
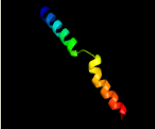

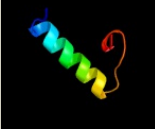
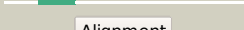






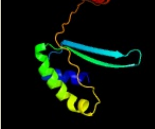

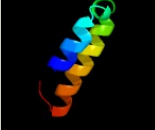

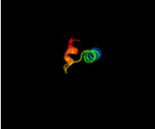
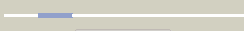






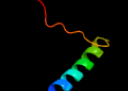






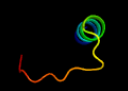


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0184 (- )_214967_215716
Date	Tue Jul 23 14:50:23 BST 2019
Unique Job ID	8dc74d809b496403

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1urqA_</a>	 Alignment		63.1	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> m-tomosyn isoform; <b>PDBTitle:</b> crystal structure of neuronal q-snares in complex with r-snares motif2 of tomosyn
2	<a href="#">c2jvdA_</a>	 Alignment		51.1	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0291 protein ynzc; <b>PDBTitle:</b> solution nmr structure of the folded n-terminal fragment of2 upf0291 protein ynzc from bacillus subtilis. northeast3 structural genomics target sr384-1-46
3	<a href="#">c3rzaA_</a>	 Alignment		42.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tripeptidase; <b>PDBTitle:</b> crystal structure of a tripeptidase (sav1512) from staphylococcus2 aureus subsp. aureus mu50 at 2.10 a resolution
4	<a href="#">c2kpiA_</a>	 Alignment		40.8	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sos-response transcriptional repressor, lexa; <b>PDBTitle:</b> solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
5	<a href="#">c6mdvA_</a>	 Alignment		36.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-n-acetylglucosaminidase; <b>PDBTitle:</b> crystal structure of streptococcus pyogenes endo-beta-n-2 acetylglucosaminidase (endos2) with high-mannose glycan
6	<a href="#">c6mx1A_</a>	 Alignment		31.4	9	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional aspartokinase/homoserine dehydrogenase 1; <b>PDBTitle:</b> the crystal structure of the regulatory domain of aspartokinase in the2 bifunctional aspartokinase/homoserine dehydrogenase 1 from3 escherichia coli str. k-12 substr. mg1655
7	<a href="#">c3wo6A_</a>	 Alignment		27.3	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane protein insertase yidc 2; <b>PDBTitle:</b> crystal structure of yidc from bacillus halodurans (form i)
8	<a href="#">d1wj7a1</a>	 Alignment		27.2	11	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
9	<a href="#">c2jowA_</a>	 Alignment		26.8	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein prgi; <b>PDBTitle:</b> differences in the electrostatic surfaces of the type iii2 secretion needle proteins
10	<a href="#">c3zhiA_</a>	 Alignment		25.8	7	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ci; <b>PDBTitle:</b> n-terminal domain of the ci repressor from bacteriophage tp901-1
11	<a href="#">c3w0ID_</a>	 Alignment		24.9	15	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> glucokinase regulatory protein; <b>PDBTitle:</b> the crystal structure of xenopus glucokinase and glucokinase2 regulatory protein complex

12	<a href="#">d1vixa1</a>	Alignment		24.8	19	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
13	<a href="#">c3rvaA</a>	Alignment		24.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> organophosphorus acid anhydrolase; <b>PDBTitle:</b> crystal structure of organophosphorus acid anhydrolase from2 alteromonas macleodii
14	<a href="#">c4wzsa</a>	Alignment		23.7	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ecu11_1470 protein; <b>PDBTitle:</b> crystal structure of the mot1 n-terminal domain in complex with tbp2 and nc2 bound to a promoter dna fragment
15	<a href="#">c2v6ll</a>	Alignment		21.2	21	<b>PDB header:</b> protein transport <b>Chain:</b> I: <b>PDB Molecule:</b> mxih; <b>PDBTitle:</b> molecular model of a type iii secretion system needle
16	<a href="#">c3epyA</a>	Alignment		20.1	29	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa-binding domain-containing protein 7; <b>PDBTitle:</b> crystal structure of human acyl-coa binding domain 7 complexed with2 palmitoyl-coa
17	<a href="#">d2g0ua1</a>	Alignment		19.3	11	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> MxiH-like <b>Family:</b> MxiH-like
18	<a href="#">c3t76A</a>	Alignment		19.2	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator vanug; <b>PDBTitle:</b> crystal structure of transcriptional regulator vanug, form ii
19	<a href="#">d2ca5a1</a>	Alignment		18.8	22	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> MxiH-like <b>Family:</b> MxiH-like
20	<a href="#">c5cnxB</a>	Alignment		18.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> aminopeptidase ypdf; <b>PDBTitle:</b> crystal structure of xaa-pro aminopeptidase from escherichia coli k12
21	<a href="#">c5ks5A</a>	Alignment	not modelled	17.5	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic elongation factor 2 kinase; <b>PDBTitle:</b> structure of the c-terminal helical repeat domain of elongation factor2 2 kinase
22	<a href="#">c2re1A</a>	Alignment	not modelled	17.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartokinase, alpha and beta subunits; <b>PDBTitle:</b> crystal structure of aspartokinase alpha and beta subunits
23	<a href="#">c3b7hA</a>	Alignment	not modelled	17.3	8	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> prophage lp1 protein 11; <b>PDBTitle:</b> crystal structure of the prophage lp1 protein 11
24	<a href="#">c4lc9A</a>	Alignment	not modelled	17.1	25	<b>PDB header:</b> transferase/transferase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase regulatory protein; <b>PDBTitle:</b> structural basis for regulation of human glucokinase by glucokinase2 regulatory protein
25	<a href="#">c2w48D</a>	Alignment	not modelled	16.8	20	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator; <b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
26	<a href="#">c2rreA</a>	Alignment	not modelled	16.3	21	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure and function of the n-terminal nucleolin binding domain of2 nuclear valocine containing protein like 2 (nvl2) harboring a3 nucleolar localization signal
27	<a href="#">c2hepA</a>	Alignment	not modelled	16.2	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0291 protein yznc; <b>PDBTitle:</b> solution nmr structure of the upf0291 protein yznc from2 bacillus subtilis. northeast structural genomics target3 sr384.
28	<a href="#">d2hepa1</a>	Alignment	not modelled	16.2	28	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> YznC-like <b>Family:</b> YznC-like

29	<a href="#">d1chma1</a>	Alignment	not modelled	16.2	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Creatinase/prolidase N-terminal domain <b>Family:</b> Creatinase/prolidase N-terminal domain
30	<a href="#">c3lisB_</a>	Alignment	not modelled	16.0	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> csp231i c protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
31	<a href="#">c3ovkD_</a>	Alignment	not modelled	15.9	4	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> aminopeptidase p, xaa-pro dipeptidase; <b>PDBTitle:</b> crystal structure of an xxa-pro aminopeptidase from streptococcus2 pyogenes
32	<a href="#">d1hb6a_</a>	Alignment	not modelled	15.8	19	<b>Fold:</b> Acyl-CoA binding protein-like <b>Superfamily:</b> Acyl-CoA binding protein <b>Family:</b> Acyl-CoA binding protein
33	<a href="#">c3ooaA_</a>	Alignment	not modelled	15.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dipeptidase; <b>PDBTitle:</b> the structure of a proline dipeptidase from streptococcus agalactiae2 2603v
34	<a href="#">c3qbwA_</a>	Alignment	not modelled	15.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anhydro-n-acetylmuramic acid kinase; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 acteylmuramic acid kinase (anmk) bound to adenosine diphosphate
35	<a href="#">c3gb0A_</a>	Alignment	not modelled	15.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase t; <b>PDBTitle:</b> crystal structure of aminopeptidase pept (np_980509.1) from bacillus2 cereus atcc 10987 at 2.04 a resolution
36	<a href="#">c1wy2B_</a>	Alignment	not modelled	15.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xaa-pro dipeptidase; <b>PDBTitle:</b> crystal structure of the prolidase from pyrococcus horikoshii ot3
37	<a href="#">c1u9gB_</a>	Alignment	not modelled	15.0	55	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pI based coiled2 coils: replacement of k(8)(9)
38	<a href="#">c3pn9C_</a>	Alignment	not modelled	14.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> proline dipeptidase; <b>PDBTitle:</b> crystal structure of a proline dipeptidase from streptococcus2 pneumoniae tigr4
39	<a href="#">c1unvA_</a>	Alignment	not modelled	14.7	55	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
40	<a href="#">c2ag3A_</a>	Alignment	not modelled	14.7	55	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4-pI; <b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pI based coiled2 coils: substitution of the k(15)-(16) amide with a triazole
41	<a href="#">c4g92C_</a>	Alignment	not modelled	14.6	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> hape; <b>PDBTitle:</b> ccaat-binding complex from aspergillus nidulans with dna
42	<a href="#">c1unvB_</a>	Alignment	not modelled	14.6	55	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
43	<a href="#">c2kwIA_</a>	Alignment	not modelled	13.9	20	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of acyl carrier protein from borrelia burgdorferi
44	<a href="#">c2rb7A_</a>	Alignment	not modelled	13.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase, m20/m25/m40 family; <b>PDBTitle:</b> crystal structure of co-catalytic metallopeptidase (yp_387682.1) from2 desulfovibrio desulfuricans g20 at 1.60 a resolution
45	<a href="#">c4hmcA_</a>	Alignment	not modelled	13.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase 60; <b>PDBTitle:</b> crystal structure of cold-adapted chitinase from moritella marina
46	<a href="#">c4bbaA_</a>	Alignment	not modelled	13.1	26	<b>PDB header:</b> protein-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase regulatory protein; <b>PDBTitle:</b> crystal structure of glucokinase regulatory protein complexed to2 phosphate
47	<a href="#">c4hjdA_</a>	Alignment	not modelled	12.8	75	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4pli(alpha/beta/acyclic gamma); <b>PDBTitle:</b> gcn4pli derivative with alpha/beta/acyclic-gamma amino acid2 substitution pattern
48	<a href="#">c4hjdB_</a>	Alignment	not modelled	12.8	75	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> gcn4pli(alpha/beta/acyclic gamma); <b>PDBTitle:</b> gcn4pli derivative with alpha/beta/acyclic-gamma amino acid2 substitution pattern
49	<a href="#">c6dmaD_</a>	Alignment	not modelled	12.6	50	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> dhd15_closed_b; <b>PDBTitle:</b> dhd15_closed
50	<a href="#">c5dowB_</a>	Alignment	not modelled	12.6	44	<b>PDB header:</b> calcium binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> chloride anion exchanger; <b>PDBTitle:</b> solution of the variably-twinned structure of a novel calmodulin-2 peptide complex in a novel configuration
51	<a href="#">c4afIA_</a>	Alignment	not modelled	12.5	6	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> inhibitor of growth protein 4; <b>PDBTitle:</b> the crystal structure of the ing4 dimerization domain2 reveals the functional organization of the ing family of3 chromatin binding proteins.
52	<a href="#">c5dowH_</a>	Alignment	not modelled	12.4	44	<b>PDB header:</b> calcium binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> chloride anion exchanger; <b>PDBTitle:</b> solution of the variably-twinned structure of a novel calmodulin-2 peptide complex in a novel configuration
53	<a href="#">c5dowF_</a>	Alignment	not modelled	12.4	44	<b>PDB header:</b> calcium binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> chloride anion exchanger; <b>PDBTitle:</b> solution of the variably-twinned structure of a novel calmodulin-2 peptide complex in a novel configuration

54	<a href="#">d2f2ab1</a>	Alignment	not modelled	11.9	6	<b>Fold:</b> GatB/YqeY motif <b>Superfamily:</b> GatB/YqeY motif <b>Family:</b> GatB/GatE C-terminal domain-like
55	<a href="#">c3s1tB</a>	Alignment	not modelled	11.6	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartokinase; <b>PDBTitle:</b> structure of the regulatory domain of aspartokinase (rv3709c; ak-beta)2 in complex with threonine from mycobacterium tuberculosis
56	<a href="#">c5dowD</a>	Alignment	not modelled	11.4	44	<b>PDB header:</b> calcium binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> chloride anion exchanger; <b>PDBTitle:</b> solution of the variably-twinned structure of a novel calmodulin-2 peptide complex in a novel configuration
57	<a href="#">d1whra</a>	Alignment	not modelled	11.0	15	<b>Fold:</b> IF3-like <b>Superfamily:</b> R3H domain <b>Family:</b> R3H domain
58	<a href="#">c1xofB</a>	Alignment	not modelled	10.8	40	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> bbahett1; <b>PDBTitle:</b> heterooligomeric beta beta alpha miniprotein
59	<a href="#">c5ds0F</a>	Alignment	not modelled	10.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> peptidase m42; <b>PDBTitle:</b> crystal structure of tet aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon scgc ab-539-e09
60	<a href="#">c6d02E</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> alpha-amyloid peptide alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
61	<a href="#">c6d02K</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> K: <b>PDB Molecule:</b> alpha-amyloid peptide alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
62	<a href="#">c6d02Z</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> Z: <b>PDB Molecule:</b> <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
63	<a href="#">c6d02J</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> J: <b>PDB Molecule:</b> alpha-amyloid peptide alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
64	<a href="#">c6d02d</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-amyloid peptide alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
65	<a href="#">c6d02A</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amyloid peptide alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
66	<a href="#">c6d02Q</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> Q: <b>PDB Molecule:</b> alpha-amyloid peptide alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
67	<a href="#">c6d02O</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> O: <b>PDB Molecule:</b> alpha-amyloid peptide alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
68	<a href="#">c6c51B</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cross-alpha amyloid-like structure alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml
69	<a href="#">c6c51A</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cross-alpha amyloid-like structure alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml
70	<a href="#">c6c51C</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> cross-alpha amyloid-like structure alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml
71	<a href="#">c6d02T</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> T: <b>PDB Molecule:</b> alpha-amyloid peptide alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
72	<a href="#">c6d02F</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> alpha-amyloid peptide alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
73	<a href="#">c6d02R</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> R: <b>PDB Molecule:</b> alpha-amyloid peptide alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
74	<a href="#">c6d02M</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> de novo protein <b>Chain:</b> M: <b>PDB Molecule:</b> alpha-amyloid peptide alphaaml; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphaaml, 2nd form
75	<a href="#">c5kp8B</a>	Alignment	not modelled	10.5	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> curb; <b>PDBTitle:</b> crystal structure of the curacin biosynthetic pathway hmg synthase in2 complex with acetyl donor-accp
76	<a href="#">d1hioa</a>	Alignment	not modelled	10.4	21	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
77	<a href="#">c4er9A</a>	Alignment	not modelled	10.0	22	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562; <b>PDBTitle:</b> crystal structure of cytochrome b562 from salmonella enterica subsp.2 enterica serovar typhimurium str. 14028s
78	<a href="#">d3dtoa1</a>	Alignment	not modelled	9.8	11	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
79	<a href="#">c2lo1A</a>	Alignment	not modelled	9.7	20	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> nmr structure of an acyl-carrier protein from rickettsia prowazekii,2 seattle structural genomics center for infectious disease (ssgcid)
80	<a href="#">c2n7c</a>	Alignment	not modelled	9.6	38	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> fusion protein between yeast variant gcn4

80	<a href="#">c2q7cc</a>	Alignment	not modelled	9.0	30	and hivgp41; <b>PDBTitle:</b> crystal structure of iqn17
81	<a href="#">c6c0dA</a>	Alignment	not modelled	9.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidase, hydantoinase/carbamoylase family; <b>PDBTitle:</b> crystal structure of an amidase (hydantoinase/carbamoylase family)2 from burkholderia phymatum
82	<a href="#">c5xevA</a>	Alignment	not modelled	9.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xaa-pro dipeptidase,peptidase-related protein; <b>PDBTitle:</b> crystal structure of a novel xaa-pro dipeptidase from deinococcus2 radiodurans
83	<a href="#">c1jfiA</a>	Alignment	not modelled	9.3	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator nc2 alpha chain; <b>PDBTitle:</b> crystal structure of the nc2-tbp-dna ternary complex
84	<a href="#">d1jfia</a>	Alignment	not modelled	9.3	21	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
85	<a href="#">c2zhoB</a>	Alignment	not modelled	9.2	6	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartokinase; <b>PDBTitle:</b> crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
86	<a href="#">d1w36c2</a>	Alignment	not modelled	9.2	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
87	<a href="#">c4go1A</a>	Alignment	not modelled	9.1	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lssr; <b>PDBTitle:</b> crystal structure of full length transcription repressor lssr from e.2 coli.
88	<a href="#">c3il0B</a>	Alignment	not modelled	9.0	7	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> aminopeptidase p; xaa-pro aminopeptidase; <b>PDBTitle:</b> the crystal structure of the aminopeptidase p,xaa-pro aminopeptidase2 from streptococcus thermophilus
89	<a href="#">d1jcna4</a>	Alignment	not modelled	9.0	9	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
90	<a href="#">c4o8bA</a>	Alignment	not modelled	9.0	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator bswr
91	<a href="#">c1vixA</a>	Alignment	not modelled	8.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase t; <b>PDBTitle:</b> crystal structure of a putative peptidase t
92	<a href="#">c4l3uA</a>	Alignment	not modelled	8.7	15	<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 duf3571 family protein (abaye3784) from2 acinetobacter baumannii aye at 1.95 a resolution
93	<a href="#">d1sbpa</a>	Alignment	not modelled	8.7	21	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
94	<a href="#">d2ctfa1</a>	Alignment	not modelled	8.7	13	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
95	<a href="#">c3pohA</a>	Alignment	not modelled	8.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-n-acetylglucosaminidase f1; <b>PDBTitle:</b> crystal structure of an endo-beta-n-acetylglucosaminidase (bt_3987)2 from bacteroides thetaiotaomicron vpi-5482 at 1.55 a resolution
96	<a href="#">d256ba</a>	Alignment	not modelled	8.5	22	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Cytochromes <b>Family:</b> Cytochrome b562
97	<a href="#">d2cyua1</a>	Alignment	not modelled	8.5	17	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
98	<a href="#">c1u9gA</a>	Alignment	not modelled	8.4	55	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(8)l(9)
99	<a href="#">c5icqA</a>	Alignment	not modelled	8.4	6	<b>PDB header:</b> periplasmic binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> methylocystis parvus obbp mbne; <b>PDBTitle:</b> methanobactin periplasmic binding protein