




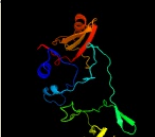





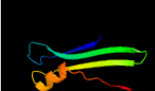






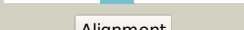







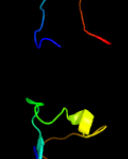

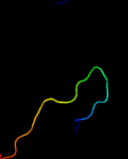

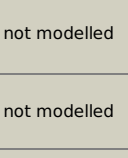


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0179c_(lprO)_209701_210810
Date	Tue Jul 23 14:50:23 BST 2019
Unique Job ID	70daf8aeee71e3ca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ohgA</a>	 Alignment		98.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein from duf2233 family; <b>PDBTitle:</b> crystal structure of a protein with unknown function from duf22332 family (bacova_00430) from bacteroides ovatus at 1.80 a resolution
2	<a href="#">c5h3kA</a>	 Alignment		98.3	27	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> slr0280 protein; <b>PDBTitle:</b> crystal structure of a hypothetical protein from synechocystis
3	<a href="#">c6ozdB</a>	 Alignment		98.1	29	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of putative exported protein (bps2145) from2 burkholderia pseudomallei k96243
4	<a href="#">c4ftdA</a>	 Alignment		64.9	26	<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 duf4623 family protein (bacegg_03550) from2 bacteroides eggerthii dsm 20697 at 1.91 a resolution
5	<a href="#">d1itva</a>	 Alignment		55.6	18	<b>Fold:</b> 4-bladed beta-propeller <b>Superfamily:</b> Hemopexin-like domain <b>Family:</b> Hemopexin-like domain
6	<a href="#">d1txka2</a>	 Alignment		51.8	39	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> MdoG-like
7	<a href="#">c1txkA</a>	 Alignment		51.5	39	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> glucans biosynthesis protein g; <b>PDBTitle:</b> crystal structure of escherichia coli oppg
8	<a href="#">c3gf8A</a>	 Alignment		49.5	22	<b>PDB header:</b> carbohydrate binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative polysaccharide binding proteins (duf1812); <b>PDBTitle:</b> crystal structure of putative polysaccharide binding proteins2 (duf1812) (np_809975.1) from bacteroides thetaiotaomicron vpi-5482 at3 2.20 a resolution
9	<a href="#">c3oyoB</a>	 Alignment		41.3	25	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemopexin fold protein cp4; <b>PDBTitle:</b> crystal structure of hemopexin fold protein cp4 from cow pea
10	<a href="#">d1gtka2</a>	 Alignment		37.1	56	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain <b>Family:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
11	<a href="#">d1pdaa2</a>	 Alignment		36.3	44	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain <b>Family:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain

12	<a href="#">d1pexa_</a>	Alignment		35.5	22	<b>Fold:</b> 4-bladed beta-propeller <b>Superfamily:</b> Hemopexin-like domain <b>Family:</b> Hemopexin-like domain
13	<a href="#">c2cltB_</a>	Alignment		33.7	34	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> interstitial collagenase; <b>PDBTitle:</b> crystal structure of the active form (full-length) of human2 fibroblast collagenase.
14	<a href="#">c3c7xA_</a>	Alignment		33.4	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrix metalloproteinase-14; <b>PDBTitle:</b> hemopexin-like domain of matrix metalloproteinase 14
15	<a href="#">c4mlqA_</a>	Alignment		32.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> porphobilinogen deaminase; <b>PDBTitle:</b> crystal structure of bacillus megaterium porphobilinogen deaminase
16	<a href="#">d1fbla1</a>	Alignment		32.2	31	<b>Fold:</b> 4-bladed beta-propeller <b>Superfamily:</b> Hemopexin-like domain <b>Family:</b> Hemopexin-like domain
17	<a href="#">c3lp9C_</a>	Alignment		28.8	24	<b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> ls-24; <b>PDBTitle:</b> crystal structure of ls24, a seed albumin from lathyrus2 sativus
18	<a href="#">d1jq5a_</a>	Alignment		28.2	28	<b>Fold:</b> GTP cyclohydrolase I feedback regulatory protein, GFRP <b>Superfamily:</b> GTP cyclohydrolase I feedback regulatory protein, GFRP <b>Family:</b> GTP cyclohydrolase I feedback regulatory protein, GFRP
19	<a href="#">d1xdna_</a>	Alignment		25.0	32	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> RNA ligase
20	<a href="#">c1su3A_</a>	Alignment		23.1	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> interstitial collagenase; <b>PDBTitle:</b> x-ray structure of human prommp-1: new insights into2 collagenase action
21	<a href="#">c5aeoA_</a>	Alignment	not modelled	21.6	33	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> r. equi vapg protein; <b>PDBTitle:</b> virulence-associated protein vapg from the intracellular2 pathogen rhodococcus equi
22	<a href="#">c4cv7A_</a>	Alignment	not modelled	21.6	33	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> virulence associated protein vapb; <b>PDBTitle:</b> crystal structure of rhodococcus equi vapb
23	<a href="#">c4csbA_</a>	Alignment	not modelled	21.4	30	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> virulence associated protein vapd; <b>PDBTitle:</b> structure of the virulence-associated protein vapd from the2 intracellular pathogen rhodococcus equi.
24	<a href="#">d1hxna_</a>	Alignment	not modelled	21.0	19	<b>Fold:</b> 4-bladed beta-propeller <b>Superfamily:</b> Hemopexin-like domain <b>Family:</b> Hemopexin-like domain
25	<a href="#">d1g47a2</a>	Alignment	not modelled	20.1	32	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
26	<a href="#">c3eq1A_</a>	Alignment	not modelled	19.6	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> porphobilinogen deaminase; <b>PDBTitle:</b> the crystal structure of human porphobilinogen deaminase at2.8a resolution
27	<a href="#">c2pnyA_</a>	Alignment	not modelled	19.1	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase 2; <b>PDBTitle:</b> structure of human isopentenyl-diphosphate delta-isomerase 2
28	<a href="#">d1lbu2</a>	Alignment	not modelled	18.6	23	<b>Fold:</b> Hedgehog/DD-peptidase <b>Superfamily:</b> Hedgehog/DD-peptidase <b>Family:</b> Muramoyl-pentapeptide carboxypeptidase

29	<a href="#">c2ypnA</a>	Alignment	not modelled	18.6	56	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hydroxymethylbilane synthase); <b>PDBTitle:</b> hydroxymethylbilane synthase
30	<a href="#">c4xfkA</a>	Alignment	not modelled	18.5	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative branched chain amino acid abc transporter, <b>PDBTitle:</b> crystal structure of leucine-, isoleucine-, valine-, threonine-, and 2 alanine-binding protein from brucella ovis
31	<a href="#">c4jxpA</a>	Alignment	not modelled	18.0	55	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-l-iduronidase; <b>PDBTitle:</b> crystal structure of human alpha-l-iduronidase, monoclinic form
32	<a href="#">c4q0pA</a>	Alignment	not modelled	17.9	31	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> l-ribose isomerase; <b>PDBTitle:</b> crystal structure of acinetobacter sp. d128 l-ribose isomerase in2 complex with l-ribose
33	<a href="#">c1gxdA</a>	Alignment	not modelled	17.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 72 kda type iv collagenase; <b>PDBTitle:</b> prommp-2/timp-2 complex
34	<a href="#">d1u2ca1</a>	Alignment	not modelled	17.6	67	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cadherin-like <b>Family:</b> Dystroglycan, N-terminal domain
35	<a href="#">c4aupA</a>	Alignment	not modelled	17.1	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a2 group xiii; <b>PDBTitle:</b> tuber borchii phospholipase a2
36	<a href="#">c4htgA</a>	Alignment	not modelled	16.7	33	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> porphobilinogen deaminase, chloroplastic; <b>PDBTitle:</b> porphobilinogen deaminase from arabidopsis thaliana
37	<a href="#">d1su3a2</a>	Alignment	not modelled	16.3	34	<b>Fold:</b> 4-bladed beta-propeller <b>Superfamily:</b> Hemopexin-like domain <b>Family:</b> Hemopexin-like domain
38	<a href="#">c5l6mA</a>	Alignment	not modelled	14.7	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> vapb family protein; <b>PDBTitle:</b> structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
39	<a href="#">c2zpaB</a>	Alignment	not modelled	14.6	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ypfi; <b>PDBTitle:</b> crystal structure of trna(met) cytidine acetyltransferase
40	<a href="#">c4g0dD</a>	Alignment	not modelled	13.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> collagenase 3; <b>PDBTitle:</b> human collagenase 3 (mmp-13) full form with peptides from pro-domain
41	<a href="#">c3anoA</a>	Alignment	not modelled	13.6	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ap-4-a phosphorylase; <b>PDBTitle:</b> crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
42	<a href="#">c2y9zB</a>	Alignment	not modelled	13.1	27	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> iswi one complex protein 3; <b>PDBTitle:</b> chromatin remodeling factor isw1a(del_atpase) in dna complex
43	<a href="#">c3ba0A</a>	Alignment	not modelled	12.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage metalloelastase; <b>PDBTitle:</b> crystal structure of full-length human mmp-12
44	<a href="#">c5nwmB</a>	Alignment	not modelled	12.5	50	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal transducer and activator of transcription 6; <b>PDBTitle:</b> insight into the molecular recognition mechanism of the coactivator2 ncoa1 by stat6
45	<a href="#">c6imfB</a>	Alignment	not modelled	12.4	18	<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
46	<a href="#">c4yycA</a>	Alignment	not modelled	12.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative trimethylamine methyltransferase; <b>PDBTitle:</b> crystal structure of trimethylamine methyltransferase from2 sinorhizobium meliloti in complex with unknown ligand
47	<a href="#">c4mi7A</a>	Alignment	not modelled	11.9	40	<b>PDB header:</b> hydrolase, toxin <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriophage encoded virulence factor; <b>PDBTitle:</b> crystal structure of salmonella effector protein gtge
48	<a href="#">d1cmra</a>	Alignment	not modelled	11.8	54	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins
49	<a href="#">c3mlhA</a>	Alignment	not modelled	11.7	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> crystal structure of the 2009 h1n1 influenza virus hemagglutinin2 receptor-binding domain
50	<a href="#">c2cisA</a>	Alignment	not modelled	11.6	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate 1-epimerase; <b>PDBTitle:</b> structure-based functional annotation: yeast ymr099c codes for a d-2 hexose-6-phosphate mutarotase. complex with tagatose-6-phosphate
51	<a href="#">c5ax7A</a>	Alignment	not modelled	11.1	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvyl transferase 1; <b>PDBTitle:</b> yeast pyruvyltransferase pvg1p
52	<a href="#">c2ec5B</a>	Alignment	not modelled	10.7	32	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> dermonecrotic toxin; <b>PDBTitle:</b> crystal structures reveal a thiol-protease like catalytic triad in the2 c-terminal region of pasteurilla multocida toxin
53	<a href="#">c3wdkA</a>	Alignment	not modelled	10.6	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-phosphopantoate--beta-alanine ligase; <b>PDBTitle:</b> crystal structure of 4-phosphopantoate-beta-alanine ligase complexed2 with reaction intermediate
54	<a href="#">c3navB</a>	Alignment	not modelled	10.3	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> putative adhesin;

54	<a href="#">c3payB</a>	Alignment	not modelled	10.3	20	<b>PDBTitle:</b> crystal structure of a putative adhesin (bacova_04077) from <i>Bacteroides ovatus</i> at 2.50 Å resolution <b>PDB header:</b> virus
55	<a href="#">c1fpvA</a>	Alignment	not modelled	10.3	14	<b>Chain:</b> A; <b>PDB Molecule:</b> feline panleukopenia virus (strain b) viral <b>PDBTitle:</b> structure determination of feline panleukopenia virus empty2 particles
56	<a href="#">c2iz4A</a>	Alignment	not modelled	9.7	11	<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
57	<a href="#">d1wk1a</a>	Alignment	not modelled	9.4	13	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
58	<a href="#">d1w91a1</a>	Alignment	not modelled	9.4	45	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
59	<a href="#">c2qnkA</a>	Alignment	not modelled	9.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-hydroxyanthranilate 3,4-dioxygenase; <b>PDBTitle:</b> crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
60	<a href="#">c4bluB</a>	Alignment	not modelled	9.3	33	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase j; <b>PDBTitle:</b> crystal structure of escherichia coli 23s rrna (a2030-n6)-2 methyltransferase rlmj
61	<a href="#">c2jxyA</a>	Alignment	not modelled	9.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> macrophage metalloelastase; <b>PDBTitle:</b> solution structure of the hemopexin-like domain of mmp12
62	<a href="#">d1gvia2</a>	Alignment	not modelled	9.2	60	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
63	<a href="#">d2viua</a>	Alignment	not modelled	9.2	29	<b>Fold:</b> Viral protein domain <b>Superfamily:</b> Viral protein domain <b>Family:</b> Influenza hemagglutinin headpiece
64	<a href="#">c2i6kA</a>	Alignment	not modelled	9.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase 1; <b>PDBTitle:</b> crystal structure of human type i isomerase complexed with a2 substrate analog
65	<a href="#">c4eogA</a>	Alignment	not modelled	8.9	38	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of csx1 of <i>pyrococcus furiosus</i>
66	<a href="#">c3isiA</a>	Alignment	not modelled	8.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> purine catabolism protein pucg; <b>PDBTitle:</b> crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from <i>Bacillus subtilis</i>
67	<a href="#">d1mqma</a>	Alignment	not modelled	8.7	24	<b>Fold:</b> Viral protein domain <b>Superfamily:</b> Viral protein domain <b>Family:</b> Influenza hemagglutinin headpiece
68	<a href="#">c2gaaA</a>	Alignment	not modelled	8.7	38	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical 39.9 kda protein; <b>PDBTitle:</b> crystal structure of yfh7 from <i>Saccharomyces cerevisiae</i> : a2 putative p-loop containing kinase with a circular3 permutation.
69	<a href="#">c2hb5A</a>	Alignment	not modelled	8.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> reverse transcriptase/ribonuclease h; <b>PDBTitle:</b> crystal structure of the moloney murine leukemia virus rnase h domain
70	<a href="#">c1hupA</a>	Alignment	not modelled	8.5	10	<b>PDB header:</b> c-type lectin <b>Chain:</b> A; <b>PDB Molecule:</b> mannose-binding protein; <b>PDBTitle:</b> human mannose binding protein carbohydrate recognition domain2 trimerizes through a triple alpha-helical coiled-coil
71	<a href="#">d2visc</a>	Alignment	not modelled	8.4	30	<b>Fold:</b> Viral protein domain <b>Superfamily:</b> Viral protein domain <b>Family:</b> Influenza hemagglutinin headpiece
72	<a href="#">c2o0tB</a>	Alignment	not modelled	8.3	22	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> the three dimensional structure of diaminopimelate decarboxylase from <i>Mycobacterium tuberculosis</i> reveals a tetrameric enzyme organisation
73	<a href="#">c3zvkg</a>	Alignment	not modelled	8.3	20	<b>PDB header:</b> antitoxin/toxin/dna <b>Chain:</b> G; <b>PDB Molecule:</b> antitoxin of toxin-antitoxin system vapb; <b>PDBTitle:</b> crystal structure of vapbc2 from <i>Rickettsia felis</i> bound to a dna fragment from their promoter
74	<a href="#">c4y90B</a>	Alignment	not modelled	8.2	26	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from <i>Deinococcus radiodurans</i>
75	<a href="#">c3fcsA</a>	Alignment	not modelled	8.2	20	<b>PDB header:</b> cell adhesion/blood clotting <b>Chain:</b> A; <b>PDB Molecule:</b> integrin, alpha 2b; <b>PDBTitle:</b> structure of complete ectodomain of integrin aiibb3
76	<a href="#">c2ww9O</a>	Alignment	not modelled	8.1	57	<b>PDB header:</b> ribosome <b>Chain:</b> O; <b>PDB Molecule:</b> 60s ribosomal protein l39; <b>PDBTitle:</b> cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
77	<a href="#">c4f15D</a>	Alignment	not modelled	8.1	24	<b>PDB header:</b> immune system <b>Chain:</b> D; <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> molecular basis of infectivity of 2009 pandemic h1n1 influenza a2 viruses
78	<a href="#">d1otga</a>	Alignment	not modelled	8.1	20	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 5-carboxymethyl-2-hydroxyruconate isomerase (CHMI)
79	<a href="#">c1q14A</a>	Alignment	not modelled	8.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hst2 protein; <b>PDBTitle:</b> structure and autoregulation of the yeast hst2 homolog of

						50	50	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> piscidin-3; <b>PDBTitle:</b> solid-state nmr structure of piscidin 3 in aligned 3:12 phosphatidylcholine/phosphoglycerol lipid bilayers
80	<a href="#">c2mcwA_</a>	Alignment	not modelled	7.8				
81	<a href="#">c2mcxA_</a>	Alignment	not modelled	7.8		50	50	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> piscidin-3; <b>PDBTitle:</b> solid-state nmr structure of piscidin 3 in aligned 1:12 phosphatidylethanolamine/phosphoglycerol lipid bilayers
82	<a href="#">d2ebfx2</a>	Alignment	not modelled	7.7		38		<b>Fold:</b> EreA/ChaN-like <b>Superfamily:</b> EreA/ChaN-like <b>Family:</b> PMT domain-like
83	<a href="#">d1czsa_</a>	Alignment	not modelled	7.7		75		<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Discoidin domain (FA58C, coagulation factor 5/8 C-terminal domain)
84	<a href="#">c5f5wC_</a>	Alignment	not modelled	7.7		20		<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> glycine--trna ligase alpha subunit; <b>PDBTitle:</b> crystal structure of the alpha subunit of glycyl trna synthetase2 (glyrs) from aquifex aeolicus in complex with an analog of glycyl3 adenylate (gly-sa)
85	<a href="#">d1dl5a2</a>	Alignment	not modelled	7.6		50		<b>Fold:</b> Protein-L-isoaspartyl O-methyltransferase, C-terminal domain <b>Superfamily:</b> Protein-L-isoaspartyl O-methyltransferase, C-terminal domain <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase, C-terminal domain
86	<a href="#">d1ti8a1</a>	Alignment	not modelled	7.6		29		<b>Fold:</b> Viral protein domain <b>Superfamily:</b> Viral protein domain <b>Family:</b> Influenza hemagglutinin headpiece
87	<a href="#">c4jppA_</a>	Alignment	not modelled	7.5		22		<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 putative carbohydrate-binding protein2 (bacuni_03838) from bacteroides uniformis atcc 8492 at 2.70 a3 resolution
88	<a href="#">c3trkA_</a>	Alignment	not modelled	7.4		50		<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> nonstructural polyprotein; <b>PDBTitle:</b> structure of the chikungunya virus nsp2 protease
89	<a href="#">c4cyzC_</a>	Alignment	not modelled	7.4		35		<b>PDB header:</b> viral protein <b>Chain:</b> C; <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> structure of the a_mallard_sweden_51_2002 h10 avian2 haemmagglutinin in complex with avian receptor analog lsta
90	<a href="#">d1rd8a_</a>	Alignment	not modelled	7.4		24		<b>Fold:</b> Viral protein domain <b>Superfamily:</b> Viral protein domain <b>Family:</b> Influenza hemagglutinin headpiece
91	<a href="#">c5nfiB_</a>	Alignment	not modelled	7.3		15		<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> minor fimbrium anchoring subunit mfa2; <b>PDBTitle:</b> the fimbrial anchor protein mfa2 from porphyromonas gingivalis
92	<a href="#">c2qrvC_</a>	Alignment	not modelled	7.3		20		<b>PDB header:</b> transferase/transferase regulator <b>Chain:</b> C; <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 3-like; <b>PDBTitle:</b> structure of dnmt3a-dnmt3l c-terminal domain complex
93	<a href="#">c5zdoA_</a>	Alignment	not modelled	7.3		19		<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamine-trna ligase; <b>PDBTitle:</b> crystal structure analysis of ttqrs in co-crystallised with atp
94	<a href="#">d1gena_</a>	Alignment	not modelled	7.2		33		<b>Fold:</b> 4-bladed beta-propeller <b>Superfamily:</b> Hemopexin-like domain <b>Family:</b> Hemopexin-like domain
95	<a href="#">d2gfva1</a>	Alignment	not modelled	7.1		58		<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
96	<a href="#">c3k6sC_</a>	Alignment	not modelled	7.0		20		<b>PDB header:</b> cell adhesion <b>Chain:</b> C; <b>PDB Molecule:</b> integrin alpha-x; <b>PDBTitle:</b> structure of integrin alphaxbeta2 ectodomain
97	<a href="#">c2btwA_</a>	Alignment	not modelled	7.0		22		<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> alr0975 protein; <b>PDBTitle:</b> crystal structure of alr0975
98	<a href="#">c4mxeA_</a>	Alignment	not modelled	6.9		58		<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> n-acetyltransferase esco1; <b>PDBTitle:</b> human esco1 (eco1/ctf7 ortholog), acetyltransferase domain in complex2 with acetyl-coa
99	<a href="#">c2ijzF_</a>	Alignment	not modelled	6.9		34		<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> probable m18-family aminopeptidase 2; <b>PDBTitle:</b> crystal structure of aminopeptidase