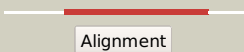
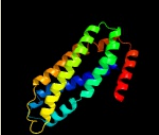
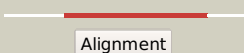

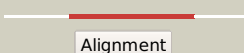
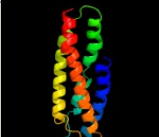
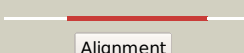
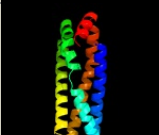





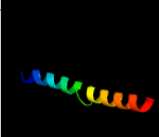
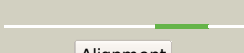
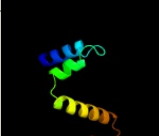
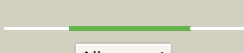




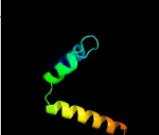







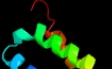



# Phyre2

Email	mdejesus@rockefeller.edu
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Date	Mon Aug 5 13:25:10 BST 2019
Unique Job ID	abd573172aceb742






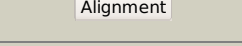
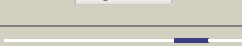






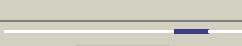
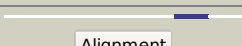
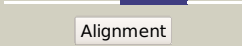
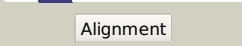
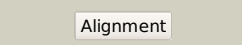
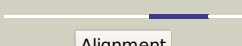

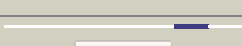
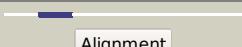

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2p0nA_</a>	 Alignment		100.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein nmb1532; <b>PDBTitle:</b> nmb1532 protein from neisseria meningitidis, unknown function
2	<a href="#">c3v5yC_</a>	 Alignment		99.8	20	<b>PDB header:</b> gene regulation <b>Chain:</b> C; <b>PDB Molecule:</b> f-box/lrr-repeat protein 5; <b>PDBTitle:</b> structure of fbxl5 hemerythrin domain, p2(1) cell
3	<a href="#">c5fnpB_</a>	 Alignment		99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> iron-sulfur cluster repair protein ytf6; <b>PDBTitle:</b> high resolution zn containing iron sulfur cluster repair2 protein ytf6
4	<a href="#">c3caxA_</a>	 Alignment		98.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein pf0695; <b>PDBTitle:</b> crystal structure of uncharacterized protein pf0695
5	<a href="#">c2awyB_</a>	 Alignment		95.1	17	<b>PDB header:</b> oxygen storage/transport <b>Chain:</b> B; <b>PDB Molecule:</b> hemerythrin-like domain protein dcrh; <b>PDBTitle:</b> met-dcrh-hr
6	<a href="#">c4xpyA_</a>	 Alignment		92.7	12	<b>PDB header:</b> oxygen binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> bacteriohemerythrin; <b>PDBTitle:</b> crystal structure of hemerythrin : I114y mutant
7	<a href="#">c3ci9B_</a>	 Alignment		63.5	18	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> heat shock factor-binding protein 1; <b>PDBTitle:</b> crystal structure of the human hsbp1
8	<a href="#">d1trra_</a>	 Alignment		58.2	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
9	<a href="#">c2wviA_</a>	 Alignment		51.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> mitotic checkpoint serine/threonine-protein <b>PDBTitle:</b> crystal structure of the n-terminal domain of bubr1
10	<a href="#">c2xusA_</a>	 Alignment		46.1	14	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> breast cancer metastasis-suppressor 1; <b>PDBTitle:</b> crystal structure of the brms1 n-terminal region
11	<a href="#">d1jhga_</a>	 Alignment		44.5	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR

12	<a href="#">c5n9qA_</a>	Alignment		40.4	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> inactive poly [adp-ribose] polymerase rcd1; <b>PDBTitle:</b> structure of a. thaliana rcd1(468-567)
13	<a href="#">c5lcwS_</a>	Alignment		34.5	8	<b>PDB header:</b> cell cycle <b>Chain:</b> S: <b>PDB Molecule:</b> mitotic checkpoint serine/threonine-protein kinase bub1 <b>PDBTitle:</b> cryo-em structure of the anaphase-promoting complex/cyclosome, in2 complex with the mitotic checkpoint complex (apc/c-mcc) at 4.23 angstrom resolution
14	<a href="#">d1g3wa2</a>	Alignment		29.4	11	<b>Fold:</b> Iron-dependent repressor protein, dimerization domain <b>Superfamily:</b> Iron-dependent repressor protein, dimerization domain <b>Family:</b> Iron-dependent repressor protein, dimerization domain
15	<a href="#">c3frwF_</a>	Alignment		28.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative trp repressor protein; <b>PDBTitle:</b> crystal structure of putative trpr protein from ruminococcus obeum
16	<a href="#">c5khuO_</a>	Alignment		27.2	8	<b>PDB header:</b> cell cycle <b>Chain:</b> Q: <b>PDB Molecule:</b> mitotic checkpoint serine/threonine-protein kinase bub1 <b>PDBTitle:</b> model of human anaphase-promoting complex/cyclosome (apc15 deletion2 mutant), in complex with the mitotic checkpoint complex (apc/c-cdc20-3 mcc) based on cryo em data at 4.8 angstrom resolution
17	<a href="#">c4lh9A_</a>	Alignment		26.9	39	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> heterocyst differentiation control protein; <b>PDBTitle:</b> crystal structure of the refolded hood domain (asp256-gly295) of hetr
18	<a href="#">d2isyA2</a>	Alignment		26.6	11	<b>Fold:</b> Iron-dependent repressor protein, dimerization domain <b>Superfamily:</b> Iron-dependent repressor protein, dimerization domain <b>Family:</b> Iron-dependent repressor protein, dimerization domain
19	<a href="#">d2bl8a1</a>	Alignment		26.3	17	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bacteriocin immunity protein-like <b>Family:</b> EntA-Im
20	<a href="#">c2lseA_</a>	Alignment		25.4	20	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> four helix bundle protein; <b>PDBTitle:</b> solution nmr structure of de novo designed four helix bundle protein,2 northeast structural genomics consortium (nesg) target or188
21	<a href="#">c4eqyC_</a>	Alignment	not modelled	22.4	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- <b>PDBTitle:</b> crystal structure of acyl-[acyl-carrier-protein]-udp-n-2 acetylglucosamine o-acyltransferase from burkholderia thailandensis
22	<a href="#">c4dckA_</a>	Alignment	not modelled	22.3	17	<b>PDB header:</b> transport protein/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium channel protein type 5 subunit alpha; <b>PDBTitle:</b> crystal structure of the c-terminus of voltage-gated sodium channel in2 complex with fgf13 and cam
23	<a href="#">c2kbiA_</a>	Alignment	not modelled	21.5	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium channel protein type 5 subunit alpha; <b>PDBTitle:</b> solution nmr structure of the c-terminal ef-hand domain of2 human cardiac sodium channel nav1.5
24	<a href="#">d2bl7a1</a>	Alignment	not modelled	20.9	12	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bacteriocin immunity protein-like <b>Family:</b> EntA-Im
25	<a href="#">d1szqa_</a>	Alignment	not modelled	20.8	12	<b>Fold:</b> 2-methylcitrate dehydratase PrpD <b>Superfamily:</b> 2-methylcitrate dehydratase PrpD <b>Family:</b> 2-methylcitrate dehydratase PrpD
26	<a href="#">d2jf2a1</a>	Alignment	not modelled	20.8	9	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> UDP N-acetylglucosamine acyltransferase
27	<a href="#">c4r36A_</a>	Alignment	not modelled	20.3	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine2 acyltransferase from bacteroides fragilis 9343 <b>PDB header:</b> cell cycle, apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> mitotic checkpoint serine/threonine-

28	<a href="#">c2lahA</a>	Alignment	not modelled	19.8	12	protein kinase bub1; <b>PDBTitle:</b> solution nmr structure of mitotic checkpoint serine/threonine-protein2 kinase bub1 n-terminal domain from homo sapiens, northeast structural3 genomics consortium target hr5460a (methods development)
29	<a href="#">c4aezC</a>	Alignment	not modelled	18.7	11	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> mitotic spindle checkpoint component mad3; <b>PDBTitle:</b> crystal structure of mitotic checkpoint complex
30	<a href="#">c5j0IC</a>	Alignment	not modelled	18.5	54	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> designed protein 3l6hc2_2; <b>PDBTitle:</b> de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
31	<a href="#">d1b77a1</a>	Alignment	not modelled	18.0	44	<b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor
32	<a href="#">c3korD</a>	Alignment	not modelled	17.5	10	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus
33	<a href="#">c2kavA</a>	Alignment	not modelled	17.3	19	<b>PDB header:</b> transport protein regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sodium channel protein type 2 subunit alpha; <b>PDBTitle:</b> solution structure of the human voltage-gated sodium channel, brain2 isoform (nav1.2)
34	<a href="#">d1fx0a1</a>	Alignment	not modelled	17.1	8	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
35	<a href="#">c6focB</a>	Alignment	not modelled	16.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase subunit alpha,atp synthase subunit alpha,atp <b>PDBTitle:</b> f1-atpase from mycobacterium smegmatis
36	<a href="#">c3deeA</a>	Alignment	not modelled	14.8	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative regulatory protein; <b>PDBTitle:</b> crystal structure of a putative regulatory protein involved in2 transcription (ngo1945) from neisseria gonorrhoeae fa 1090 at 2.25 a3 resolution
37	<a href="#">c2pg4B</a>	Alignment	not modelled	14.7	21	<b>PDB header:</b> chaperone/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic nitrate reductase precursor; <b>PDBTitle:</b> nmr solution structure of napd in complex with napa1-352 signal peptide
38	<a href="#">c6dkmB</a>	Alignment	not modelled	14.2	21	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> dhd131_b; <b>PDBTitle:</b> dhd131
39	<a href="#">c2xu6B</a>	Alignment	not modelled	14.0	21	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> mdv1 coiled coil; <b>PDBTitle:</b> mdv1 coiled coil domain
40	<a href="#">c2fynO</a>	Alignment	not modelled	14.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur <b>PDBTitle:</b> crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
41	<a href="#">c6n63A</a>	Alignment	not modelled	14.0	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> encapsulin cargo protein; <b>PDBTitle:</b> crystal structure of an iron binding protein
42	<a href="#">c6fo2R</a>	Alignment	not modelled	13.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> R: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit rieske, mitochondrial; <b>PDBTitle:</b> cryoem structure of bovine cytochrome bc1 with no ligand bound
43	<a href="#">d1czda1</a>	Alignment	not modelled	13.1	56	<b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor
44	<a href="#">c4ynlB</a>	Alignment	not modelled	12.7	39	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> heterocyst differentiation control protein; <b>PDBTitle:</b> crystal structure of the hood domain of anaabaena hetr in complex with2 the hexapeptide ergsgr derived from pats
45	<a href="#">c5vnyA</a>	Alignment	not modelled	12.6	25	<b>PDB header:</b> endocytosis, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> lethal (2) giant discs 1, isoform b; <b>PDBTitle:</b> crystal structure of dm14-3 domain of lgd
46	<a href="#">d1iapa</a>	Alignment	not modelled	12.2	22	<b>Fold:</b> Regulator of G-protein signaling, RGS <b>Superfamily:</b> Regulator of G-protein signaling, RGS <b>Family:</b> Regulator of G-protein signaling, RGS
47	<a href="#">c5muxB</a>	Alignment	not modelled	12.1	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-methylcitrate dehydratase; <b>PDBTitle:</b> crystal structure of 2-methylcitrate dehydratase (mmge) from bacillus2 subtilis.
48	<a href="#">c5dg3D</a>	Alignment	not modelled	11.9	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- <b>PDBTitle:</b> structure of pseudomonas aeruginosa lpxa in complex with udp-3-o-(r-3-2 hydroxydecanoyl)-glcnaac
49	<a href="#">c2lfhA</a>	Alignment	not modelled	11.9	14	<b>PDB header:</b> dna binding protein inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein inhibitor id-3; <b>PDBTitle:</b> solution nmr structure of the helix-loop-helix domain of human id32 protein, northeast structural genomics consortium target hr3111a
50	<a href="#">d1z0xa2</a>	Alignment	not modelled	11.8	19	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
51	<a href="#">c2m4gA</a>	Alignment	not modelled	11.6	19	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> murine norovirus vpg protein; <b>PDBTitle:</b> solution structure of the core domain (11-85) of the murine norovirus2 vpg protein <b>PDB header:</b> transferase

52	<a href="#">c4e6tA</a>	Alignment	not modelled	11.5	9	<b>Chain:</b> A: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- <b>PDBTitle:</b> structure of lpxa from acinetobacter baumannii at 1.8a resolution2 (p212121 form)
53	<a href="#">d1topa</a>	Alignment	not modelled	11.2	10	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
54	<a href="#">c4rd8B</a>	Alignment	not modelled	10.6	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally-unknown protein from2 legionella pneumophila subsp. pneumophila str. philadelphia 1
55	<a href="#">d2etha1</a>	Alignment	not modelled	10.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
56	<a href="#">c6fddC</a>	Alignment	not modelled	10.0	11	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> whirlin; <b>PDBTitle:</b> crystal structure of the hhd2 domain of whirlin
57	<a href="#">c1b8hA</a>	Alignment	not modelled	9.7	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase processivity component; <b>PDBTitle:</b> sliding clamp, dna polymerase
58	<a href="#">c6iu8C</a>	Alignment	not modelled	9.5	13	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> vit1; <b>PDBTitle:</b> crystal structure of cytoplasmic metal binding domain with cobalt ions
59	<a href="#">c1kveA</a>	Alignment	not modelled	9.2	75	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> smk toxin; <b>PDBTitle:</b> killer toxin from halotolerant yeast
60	<a href="#">c3i3aC</a>	Alignment	not modelled	9.1	10	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n- <b>PDBTitle:</b> structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
61	<a href="#">d1i4ya</a>	Alignment	not modelled	9.0	16	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Hemerythrin-like <b>Family:</b> Hemerythrin-like
62	<a href="#">c2ip6A</a>	Alignment	not modelled	9.0	20	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> papb; <b>PDBTitle:</b> crystal structure of pedb
63	<a href="#">c5jxxC</a>	Alignment	not modelled	8.9	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n- <b>PDBTitle:</b> crystal structure of udp-n-acetylglucosamine o- acyltransferase (lpxa)2 from moraxella catarrhalis rh4.
64	<a href="#">c6egnA</a>	Alignment	not modelled	8.9	18	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> hg(ii)(grand coilser16cl19(dle))3-; <b>PDBTitle:</b> crystal structure of a three-stranded coiled coil peptide containing a2 trigonal planar hg(ii)s3 site modified by d-leu in the second3 coordination sphere
65	<a href="#">c4uetA</a>	Alignment	not modelled	8.9	10	<b>PDB header:</b> retinol-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nematode fatty acid retinoid binding protein; <b>PDBTitle:</b> diversity in the structures and ligand binding sites among2 the fatty acid and retinol binding proteins of nematodes3 revealed by na-far-1 from necator americanus
66	<a href="#">c2ak0A</a>	Alignment	not modelled	8.8	25	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-conotoxin mii; <b>PDBTitle:</b> structure of cyclic conotoxin mii-7
67	<a href="#">d1avsa</a>	Alignment	not modelled	8.7	10	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
68	<a href="#">c6egnC</a>	Alignment	not modelled	8.7	18	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> hg(ii)(grand coilser16cl19(dle))3-; <b>PDBTitle:</b> crystal structure of a three-stranded coiled coil peptide containing a2 trigonal planar hg(ii)s3 site modified by d-leu in the second3 coordination sphere
69	<a href="#">c6egmA</a>	Alignment	not modelled	8.7	18	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> apo-(grand coilser16cl19(dle))3; <b>PDBTitle:</b> crystal structure of a de novo three-stranded coiled coil peptide2 containing d-leu in a d-site position of a tris-thiolate binding site
70	<a href="#">d1zs3a1</a>	Alignment	not modelled	8.6	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
71	<a href="#">c5mc9B</a>	Alignment	not modelled	8.5	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> laminin subunit beta-1; <b>PDBTitle:</b> crystal structure of the heterotrimeric integrin-binding region of2 laminin-111
72	<a href="#">c1w0jB</a>	Alignment	not modelled	8.3	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase alpha chain heart isoform, <b>PDBTitle:</b> beryllium fluoride inhibited bovine f1-atpase
73	<a href="#">d2hmza</a>	Alignment	not modelled	8.1	24	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Hemerythrin-like <b>Family:</b> Hemerythrin-like
74	<a href="#">d1af7a1</a>	Alignment	not modelled	8.0	15	<b>Fold:</b> Chemotaxis receptor methyltransferase CheR, N-terminal domain <b>Superfamily:</b> Chemotaxis receptor methyltransferase CheR, N-terminal domain <b>Family:</b> Chemotaxis receptor methyltransferase CheR, N-terminal domain
75	<a href="#">d1cg5b</a>	Alignment	not modelled	7.8	13	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
76	<a href="#">d2dn3b1</a>	Alignment	not modelled	7.8	6	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins

77	<a href="#">c4n4uA</a>		not modelled	7.8	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter periplasmic solute-binding <b>PDBTitle:</b> crystal structure of abc transporter solute binding protein bb07192 from bordetella bronchiseptica rb50, target efi-510049
78	<a href="#">d1zaca</a>		not modelled	7.6	10	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
79	<a href="#">c3t57A</a>		not modelled	7.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine o-acyltransferase domain-containing <b>PDBTitle:</b> activity and crystal structure of arabidopsis udp-n-acetylglucosamine2 acyltransferase
80	<a href="#">c3oeoD</a>		not modelled	7.2	8	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> spheroplast protein y; <b>PDBTitle:</b> the crystal structure e. coli spy
81	<a href="#">c4l9mA</a>		not modelled	7.0	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ras guanyl-releasing protein 1; <b>PDBTitle:</b> autoinhibited state of the ras-specific exchange factor rasgrp1
82	<a href="#">d1hrba</a>		not modelled	7.0	16	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Hemerythrin-like <b>Family:</b> Hemerythrin-like
83	<a href="#">d1ozbg</a>		not modelled	7.0	31	<b>Fold:</b> SecB-like <b>Superfamily:</b> SecB-like <b>Family:</b> Bacterial protein-export protein SecB
84	<a href="#">c4xngC</a>		not modelled	6.9	21	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein mg218.1; <b>PDBTitle:</b> central domain of mycoplasma genitalium terminal organelle protein2 mg491
85	<a href="#">c3lw5H</a>		not modelled	6.9	22	<b>PDB header:</b> photosynthesis <b>Chain:</b> H: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> improved model of plant photosystem i
86	<a href="#">c2kvcA</a>		not modelled	6.8	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of the mycobacterium tuberculosis protein rv0543c.2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
87	<a href="#">c4k6jA</a>		not modelled	6.8	10	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> wings apart-like protein homolog; <b>PDBTitle:</b> human cohesin inhibitor wapl
88	<a href="#">d1gcvb</a>		not modelled	6.7	9	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
89	<a href="#">c4p47A</a>		not modelled	6.6	6	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 ochrobactrum anthropi (oant_4429), target efi-510151, c-terminus bound3 in ligand binding pocket
90	<a href="#">d2efva1</a>		not modelled	6.6	12	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> MJ0366-like
91	<a href="#">c2k7bA</a>		not modelled	6.5	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-binding protein 1; <b>PDBTitle:</b> nmr structure of mg2+-bound cabp1 n-domain
92	<a href="#">d3d1kb1</a>		not modelled	6.5	9	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
93	<a href="#">d1lifa</a>		not modelled	6.4	7	<b>Fold:</b> PABP domain-like <b>Superfamily:</b> PABC (PABP) domain <b>Family:</b> PABC (PABP) domain
94	<a href="#">c2fyuE</a>		not modelled	6.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit, <b>PDBTitle:</b> crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
95	<a href="#">d2qssb1</a>		not modelled	6.3	9	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
96	<a href="#">c4p8bA</a>		not modelled	6.2	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap-type transporter, periplasmic component; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 ralstonia eutropha h16 (h16_a1328), target efi-510189, with bound3 (s)-2-hydroxy-2-methyl-3-oxobutanoate ((s)-2-acetolactate)
97	<a href="#">c4h7yD</a>		not modelled	6.2	9	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dual specificity protein kinase ttk; <b>PDBTitle:</b> crystal structure of the tetratricopeptide repeat (tpr) motif of human2 dual specificity protein kinase mps1
98	<a href="#">d1wmub</a>		not modelled	6.2	6	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
99	<a href="#">c1p84E</a>		not modelled	6.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> hdbt inhibited yeast cytochrome bc1 complex