDB Molecule:</b> copc; <b>PDBTitle:</b> crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
30	<a href="#">d1tfpa</a>	Alignment	not modelled	29.5	16	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
31	<a href="#">c4ic7B</a>	Alignment	not modelled	28.4	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dual specificity mitogen-activated protein kinase kinase 5; <b>PDBTitle:</b> crystal structure of the erk5 kinase domain in complex with an mkk52 binding fragment
32	<a href="#">c2di7A</a>	Alignment	not modelled	25.8	9	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> bk158_1; <b>PDBTitle:</b> solution structure of the filamin domain from human bk158_12 protein
33	<a href="#">c2qz5A</a>	Alignment	not modelled	24.7	14	<b>PDB header:</b> signaling protein, lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> axin interactor, dorsalization associated <b>PDBTitle:</b> crystal structure of the c-terminal domain of aida
34	<a href="#">c6imfB</a>	Alignment	not modelled	24.5	19	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> small serum protein 2; <b>PDBTitle:</b> crystal structure of toxin/antitoxin complex
35	<a href="#">c3t69A</a>	Alignment	not modelled	22.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 2-dehydro-3-deoxygalactonokinase; <b>PDBTitle:</b> crystal structure of a putative 2-dehydro-3-deoxygalactonokinase2 protein from sinorhizobium meliloti
36	<a href="#">c3wp9A</a>	Alignment	not modelled	22.2	36	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> ice-binding protein; <b>PDBTitle:</b> crystal structure of antifreeze protein from an antarctic sea ice2 bacterium colwellia sp.
37	<a href="#">c3hh1D</a>	Alignment	not modelled	22.0	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> tetrapyrrole methylase family protein; <b>PDBTitle:</b> the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum t1s
38	<a href="#">d2fyta1</a>	Alignment	not modelled	21.4	9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
39	<a href="#">c4jdeB</a>	Alignment	not modelled	21.3	53	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein f15e11.1; <b>PDBTitle:</b> crystal structure of pud-1/pud-2 heterodimer
40	<a href="#">c1o7dA</a>	Alignment	not modelled	20.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysosomal alpha-mannosidase; <b>PDBTitle:</b> the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
41	<a href="#">d1wi0a</a>	Alignment	not modelled	20.6	27	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
42	<a href="#">c4c3iA</a>	Alignment	not modelled	20.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase i subunit rpa190; <b>PDBTitle:</b> structure of 14-subunit rna polymerase i at 3.0 a resolution, crystal2 form c2-100
43	<a href="#">c5lmxA</a>	Alignment	not modelled	20.5	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase i subunit rpa190; <b>PDBTitle:</b> monomeric rna polymerase i at 4.9 a resolution
44	<a href="#">d1ci3m2</a>	Alignment	not modelled	20.1	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
45	<a href="#">c3osvC</a>	Alignment	not modelled	20.0	14	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> flagellar basal-body rod modification protein flgd; <b>PDBTitle:</b> the crytsal structure of flgd from p. aeruginosa
46	<a href="#">c3w5mA</a>	Alignment	not modelled	19.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative rhamnosidase; <b>PDBTitle:</b> crystal structure of streptomyces avermitilis alpha-l-rhamnosidase
47	<a href="#">c2ymaB</a>	Alignment	not modelled	18.9	40	<b>PDB header:</b> carbohydrate binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein os-9 homolog; <b>PDBTitle:</b> x-ray structure of the yos9 dimerization domain
48	<a href="#">d3bvua3</a>	Alignment	not modelled	18.6	19	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> alpha-mannosidase
49	<a href="#">c5m3fA</a>	Alignment	not modelled	18.5	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase i subunit rpa190; <b>PDBTitle:</b> yeast rna polymerase i elongation complex at 3.8a
50	<a href="#">d1jmxa5</a>	Alignment	not modelled	17.7	28	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> Quinohemoprotein amine dehydrogenase A chain, domain 3 <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domain 3
51	<a href="#">d1cwva2</a>	Alignment	not modelled	17.7	24	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Invasin/intimin cell-adhesion fragments <b>Family:</b> Invasin/intimin cell-adhesion fragments
52	<a href="#">c3obaA</a>	Alignment	not modelled	17.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> structure of the beta-galactosidase from kluveromyces lactis
53	<a href="#">c2kxrA</a>	Alignment	not modelled	17.1	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> tight junction protein zo-1; <b>PDBTitle:</b> zo1 zu5 domain mc/aa mutation
54	<a href="#">d1uena</a>	Alignment	not modelled	17.0	29	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III

55	<a href="#">d1jz8a1</a>	Alignment	not modelled	17.0	22	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> beta-Galactosidase/glucuronidase domain <b>Family:</b> beta-Galactosidase/glucuronidase domain
56	<a href="#">c6gcsC</a>	Alignment	not modelled	16.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 49-kda protein (nucm); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
57	<a href="#">c3j9qc</a>	Alignment	not modelled	16.9	13	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> sheath; <b>PDBTitle:</b> atomic structures of a bactericidal contractile nanotube in its pre-2 and post-contraction states
58	<a href="#">c2ow7A</a>	Alignment	not modelled	16.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-mannosidase 2; <b>PDBTitle:</b> golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thioniabicyclo[4.3.0]nonan-7,8-diol chloride
59	<a href="#">c2x5pA</a>	Alignment	not modelled	16.2	27	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fibronectin binding protein; <b>PDBTitle:</b> crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
60	<a href="#">c2iz4A</a>	Alignment	not modelled	16.2	33	<b>PDB header:</b> inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> beta-microseminoprotein; <b>PDBTitle:</b> solution structure of human and porcine beta-2 microseminoprotein
61	<a href="#">c3uyuA</a>	Alignment	not modelled	16.1	40	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> antifreeze protein; <b>PDBTitle:</b> structural basis for the antifreeze activity of an ice-binding protein2 (leibp) from arctic yeast
62	<a href="#">c4lg3B</a>	Alignment	not modelled	16.1	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf487 family protein (despig_00776) from2 desulfovibrio piger atcc 29098 at 2.49 a resolution
63	<a href="#">d2vzsa3</a>	Alignment	not modelled	15.8	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> beta-Galactosidase/glucuronidase domain <b>Family:</b> beta-Galactosidase/glucuronidase domain
64	<a href="#">c2zp2B</a>	Alignment	not modelled	15.3	15	<b>PDB header:</b> transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> kinase a inhibitor; <b>PDBTitle:</b> c-terminal domain of kipi from bacillus subtilis
65	<a href="#">c3pe9D</a>	Alignment	not modelled	15.2	13	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> fibronectin(iii)-like module; <b>PDBTitle:</b> structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
66	<a href="#">d1zdxa1</a>	Alignment	not modelled	14.7	23	<b>Fold:</b> FimD N-terminal domain-like <b>Superfamily:</b> FimD N-terminal domain-like <b>Family:</b> Usher N-domain
67	<a href="#">c3g5bA</a>	Alignment	not modelled	14.4	20	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> netrin receptor unc5b; <b>PDBTitle:</b> the structure of unc5b cytoplasmic domain
68	<a href="#">d1kula</a>	Alignment	not modelled	14.4	9	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Starch-binding domain-like <b>Family:</b> Starch-binding domain
69	<a href="#">c3pe9B</a>	Alignment	not modelled	14.3	13	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> fibronectin(iii)-like module; <b>PDBTitle:</b> structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
70	<a href="#">d1kgia</a>	Alignment	not modelled	14.0	16	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
71	<a href="#">d1ttaa</a>	Alignment	not modelled	13.9	19	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
72	<a href="#">c4e9lA</a>	Alignment	not modelled	13.8	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> attaching and effacing protein, pathogenesis factor; <b>PDBTitle:</b> fdec, a novel broadly conserved escherichia coli adhesin eliciting2 protection against urinary tract infections
73	<a href="#">c2qbuA</a>	Alignment	not modelled	13.6	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> precorrin-2 methyltransferase; <b>PDBTitle:</b> crystal structure of methanothermobacter thermautotrophicus cbil
74	<a href="#">c2rpsA</a>	Alignment	not modelled	13.5	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> chemokine; <b>PDBTitle:</b> solution structure of a novel insect chemokine isolated from2 integument
75	<a href="#">d1pbya5</a>	Alignment	not modelled	13.5	38	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> Quinohemoprotein amine dehydrogenase A chain, domain 3 <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domain 3
76	<a href="#">c6eioA</a>	Alignment	not modelled	13.3	26	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> antifreeze protein; <b>PDBTitle:</b> crystal structure of an ice binding protein from an antarctic2 biological consortium
77	<a href="#">c2phcB</a>	Alignment	not modelled	13.3	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ph0987; <b>PDBTitle:</b> crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
78	<a href="#">c2h1xB</a>	Alignment	not modelled	13.2	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-hydroxyisourate hydrolase (formerly known as <b>PDBTitle:</b> crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
79	<a href="#">c5fjaA</a>	Alignment	not modelled	13.1	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc1; <b>PDBTitle:</b> cryo-em structure of yeast rna polymerase iii at 4.7 a
80	<a href="#">c3qvaB</a>	Alignment	not modelled	13.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> transthyretin-like protein; <b>PDBTitle:</b> structure of klebsiella pneumoniae 5-hydroxyisourate

						hydrolase
81	<a href="#">c5dudB</a>	Alignment	not modelled	12.7	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ybgj; <b>PDBTitle:</b> crystal structure of e. coli ybgjk
82	<a href="#">c3isyA</a>	Alignment	not modelled	12.7	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> intracellular proteinase inhibitor; <b>PDBTitle:</b> crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
83	<a href="#">c3o27B</a>	Alignment	not modelled	12.6	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the crystal structure of c68 from the hybrid virus-plasmid pssvx
84	<a href="#">d1oo2a</a>	Alignment	not modelled	12.4	16	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
85	<a href="#">c2e0kA</a>	Alignment	not modelled	12.3	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> precorrin-2 c20-methyltransferase; <b>PDBTitle:</b> crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
86	<a href="#">d1fzda</a>	Alignment	not modelled	12.0	17	<b>Fold:</b> Fibrinogen C-terminal domain-like <b>Superfamily:</b> Fibrinogen C-terminal domain-like <b>Family:</b> Fibrinogen C-terminal domain-like
87	<a href="#">c4qt6A</a>	Alignment	not modelled	12.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable e3 ubiquitin-protein ligase herc1; <b>PDBTitle:</b> crystal structure of the spry domain of human herc1
88	<a href="#">c3kwpA</a>	Alignment	not modelled	11.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from lactobacillus2 brevis
89	<a href="#">d1f86a</a>	Alignment	not modelled	11.9	24	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
90	<a href="#">c3mv14</a>	Alignment	not modelled	11.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> 4: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> e.coli (lacz) beta-galactosidase (r599a) in complex with guanidinium
91	<a href="#">c4qiwa</a>	Alignment	not modelled	11.7	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
92	<a href="#">c1jz6C</a>	Alignment	not modelled	11.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole
93	<a href="#">c1htyA</a>	Alignment	not modelled	11.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-mannosidase ii; <b>PDBTitle:</b> golgi alpha-mannosidase ii
94	<a href="#">c2vz1A</a>	Alignment	not modelled	11.2	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> galactose oxidase; <b>PDBTitle:</b> premat-galactose oxidase
95	<a href="#">c4puxA</a>	Alignment	not modelled	11.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a beta-barrel like protein (abaye2633) from2 acinetobacter baumannii aye at 1.43 a resolution
96	<a href="#">d2phcb1</a>	Alignment	not modelled	10.8	23	<b>Fold:</b> Cyclophilin-like <b>Superfamily:</b> Cyclophilin-like <b>Family:</b> PH0987 C-terminal domain-like
97	<a href="#">c2lieA</a>	Alignment	not modelled	10.7	31	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cc12 lectin; <b>PDBTitle:</b> nmr structure of the lectin ccl2
98	<a href="#">c5x5sA</a>	Alignment	not modelled	10.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amylase; <b>PDBTitle:</b> ligand induced structure of amyp-sbd
99	<a href="#">c2iz3A</a>	Alignment	not modelled	10.5	27	<b>PDB header:</b> inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> beta-microseminoprotein; <b>PDBTitle:</b> solution structure of human and porcine beta-2 microseminoprotein