






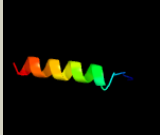

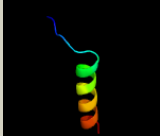

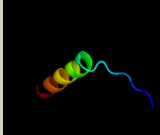



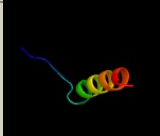



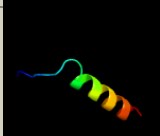

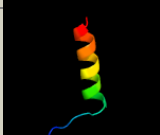
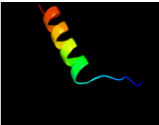
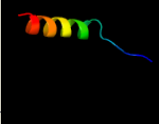

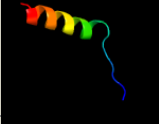



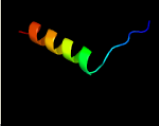



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1490_(-)_1679328_1680635
Date	Fri Aug 2 13:30:07 BST 2019
Unique Job ID	2c99e2f8cb9c4f19

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4kppA_</a>	 Alignment		41.6	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of h+/ca2+ exchanger cax
2	<a href="#">c6iu3A_</a>	 Alignment		37.4	16	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> vit1; <b>PDBTitle:</b> crystal structure of iron transporter vit1 with zinc ions
3	<a href="#">c5jyfB_</a>	 Alignment		33.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> structures of streptococcus agalactiae gbs gapdh in different2 enzymatic states
4	<a href="#">c1rm4O_</a>	 Alignment		32.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase a; <b>PDBTitle:</b> crystal structure of recombinant photosynthetic glyceraldehyde-3-2 phosphate dehydrogenase a4 isoform, complexed with nadp
5	<a href="#">c3hq4R_</a>	 Alignment		32.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution
6	<a href="#">c2pkrl_</a>	 Alignment		32.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase aor; <b>PDBTitle:</b> crystal structure of (a+cte)4 chimeric form of photosynthetic2 glyceraldehyde-3-phosphate dehydrogenase, complexed with nadp
7	<a href="#">c4qx6A_</a>	 Alignment		31.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 streptococcus agalactiae nem316 at 2.46 angstrom resolution
8	<a href="#">c5ld5C_</a>	 Alignment		31.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of a bacterial dehydrogenase at 2.19 angstroms2 resolution
9	<a href="#">c2x5kO_</a>	 Alignment		30.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> d-erythrose-4-phosphate dehydrogenase; <b>PDBTitle:</b> structure of an active site mutant of the d-erythrose-4-phosphate2 dehydrogenase from e. coli
10	<a href="#">c4dibF_</a>	 Alignment		30.3	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 bacillus anthracis str. Sterne
11	<a href="#">c1hdgO_</a>	 Alignment		30.3	17	<b>PDB header:</b> oxidoreductase (aldehy(d)-nad(a)) <b>Chain:</b> O: <b>PDB Molecule:</b> holo-d-glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of holo-glyceraldehyde-3-phosphate dehydrogenase2 from the hyperthermophilic bacterium thermotoga maritima at 2.53 angstroms resolution

12	<a href="#">c3cieC</a>	Alignment		30.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
13	<a href="#">c3docD</a>	Alignment		30.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of trka glyceraldehyde-3-phosphate dehydrogenase2 from brucella melitensis
14	<a href="#">c5ur0B</a>	Alignment		29.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystallographic structure of glyceraldehyde-3-phosphate dehydrogenase2 from naegleria gruberi
15	<a href="#">c3b20R</a>	Alignment		29.4	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase (nadp+); <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase2 complexed with nadfrom synechococcus elongatus"
16	<a href="#">c3h9eO</a>	Alignment		29.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase, testis-specific; <b>PDBTitle:</b> crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
17	<a href="#">c2d2iO</a>	Alignment		29.2	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of nadp-dependent glyceraldehyde-3-2 phosphate dehydrogenase from synechococcus sp. complexed3 with nadp+
18	<a href="#">d2ca1a1</a>	Alignment		29.1	20	<b>Fold:</b> Nucleocapsid protein dimerization domain <b>Superfamily:</b> Nucleocapsid protein dimerization domain <b>Family:</b> Coronavirus nucleocapsid protein
19	<a href="#">c1cerC</a>	Alignment		29.0	17	<b>PDB header:</b> oxidoreductase (aldehyde(d)-nad(a)) <b>Chain:</b> C: <b>PDB Molecule:</b> holo-d-glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> determinants of enzyme thermostability observed in the2 molecular structure of thermus aquaticus d-glyceraldehyde-3 3-phosphate dehydrogenase at 2.5 angstroms resolution
20	<a href="#">c2ep7B</a>	Alignment		28.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> structural study of project id aq_1065 from aquifex aeolicus vf5
21	<a href="#">c2b4rQ</a>	Alignment	not modelled	28.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falciparum at 2.25 angstrom resolution reveals intriguing3 extra electron density in the active site
22	<a href="#">c1i32D</a>	Alignment	not modelled	28.8	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
23	<a href="#">d2ge7a1</a>	Alignment	not modelled	28.7	20	<b>Fold:</b> Nucleocapsid protein dimerization domain <b>Superfamily:</b> Nucleocapsid protein dimerization domain <b>Family:</b> Coronavirus nucleocapsid protein
24	<a href="#">c6ok4A</a>	Alignment	not modelled	28.7	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase (gapdh)2 from chlamydia trachomatis with bound nad
25	<a href="#">c1ihxD</a>	Alignment	not modelled	28.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of two d-glyceraldehyde-3-phosphate2 dehydrogenase complexes: a case of asymmetry
26	<a href="#">c2i5pO</a>	Alignment	not modelled	28.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase isoform 1 from k. marxianus
27	<a href="#">c1s7cA</a>	Alignment	not modelled	26.5	13	<b>PDB header:</b> structural genomics, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase a;

						<b>PDBTitle:</b> crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli <b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor <b>Family:</b> Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
28	<a href="#">d1kqfb2</a>	Alignment	not modelled	26.3	32	<b>PDB header:</b> glycolytic pathway <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from alcaligenes xylooxidans at 1.7 a3 resolution.
29	<a href="#">c1obfO_</a>	Alignment	not modelled	24.8	17	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> c-terminal domain of human coronavirus nl63 nucleocapsid protein
30	<a href="#">c5epwB_</a>	Alignment	not modelled	22.8	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 borrelia burgdorferi
31	<a href="#">c3hjaB_</a>	Alignment	not modelled	22.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-p dehydrogenase; <b>PDBTitle:</b> structure of lactobacillus acidophilus glyceraldehyde-3-phosphate2 dehydrogenase at 2.21 angstrom resolution
32	<a href="#">c5j9gB_</a>	Alignment	not modelled	22.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
33	<a href="#">c3sthA_</a>	Alignment	not modelled	18.5	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase slyd; <b>PDBTitle:</b> solution structure of helicobacter pylori slyd
34	<a href="#">c2kr7A_</a>	Alignment	not modelled	17.6	33	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 100mm dpc)
35	<a href="#">c1r7gA_</a>	Alignment	not modelled	16.9	63	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 50% tfe)
36	<a href="#">c1r7cA_</a>	Alignment	not modelled	16.9	63	<b>PDB header:</b> oxidoreductase(aldehyde(d)-nad(a)) <b>Chain:</b> P: <b>PDB Molecule:</b> apo-d-glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> coenzyme-induced conformational changes in glyceraldehyde-3-2 phosphate dehydrogenase from bacillus stearothermophilus
37	<a href="#">c2gd1P_</a>	Alignment	not modelled	16.7	23	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> semb cab41934.1;
38	<a href="#">c2ntxB_</a>	Alignment	not modelled	16.7	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium release-activated calcium channel protein 1; <b>PDBTitle:</b> calcium release-activated calcium (crac) channel orai
39	<a href="#">c4hkrA_</a>	Alignment	not modelled	16.5	21	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> 2.70 a cytochrome b6f complex structure from nostoc pcc 7120
40	<a href="#">c4h44E_</a>	Alignment	not modelled	16.5	50	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
41	<a href="#">c2zt9E_</a>	Alignment	not modelled	16.5	50	<b>PDB header:</b> electron transport <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> internal lipid architecture of the hetero-oligomeric cytochrome b6f2 complex
42	<a href="#">c4ogqE_</a>	Alignment	not modelled	16.5	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell surface protein (putative cell surface-associated) <b>PDBTitle:</b> the crystal structure of the cysteine protease and lectin-like2 domains of cwp84, a surface layer associated protein of clostridium3 difficile
43	<a href="#">d2giba1</a>	Alignment	not modelled	15.4	29	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
44	<a href="#">c4ci7A_</a>	Alignment	not modelled	14.5	17	<b>Fold:</b> Nucleocapsid protein dimerization domain <b>Superfamily:</b> Nucleocapsid protein dimerization domain <b>Family:</b> Coronavirus nucleocapsid protein
45	<a href="#">c3pr9A_</a>	Alignment	not modelled	14.1	11	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Long-chain cytokines
46	<a href="#">d2cjr1</a>	Alignment	not modelled	13.9	29	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
47	<a href="#">d1pvhb_</a>	Alignment	not modelled	13.9	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> Dhaf3308-like <b>Family:</b> Dhaf3308-like
48	<a href="#">d3buxb1</a>	Alignment	not modelled	13.8	36	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> c-terminal domain of mers-cov nucleocapsid
49	<a href="#">d2h1qa1</a>	Alignment	not modelled	13.0	26	
50	<a href="#">c6g13B_</a>	Alignment	not modelled	12.9	26	

51	<a href="#">c4olsA</a>	Alignment	not modelled	12.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endolysin; <b>PDBTitle:</b> the amidase-2 domain of lysgh15
52	<a href="#">c5i0cA</a>	Alignment	not modelled	11.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yjdj; <b>PDBTitle:</b> crystal structure of predicted acyltransferase yjdj with acyl-coa n-2 acyltransferase domain from escherichia coli str. k-12
53	<a href="#">c6g9oA</a>	Alignment	not modelled	11.7	28	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> volume-regulated anion channel subunit lrrc8a; <b>PDBTitle:</b> structure of full-length homomeric mlrrc8a volume-regulated anion2 channel at 4.25 a resolution
54	<a href="#">d2auwa1</a>	Alignment	not modelled	11.7	25	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE0471 C-terminal domain-like
55	<a href="#">c3wmjB</a>	Alignment	not modelled	11.6	24	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> eiaiv vaccine gp45; <b>PDBTitle:</b> crystal structure of eiaiv vaccine gp45
56	<a href="#">d1a7ja</a>	Alignment	not modelled	10.3	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
57	<a href="#">c3srjB</a>	Alignment	not modelled	9.8	29	<b>PDB header:</b> cell invasion/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> apical membrane antigen 1, ama1; <b>PDBTitle:</b> pfama1 in complex with invasion-inhibitory peptide r1
58	<a href="#">c4jo6Z</a>	Alignment	not modelled	9.5	50	<b>PDB header:</b> unknown function <b>Chain:</b> Z: <b>PDB Molecule:</b> sbp-tag; <b>PDBTitle:</b> streptavidin complex with sbp-tag
59	<a href="#">c4jo6Y</a>	Alignment	not modelled	9.5	50	<b>PDB header:</b> unknown function <b>Chain:</b> Y: <b>PDB Molecule:</b> sbp-tag; <b>PDBTitle:</b> streptavidin complex with sbp-tag
60	<a href="#">c5n5xN</a>	Alignment	not modelled	9.3	40	<b>PDB header:</b> transcription <b>Chain:</b> N: <b>PDB Molecule:</b> rna polymerase i-specific transcription initiation factor <b>PDBTitle:</b> crystal structure of s. cerevisiae core factor at 3.2a resolution
61	<a href="#">c5yq7H</a>	Alignment	not modelled	9.1	65	<b>PDB header:</b> photosynthesis <b>Chain:</b> H: <b>PDB Molecule:</b> alpha subunit of light-harvesting 1; <b>PDBTitle:</b> cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
62	<a href="#">d1cwpA</a>	Alignment	not modelled	8.9	42	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Bromoviridae-like VP
63	<a href="#">c5vlaZ</a>	Alignment	not modelled	8.9	58	<b>PDB header:</b> hydrolase <b>Chain:</b> Z: <b>PDB Molecule:</b> thr-val-phe-thr-ser-trp-glu-glu-tyr-leu-asp-trp-val-met- <b>PDBTitle:</b> short pcsk9 delta-p' complex with fusion2 peptide
64	<a href="#">d1r3ba</a>	Alignment	not modelled	8.9	23	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Mob1/phocein <b>Family:</b> Mob1/phocein
65	<a href="#">d1wjva1</a>	Alignment	not modelled	8.8	18	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> C2HC finger
66	<a href="#">c3npgD</a>	Alignment	not modelled	8.8	26	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized duf364 family protein; <b>PDBTitle:</b> crystal structure of a protein with unknown function from duf3642 family (ph1506) from pyrococcus horikoshii at 2.70 a resolution
67	<a href="#">c2k8iA</a>	Alignment	not modelled	8.8	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> solution structure of e.coli slyd
68	<a href="#">d1ix5a</a>	Alignment	not modelled	8.7	11	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
69	<a href="#">d1xmta</a>	Alignment	not modelled	8.6	15	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
70	<a href="#">c2kvIA</a>	Alignment	not modelled	8.5	27	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> major outer capsid protein vp7; <b>PDBTitle:</b> nmr structure of the c-terminal domain of vp7
71	<a href="#">c2jagA</a>	Alignment	not modelled	8.5	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> halorhodopsin; <b>PDBTitle:</b> I1-intermediate of halorhodopsin t203v
72	<a href="#">d1wxxa1</a>	Alignment	not modelled	8.4	55	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Hypothetical RNA methyltransferase domain (HRMD)
73	<a href="#">d2fmma1</a>	Alignment	not modelled	8.4	31	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Chromo domain-like <b>Family:</b> Chromo domain
74	<a href="#">c3cgnA</a>	Alignment	not modelled	8.4	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> crystal structure of thermophilic slyd
75	<a href="#">c2kfwA</a>	Alignment	not modelled	8.3	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase <b>PDBTitle:</b> solution structure of full-length slyd from e.coli
76	<a href="#">c6go1A</a>	Alignment	not modelled	8.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> polysaccharide deacetylase-like protein; <b>PDBTitle:</b> crystal structure of a bacillus anthracis peptidoglycan deacetylase
77	<a href="#">c4ln0C</a>	Alignment	not modelled	8.2	24	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcription cofactor vestigial-like protein

77	<a href="#">c4mhc_</a>	Alignment	not modelled	8.2	34	4; <b>PDB header:</b> crystal structure of the vgl14-tead4 complex <b>PDB header:</b> chaperone, isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
78	<a href="#">c3prdA_</a>	Alignment	not modelled	8.2	13	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> CCP-like
79	<a href="#">d1fhfa_</a>	Alignment	not modelled	7.8	13	<b>PDB header:</b> virus/rna <b>Chain:</b> B; <b>PDB Molecule:</b> coat protein; <b>PDBTitle:</b> structures of the native and swollen forms of cowpea2 chlorotic mottle virus determined by x-ray crystallography3 and cryo-electron microscopy
80	<a href="#">c1cwpB_</a>	Alignment	not modelled	7.8	42	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> fkbp-type 16 kda peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> crystal structure of the ppiase-chaperone slpa with the chaperone2 binding site occupied by the linker of the purification tag
81	<a href="#">c4dt4A_</a>	Alignment	not modelled	7.7	38	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> son of sevenless homolog 1; <b>PDBTitle:</b> crystal structure of the histone domain, dh-ph unit, and catalytic2 unit of the ras activator son of sevenless (sos)
82	<a href="#">c3ksyA_</a>	Alignment	not modelled	7.7	34	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> glutathione s-transferase homolog; <b>PDBTitle:</b> ligg from sphingobium sp. syk-6 is related to the glutathione2 transferase omega class
83	<a href="#">c4g10A_</a>	Alignment	not modelled	7.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> namn:dmb phosphoribosyltransferase; <b>PDBTitle:</b> the structure of cobt from pyrococcus horikoshii
84	<a href="#">c3u4gA_</a>	Alignment	not modelled	7.6	50	<b>Fold:</b> Family A G protein-coupled receptor-like <b>Superfamily:</b> Family A G protein-coupled receptor-like <b>Family:</b> Bacteriorhodopsin-like
85	<a href="#">d1e12a_</a>	Alignment	not modelled	7.6	11	<b>Fold:</b> Another 3-helical bundle <b>Superfamily:</b> IscX-like <b>Family:</b> IscX-like
86	<a href="#">d1uj8a1</a>	Alignment	not modelled	7.5	38	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> calcium release-activated calcium channel protein 1; <b>PDBTitle:</b> calcium release-activated calcium (crac) channel orai
87	<a href="#">c4hkrB_</a>	Alignment	not modelled	7.3	21	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Bromoviridae-like VP
88	<a href="#">d1yc611</a>	Alignment	not modelled	7.2	42	<b>PDB header:</b> signaling protein <b>Chain:</b> P; <b>PDB Molecule:</b> erythropoietin receptor; <b>PDBTitle:</b> structure of human jak2 ferm/sh2 in complex with erythropoietin2 receptor
89	<a href="#">c6e2qP_</a>	Alignment	not modelled	6.9	14	<b>PDB header:</b> metal transport <b>Chain:</b> B; <b>PDB Molecule:</b> integral membrane channel and cytosolic domains; <b>PDBTitle:</b> crystal structure of an inward rectifier potassium channel
90	<a href="#">c1p7bB_</a>	Alignment	not modelled	6.7	20	<b>PDB header:</b> metal binding protein/transferase <b>Chain:</b> B; <b>PDB Molecule:</b> eukaryotic elongation factor 2 kinase; <b>PDBTitle:</b> structure of calmodulin in a complex with a peptide derived from a2 calmodulin-dependent kinase
91	<a href="#">c5j8hB_</a>	Alignment	not modelled	6.5	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M; <b>PDB Molecule:</b> isocitrate dehydrogenase [nad] subunit 1; <b>PDBTitle:</b> yeast isocitrate dehydrogenase (apo form)
92	<a href="#">c3blxM_</a>	Alignment	not modelled	6.4	22	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Bromoviridae-like VP
93	<a href="#">d1js9c_</a>	Alignment	not modelled	6.4	42	<b>PDB header:</b> virus <b>Chain:</b> Z; <b>PDB Molecule:</b> highly immunogenic outer capsid protein; <b>PDBTitle:</b> bacteriophage t4 isometric capsid
94	<a href="#">c5vf3Z_</a>	Alignment	not modelled	6.3	60	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> deoxynucleotidyltransferase terminal-interacting protein 1; <b>PDBTitle:</b> the structure of the carboxy-terminal domain of dnttip1
95	<a href="#">c2mwiA_</a>	Alignment	not modelled	6.1	67	<b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
96	<a href="#">d3d37a1</a>	Alignment	not modelled	6.0	18	<b>PDB header:</b> chaperone <b>Chain:</b> T; <b>PDB Molecule:</b> heat shock protein beta-1; <b>PDBTitle:</b> oligomeric complex of a hsp27 24-mer at 3.6 a resolution
97	<a href="#">c6dv5T_</a>	Alignment	not modelled	5.9	17	<b>PDB header:</b> photosynthesis <b>Chain:</b> L; <b>PDB Molecule:</b> cytochrome b559 beta subunit; <b>PDBTitle:</b> photosystem ii from thermosynechococcus elongatus
98	<a href="#">c1w5cL_</a>	Alignment	not modelled	5.9	42	<b>PDB header:</b> electron transport <b>Chain:</b> P; <b>PDB Molecule:</b> prokaryotic respiratory supercomplex associate factor 1 <b>PDBTitle:</b> respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
99	<a href="#">c6adqP_</a>	Alignment	not modelled	5.9	27	