
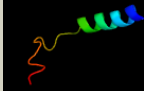

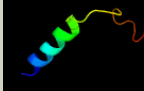



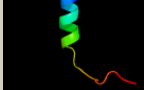
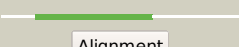
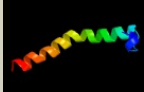
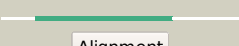


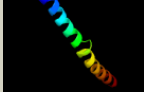





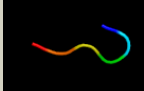




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1740_(-)_1967712_1967924
Date	Fri Aug 2 13:30:34 BST 2019
Unique Job ID	b336b5b9bc4e8335

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4xgqD_</a>	 Alignment		98.5	69	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> D; <b>PDB Molecule:</b> antitoxin vapp30; <b>PDBTitle:</b> crystal structure of addiction module from mycobacterial species
2	<a href="#">c4xgqB_</a>	 Alignment		98.5	69	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> B; <b>PDB Molecule:</b> antitoxin vapp30; <b>PDBTitle:</b> crystal structure of addiction module from mycobacterial species
3	<a href="#">c4xgrH_</a>	 Alignment		97.9	64	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> H; <b>PDB Molecule:</b> antitoxin vapp30; <b>PDBTitle:</b> crystal structure of addiction module from mycobacterial species
4	<a href="#">c4xgrF_</a>	 Alignment		97.7	68	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> F; <b>PDB Molecule:</b> antitoxin vapp30; <b>PDBTitle:</b> crystal structure of addiction module from mycobacterial species
5	<a href="#">c4d8jD_</a>	 Alignment		58.9	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> macrodomain ter protein; <b>PDBTitle:</b> structure of e. coli matp-mats complex
6	<a href="#">c3lt6D_</a>	 Alignment		40.0	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> D; <b>PDB Molecule:</b> adhesin yada; <b>PDBTitle:</b> a transition from strong right-handed to canonical left-handed2 supercoiling in a conserved coiled coil segment of trimeric3 autotransporter adhesins - the mutant 4 structure
7	<a href="#">c3lt7D_</a>	 Alignment		33.2	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> D; <b>PDB Molecule:</b> adhesin yada; <b>PDBTitle:</b> a transition from strong right-handed to canonical left-handed2 supercoiling in a conserved coiled coil segment of trimeric3 autotransporter adhesins - the m3 mutant structure
8	<a href="#">d2jeka1</a>	 Alignment		27.5	20	<b>Fold:</b> Rv1873-like <b>Superfamily:</b> Rv1873-like <b>Family:</b> Rv1873-like
9	<a href="#">c4kvcC_</a>	 Alignment		26.4	37	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-l17c-w224bf; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-l17c-w224bf
10	<a href="#">c5bs7F_</a>	 Alignment		26.1	67	<b>PDB header:</b> transcription regulator <b>Chain:</b> F; <b>PDB Molecule:</b> protein spt2 homolog; <b>PDBTitle:</b> structure of histone h3/h4 in complex with spt2
11	<a href="#">c5bsaF_</a>	 Alignment		25.6	67	<b>PDB header:</b> transcription regulator <b>Chain:</b> F; <b>PDB Molecule:</b> protein spt2 homolog; <b>PDBTitle:</b> structure of histone h3/h4 in complex with spt2

12	<a href="#">c4kvuA_</a>	Alignment		22.9	37	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-l17c-w224bf; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-l17c-w224bf
13	<a href="#">c4kvuB_</a>	Alignment		22.9	37	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> 6-helix coiled coil cc-hex-l17c-w224bf; <b>PDBTitle:</b> crystal structure of a 6-helix coiled coil cc-hex-l17c-w224bf
14	<a href="#">c4zrjB_</a>	Alignment		22.6	21	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> merlin; <b>PDBTitle:</b> structure of merlin-ferm and ctd
15	<a href="#">c1wkbA_</a>	Alignment		18.2	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> crystal structure of leucyl-trna synthetase from the2 archaeon pyrococcus horikoshii reveals a novel editing3 domain orientation
16	<a href="#">c5bsaE_</a>	Alignment		17.9	50	<b>PDB header:</b> transcription regulator <b>Chain:</b> E: <b>PDB Molecule:</b> protein spt2 homolog; <b>PDBTitle:</b> structure of histone h3/h4 in complex with spt2
17	<a href="#">d1uf2c1</a>	Alignment		16.9	28	<b>Fold:</b> A virus capsid protein alpha-helical domain <b>Superfamily:</b> A virus capsid protein alpha-helical domain <b>Family:</b> Phytoreovirus capsid
18	<a href="#">c1uf2F_</a>	Alignment		15.6	28	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> outer capsid protein p8; <b>PDBTitle:</b> the atomic structure of rice dwarf virus (rdv)
19	<a href="#">c2w6jG_</a>	Alignment		14.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase subunit gamma, mitochondrial; <b>PDBTitle:</b> low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 5.
20	<a href="#">c3go5A_</a>	Alignment		14.3	18	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> multidomain protein with s1 rna-binding domains; <b>PDBTitle:</b> crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
21	<a href="#">c1wloA_</a>	Alignment	not modelled	14.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sufe protein; <b>PDBTitle:</b> solution structure of the hypothetical protein from thermus2 thermophilus hb8
22	<a href="#">c4lgjA_</a>	Alignment	not modelled	14.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure and mechanism of a type iii secretion protease
23	<a href="#">c3r4hD_</a>	Alignment	not modelled	13.9	40	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> coiled coil helix cc-tet-phi22; <b>PDBTitle:</b> crystal structure of the 4-helix coiled coil cc-tet-phi22
24	<a href="#">c6f5dG_</a>	Alignment	not modelled	13.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase gamma subunit; <b>PDBTitle:</b> trypanosoma brucei f1-atpase
25	<a href="#">d1mzga_</a>	Alignment	not modelled	13.7	21	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SufE-like
26	<a href="#">c5m1gB_</a>	Alignment	not modelled	13.6	34	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gag protein; <b>PDBTitle:</b> structure of a spumaretrovirus gag central domain reveals an ancient2 retroviral capsid
27	<a href="#">c3r4hE_</a>	Alignment	not modelled	13.3	40	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> coiled coil helix cc-tet-phi22; <b>PDBTitle:</b> crystal structure of the 4-helix coiled coil cc-tet-phi22
28	<a href="#">c2xokG_</a>	Alignment	not modelled	12.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase subunit gamma, mitochondrial; <b>PDBTitle:</b> refined structure of yeast f1c10 atpase complex to 3 a resolution

29	<a href="#">c2kelB_</a>	Alignment	not modelled	12.5	50	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein 56b; <b>PDBTitle:</b> structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
30	<a href="#">c3r4hF_</a>	Alignment	not modelled	12.4	40	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> coiled coil helix cc-tet-phi22; <b>PDBTitle:</b> crystal structure of the 4-helix coiled coil cc-tet-phi22
31	<a href="#">c3r4hA_</a>	Alignment	not modelled	12.4	40	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled coil helix cc-tet-phi22; <b>PDBTitle:</b> crystal structure of the 4-helix coiled coil cc-tet-phi22
32	<a href="#">c3r4hC_</a>	Alignment	not modelled	12.4	40	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coiled coil helix cc-tet-phi22; <b>PDBTitle:</b> crystal structure of the 4-helix coiled coil cc-tet-phi22
33	<a href="#">c3r4hB_</a>	Alignment	not modelled	12.4	40	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coiled coil helix cc-tet-phi22; <b>PDBTitle:</b> crystal structure of the 4-helix coiled coil cc-tet-phi22
34	<a href="#">c3terA_</a>	Alignment	not modelled	12.2	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mammalian stromal interaction molecule-1; <b>PDBTitle:</b> crystal structure of soar domain with inhibition helix from c. elegans
35	<a href="#">c4k6IG_</a>	Alignment	not modelled	12.2	30	<b>PDB header:</b> toxin <b>Chain:</b> G: <b>PDB Molecule:</b> putative pertussis-like toxin subunit; <b>PDBTitle:</b> structure of typhoid toxin
36	<a href="#">c4z9dA_</a>	Alignment	not modelled	12.1	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pertussis toxin-like subunit arta; <b>PDBTitle:</b> ecplta
37	<a href="#">c4ariA_</a>	Alignment	not modelled	11.9	50	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> leucine--trna ligase; <b>PDBTitle:</b> ternary complex of e. coli leucyl-trna synthetase, trna(leu) and the2 benzoxaborole an2679 in the editing conformation
38	<a href="#">c5ca8A_</a>	Alignment	not modelled	11.7	58	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein sey1; <b>PDBTitle:</b> structures of the yeast dynamin-like gtpase sey1p in complex with gdp
39	<a href="#">d1mnta_</a>	Alignment	not modelled	11.7	20	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
40	<a href="#">c4xd7G_</a>	Alignment	not modelled	11.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase gamma chain; <b>PDBTitle:</b> structure of thermophilic f1-atpase inhibited by epsilon subunit
41	<a href="#">c4lgiD_</a>	Alignment	not modelled	10.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> n-terminal truncated nlec structure
42	<a href="#">c4z9cA_</a>	Alignment	not modelled	10.9	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pertussis toxin-like subunit arta; <b>PDBTitle:</b> ecpltab oxidized
43	<a href="#">c4tlwA_</a>	Alignment	not modelled	10.9	38	<b>PDB header:</b> toxin, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylating toxin cards; <b>PDBTitle:</b> cards toxin, full-length
44	<a href="#">c1wz2B_</a>	Alignment	not modelled	10.8	20	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
45	<a href="#">d1ni7a_</a>	Alignment	not modelled	10.3	7	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SufE-like
46	<a href="#">c3oaaO_</a>	Alignment	not modelled	10.1	21	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> O: <b>PDB Molecule:</b> atp synthase gamma chain; <b>PDBTitle:</b> structure of the e.coli f1-atp synthase inhibited by subunit epsilon
47	<a href="#">c5lqxG_</a>	Alignment	not modelled	9.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase gamma subunit; <b>PDBTitle:</b> structure of f-atpase from pichia angusta, state3
48	<a href="#">c4r33A_</a>	Alignment	not modelled	9.6	42	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> nosl; <b>PDBTitle:</b> x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
49	<a href="#">c3teqB_</a>	Alignment	not modelled	9.6	45	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> stromal interaction molecule 1; <b>PDBTitle:</b> crystal structure of soar domain
50	<a href="#">c2xpiE_</a>	Alignment	not modelled	9.4	50	<b>PDB header:</b> cell cycle <b>Chain:</b> E: <b>PDB Molecule:</b> anaphase-promoting complex subunit hcn1 hcn1/cdc26,20s <b>PDBTitle:</b> crystal structure of apc/c hetero-tetramer cut9-hcn1
51	<a href="#">c2mc7A_</a>	Alignment	not modelled	9.0	38	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory peptide; <b>PDBTitle:</b> structure of salmonella mgtr
52	<a href="#">c4hsrA_</a>	Alignment	not modelled	8.9	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaryl-7-aminocephalosporanic acid acylase alpha chain; <b>PDBTitle:</b> crystal structure of a class iii engineered cephalosporin acylase
53	<a href="#">c2bytD_</a>	Alignment	not modelled	8.9	50	<b>PDB header:</b> synthetase <b>Chain:</b> D: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> thermus thermophilus leucyl-trna synthetase complexed with2 a trnaleu transcript in the post-editing conformation
54	<a href="#">c2dcqA_</a>	Alignment	not modelled	8.9	38	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative protein at4g01050; <b>PDBTitle:</b> fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana

55	<a href="#">c5ady6</a>	Alignment	not modelled	8.9	22	<b>PDB header:</b> ribosome <b>Chain:</b> 6: <b>PDB Molecule:</b> gtpase hflx; <b>PDBTitle:</b> cryo-em structures of the 50s ribosome subunit bound with hflx
56	<a href="#">c5dazA</a>	Alignment	not modelled	8.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> scabin; <b>PDBTitle:</b> crystal structure of scabin, a mono- <i>adp</i> -ribosyltransferase from <i>Streptomyces scabies</i>
57	<a href="#">c1qu2A</a>	Alignment	not modelled	8.8	50	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> isoleucyl-trna synthetase; <b>PDBTitle:</b> insights into editing from an ile-trna synthetase structure2 with trna(ile) and mupirocin
58	<a href="#">c6re1S</a>	Alignment	not modelled	8.8	23	<b>PDB header:</b> proton transport <b>Chain:</b> S: <b>PDB Molecule:</b> atp synthase gamma chain, mitochondrial; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 2a,2 focussed refinement of f1 head and rotor
59	<a href="#">c6q8aA</a>	Alignment	not modelled	8.7	40	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine--trna ligase; <b>PDBTitle:</b> neisseria gonorrhoeae leucyl-trna synthetase in complex with 5'-o-(n-2 (l-leucyl)-sulfamoyl)cytidine
60	<a href="#">c6fkig</a>	Alignment	not modelled	8.5	21	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase subunit c, chloroplastic; <b>PDBTitle:</b> chloroplast f1fo conformation 3
61	<a href="#">c6ax5A</a>	Alignment	not modelled	8.5	25	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> swi/snf-related matrix-associated actin-dependent regulator <b>PDBTitle:</b> rpt1 region of ini1/snf5/smarcb1_human - swi/snf-related matrix-2 associated actin-dependent regulator of chromatin subfamily b member3 1.
62	<a href="#">c5ah5B</a>	Alignment	not modelled	8.4	50	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> leucine--trna ligase; <b>PDBTitle:</b> crystal structure of the ternary complex of agrobacterium2 radiobacter k84 agnb2 leu-trna-leuams
63	<a href="#">c5m1hA</a>	Alignment	not modelled	8.4	33	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gag protein; <b>PDBTitle:</b> structure of a spumaretrovirus gag central domain reveals an ancient2 retroviral capsid
64	<a href="#">c3r4aA</a>	Alignment	not modelled	8.3	41	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled coil helix cc-tet; <b>PDBTitle:</b> crystal structure of the 4-helix coiled coil cc-tet
65	<a href="#">c2xp1B</a>	Alignment	not modelled	8.2	50	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> anaphase-promoting complex subunit hcn1 hcn1/cdc26,20s <b>PDBTitle:</b> crystal structure of apc/c hetero-tetramer cut9-hcn1
66	<a href="#">d1em7a</a>	Alignment	not modelled	8.0	35	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> immunoglobulin-binding domains <b>Family:</b> immunoglobulin-binding domains
67	<a href="#">c2yy0D</a>	Alignment	not modelled	7.9	40	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> c-myc-binding protein; <b>PDBTitle:</b> crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
68	<a href="#">c3r4aD</a>	Alignment	not modelled	7.9	41	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> coiled coil helix cc-tet; <b>PDBTitle:</b> crystal structure of the 4-helix coiled coil cc-tet
69	<a href="#">c3r4aC</a>	Alignment	not modelled	7.8	41	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coiled coil helix cc-tet; <b>PDBTitle:</b> crystal structure of the 4-helix coiled coil cc-tet
70	<a href="#">c3r4aB</a>	Alignment	not modelled	7.8	41	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coiled coil helix cc-tet; <b>PDBTitle:</b> crystal structure of the 4-helix coiled coil cc-tet
71	<a href="#">c1ileA</a>	Alignment	not modelled	7.7	45	<b>PDB header:</b> aminoacyl-trna synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> isoleucyl-trna synthetase; <b>PDBTitle:</b> isoleucyl-trna synthetase
72	<a href="#">c2akfB</a>	Alignment	not modelled	7.6	38	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
73	<a href="#">c2akfA</a>	Alignment	not modelled	7.6	38	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
74	<a href="#">c2akfC</a>	Alignment	not modelled	7.6	38	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
75	<a href="#">c6ajnF</a>	Alignment	not modelled	7.6	23	<b>PDB header:</b> toxin <b>Chain:</b> F: <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> crystal structure of atatr bound with accoa
76	<a href="#">d1fd6a</a>	Alignment	not modelled	7.2	40	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> immunoglobulin-binding domains <b>Family:</b> immunoglobulin-binding domains
77	<a href="#">c1tiiA</a>	Alignment	not modelled	7.1	33	<b>PDB header:</b> enterotoxin <b>Chain:</b> A: <b>PDB Molecule:</b> heat labile enterotoxin type iib; <b>PDBTitle:</b> escherichia coli heat labile enterotoxin type iib
78	<a href="#">d2jdig1</a>	Alignment	not modelled	7.1	30	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> ATP synthase (F1-ATPase), gamma subunit <b>Family:</b> ATP synthase (F1-ATPase), gamma subunit
79	<a href="#">c2yskA</a>	Alignment	not modelled	7.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha1432; <b>PDBTitle:</b> crystal structure of a hypothetical protein ttha1432 from thermus2 thermophilus
80	<a href="#">c2w6hG</a>	Alignment	not modelled	6.9	30	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase subunit gamma, mitochondrial; <b>PDBTitle:</b> low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 4a.

81	<a href="#">d2a5db1</a>	Alignment	not modelled	6.9	44	<b>Fold:</b> ADP-ribosylation <b>Superfamily:</b> ADP-ribosylation <b>Family:</b> ADP-ribosylating toxins
82	<a href="#">c1obhA</a>	Alignment	not modelled	6.8	50	<b>PDB header:</b> synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> leucyl-trna synthetase from thermus thermophilus complexed2 with a pre-transfer editing substrate analogue in both3 synthetic active site and editing site
83	<a href="#">c6q45G</a>	Alignment	not modelled	6.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase gamma chain; <b>PDBTitle:</b> f1-atpase from fusobacterium nucleatum
84	<a href="#">c4egcA</a>	Alignment	not modelled	6.7	58	<b>PDB header:</b> transcription/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, homeobox protein six1 <b>PDBTitle:</b> crystal structure of mbp-fused human six1 bound to human eya2 eya2 domain
85	<a href="#">c3m92B</a>	Alignment	not modelled	6.5	83	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein ycin; <b>PDBTitle:</b> the structure of ycin, an uncharacterized protein from shigella2 flexneri.
86	<a href="#">c5vwwD</a>	Alignment	not modelled	6.4	38	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> bak core latch dimer in complex with bim-rt - tetragonal
87	<a href="#">c3g5jA</a>	Alignment	not modelled	6.4	22	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative atp/gtp binding protein; <b>PDBTitle:</b> crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
88	<a href="#">c2llzA</a>	Alignment	not modelled	6.4	42	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yjdk; <b>PDBTitle:</b> ghos (yjdk) monomer
89	<a href="#">c4qvrA</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hypothetical protein ftt_1539c; <b>PDBTitle:</b> 2.3 angstrom crystal structure of hypothetical protein ftt1539c from2 francisella tularensis.
90	<a href="#">c3eabK</a>	Alignment	not modelled	6.0	25	<b>PDB header:</b> cell cycle <b>Chain:</b> K: <b>PDB Molecule:</b> chmp1b; <b>PDBTitle:</b> crystal structure of spastin mit in complex with escrt iii
91	<a href="#">d1fcla</a>	Alignment	not modelled	6.0	40	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
92	<a href="#">d1pgaa</a>	Alignment	not modelled	5.8	40	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
93	<a href="#">c2jwuA</a>	Alignment	not modelled	5.8	20	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> gb88; <b>PDBTitle:</b> solution nmr structures of two designed proteins with 88%2 sequence identity but different fold and function
94	<a href="#">d1gb4a</a>	Alignment	not modelled	5.7	30	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
95	<a href="#">c3fksY</a>	Alignment	not modelled	5.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> Y: <b>PDB Molecule:</b> atp synthase subunit gamma, mitochondrial; <b>PDBTitle:</b> yeast f1 atpase in the absence of bound nucleotides
96	<a href="#">c3gkuB</a>	Alignment	not modelled	5.7	33	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable rna-binding protein; <b>PDBTitle:</b> crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
97	<a href="#">d1p7ea</a>	Alignment	not modelled	5.5	35	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
98	<a href="#">c2dytA</a>	Alignment	not modelled	5.3	38	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> autophagy-related protein 3; <b>PDBTitle:</b> the crystal structure of saccharomyces cerevisiae atg3
99	<a href="#">c5dn6G</a>	Alignment	not modelled	5.3	25	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase gamma chain; <b>PDBTitle:</b> atp synthase from paracoccus denitrificans