

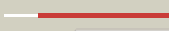






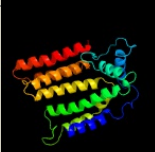







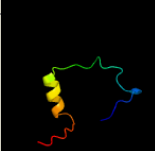

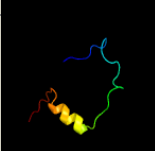



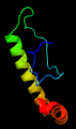
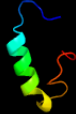
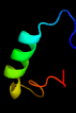




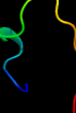


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3805c_(-)_4267131_4269014
Date	Fri Aug 9 18:20:51 BST 2019
Unique Job ID	11153af62f9e66af

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5f15A_</a>	 Alignment		99.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; <b>PDBTitle:</b> crystal structure of arnt from cupriavidus metallidurans bound to 2 undecaprenyl phosphate
2	<a href="#">c3wajA_</a>	 Alignment		98.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane oligosaccharyl transferase; <b>PDBTitle:</b> crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
3	<a href="#">c3rceA_</a>	 Alignment		98.0	16	<b>PDB header:</b> transferase/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> oligosaccharide transferase to n-glycosylate proteins; <b>PDBTitle:</b> bacterial oligosaccharyltransferase pglb
4	<a href="#">c6p2rB_</a>	 Alignment		97.4	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dolichyl-phosphate-mannose--protein mannosyltransferase 2; <b>PDBTitle:</b> structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
5	<a href="#">c6p25A_</a>	 Alignment		97.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dolichyl-phosphate-mannose--protein mannosyltransferase 1; <b>PDBTitle:</b> structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
6	<a href="#">c6eznF_</a>	 Alignment		96.4	13	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
7	<a href="#">d2d6fc2</a>	 Alignment		62.9	21	<b>Fold:</b> DCoH-like <b>Superfamily:</b> GAD domain-like <b>Family:</b> GAD domain
8	<a href="#">dlzqlc2</a>	 Alignment		58.9	26	<b>Fold:</b> DCoH-like <b>Superfamily:</b> GAD domain-like <b>Family:</b> GAD domain
9	<a href="#">c4j7bF_</a>	 Alignment		36.1	26	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> 205 kda microtubule-associated protein; <b>PDBTitle:</b> crystal structure of polo-like kinase 1
10	<a href="#">c4j7bC_</a>	 Alignment		36.1	26	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 205 kda microtubule-associated protein; <b>PDBTitle:</b> crystal structure of polo-like kinase 1
11	<a href="#">c5uz9D_</a>	 Alignment		35.3	30	<b>PDB header:</b> immune system/rna <b>Chain:</b> D: <b>PDB Molecule:</b> crispr-associated protein csy3; <b>PDBTitle:</b> cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crna-guided crispr surveillance complex

12	<a href="#">c4eogA</a>	Alignment		31.6	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of csx1 of pyrococcus furiosus
13	<a href="#">d1usua</a>	Alignment		19.8	12	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Hsp90 middle domain
14	<a href="#">d1s4na</a>	Alignment		19.0	19	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Glycolipid 2-alpha-mannosyltransferase
15	<a href="#">c1s4pA</a>	Alignment		17.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycolipid 2-alpha-mannosyltransferase; <b>PDBTitle:</b> crystal structure of yeast alpha1,2-mannosyltransferase kre2p/mtt1.p:2 ternary complex with gdp/mn and methyl-alpha-mannoside acceptor
16	<a href="#">d1g8fa2</a>	Alignment		17.9	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
17	<a href="#">d2prra1</a>	Alignment		17.6	7	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> Atu0492-like
18	<a href="#">c2gx8B</a>	Alignment		17.2	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> nif3-related protein; <b>PDBTitle:</b> the crystal structure of bacillus cereus protein related to nif3
19	<a href="#">c5ve9C</a>	Alignment		16.9	50	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> microtubule-actin cross-linking factor 1, isoforms 1/2/3/5; <b>PDBTitle:</b> structure of hacf7 ef1-ef2-gar domains
20	<a href="#">d1ht6a1</a>	Alignment		16.8	17	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
21	<a href="#">d2gx8a1</a>	Alignment	not modelled	15.7	22	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
22	<a href="#">d1v5ra1</a>	Alignment	not modelled	15.3	38	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GAS2 domain-like <b>Family:</b> GAS2 domain
23	<a href="#">c3arcl</a>	Alignment	not modelled	15.1	33	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
24	<a href="#">c4ub6L</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
25	<a href="#">c4tnhl</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
26	<a href="#">c3a0bl</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure of br-substituted photosystem ii complex
27	<a href="#">c4il6L</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> structure of sr-substituted photosystem ii
28	<a href="#">c5e7cl</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> macromolecular diffractive imaging using imperfect crystals - bragg2 data
						<b>PDB header:</b> electron transport,photosynthesis

29	<a href="#">c4tnkL</a>	Alignment	not modelled	14.6	33	<b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt xfel structure of photosystem ii 250 microsec after the third illumination at 5.2 a resolution
30	<a href="#">c4rvyl</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> serial time resolved crystallography of photosystem ii using a 2 femtosecond x-ray laser. the s state after two flashes (s3)
31	<a href="#">c4ixrl</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt fs x-ray diffraction of photosystem ii, first illuminated state
32	<a href="#">c4fbyL</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> fs x-ray diffraction of photosystem ii
33	<a href="#">c4tnil</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt xfel structure of photosystem ii 500 ms after the third illumination at 4.6 a resolution
34	<a href="#">c4ixql</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt fs x-ray diffraction of photosystem ii, dark state
35	<a href="#">c3wu2L</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure analysis of photosystem ii complex
36	<a href="#">c4ub8L</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
37	<a href="#">c4tnjL</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
38	<a href="#">c3arcL</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
39	<a href="#">c4ub6L</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
40	<a href="#">c4tniL</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt xfel structure of photosystem ii 500 ms after the third illumination at 4.6 a resolution
41	<a href="#">c4ixrL</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt fs x-ray diffraction of photosystem ii, first illuminated state
42	<a href="#">c4il6L</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> structure of sr-substituted photosystem ii
43	<a href="#">c3kziL</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure of monomeric form of cyanobacterial photosystem ii
44	<a href="#">c4ixqL</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt fs x-ray diffraction of photosystem ii, dark state
45	<a href="#">c3prrl</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii in complex with 2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
46	<a href="#">c4tnkL</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt xfel structure of photosystem ii 250 microsec after the third illumination at 5.2 a resolution
47	<a href="#">c5e7cL</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> macromolecular diffractive imaging using imperfect crystals - bragg2 data
48	<a href="#">c4ub8L</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
49	<a href="#">c3a0hl</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
50	<a href="#">c2axtL</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center I protein; <b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus
51	<a href="#">c1s5ll</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center I protein; <b>PDBTitle:</b> architecture of the photosynthetic oxygen evolving center
52	<a href="#">c2axtL</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center I protein; <b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus
53	<a href="#">c4fbyd</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> photosystem ii d2 protein; <b>PDBTitle:</b> fs x-ray diffraction of photosystem ii
54	<a href="#">c3wu2L</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure analysis of photosystem ii complex
						<b>PDB header:</b> electron transport

55	<a href="#">c3bz1L_</a>	Alignment	not modelled	14.6	33	<b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii (part 1 of 2). this2 file contains first monomer of psii dimer
56	<a href="#">d2axtl1</a>	Alignment	not modelled	14.6	33	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein L, PsbL <b>Family:</b> PsbL-like
57	<a href="#">c1s5L_</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center I protein; <b>PDBTitle:</b> architecture of the photosynthetic oxygen evolving center
58	<a href="#">c3prqL_</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
59	<a href="#">c3bz2L_</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii (part 2 of 2). this2 file contains second monomer of psii dimer
60	<a href="#">c4rvyL_</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> serial time resolved crystallography of photosystem ii using a2 femtosecond x-ray laser. the s state after two flashes (s3)
61	<a href="#">c3a0hL_</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
62	<a href="#">c4tnjL_</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
63	<a href="#">c4tnhL_</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
64	<a href="#">c3a0bL_</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> crystal structure of br-substituted photosystem ii complex
65	<a href="#">c4pj0L_</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> oxidoreductase, electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
66	<a href="#">c4pj0L_</a>	Alignment	not modelled	14.6	33	<b>PDB header:</b> oxidoreductase, electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii reaction center protein I; <b>PDBTitle:</b> structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
67	<a href="#">c6nd1A_</a>	Alignment	not modelled	14.3	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein translocation protein sec63; <b>PDBTitle:</b> cryoem structure of the sec complex from yeast
68	<a href="#">d1su3a1</a>	Alignment	not modelled	14.1	50	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> MMP N-terminal domain
69	<a href="#">c3cr8C_</a>	Alignment	not modelled	14.0	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfate adenylyltransferase, adenylylsulfate kinase; <b>PDBTitle:</b> hexameric aps kinase from thiobacillus denitrificans
70	<a href="#">d1pama3</a>	Alignment	not modelled	13.9	47	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
71	<a href="#">d1slma1</a>	Alignment	not modelled	13.9	50	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> MMP N-terminal domain
72	<a href="#">c6hkeB_</a>	Alignment	not modelled	13.7	18	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> possible tctc subunit of the tripartite tricarboxylate <b>PDBTitle:</b> matc (rpa3494) from rhodopseudomonas palustris with bound malate
73	<a href="#">d1t5la1</a>	Alignment	not modelled	13.6	25	<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
74	<a href="#">c3jcul_</a>	Alignment	not modelled	13.6	46	<b>PDB header:</b> membrane protein <b>Chain:</b> L: <b>PDB Molecule:</b> protein photosystem ii reaction center protein I; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
75	<a href="#">d1m55a_</a>	Alignment	not modelled	13.4	15	<b>Fold:</b> Origin of replication-binding domain, RBD-like <b>Superfamily:</b> Origin of replication-binding domain, RBD-like <b>Family:</b> Replication protein Rep, nuclease domain
76	<a href="#">d1m8pa2</a>	Alignment	not modelled	13.3	27	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
77	<a href="#">c2nydB_</a>	Alignment	not modelled	13.2	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0135 protein sa1388; <b>PDBTitle:</b> crystal structure of staphylococcus aureus hypothetical protein sa1388
78	<a href="#">c3n3fB_</a>	Alignment	not modelled	13.1	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-1(xv) chain; <b>PDBTitle:</b> crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens
79	<a href="#">d1x6va2</a>	Alignment	not modelled	13.1	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
80	<a href="#">c1r6xA_</a>	Alignment	not modelled	12.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp:sulfate adenylyltransferase; <b>PDBTitle:</b> the crystal structure of a truncated form of yeast atp2 sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate

81	<a href="#">d1ku1a_</a>	Alignment	not modelled	12.7	12	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Sec7 domain <b>Family:</b> Sec7 domain
82	<a href="#">c3i71B_</a>	Alignment	not modelled	12.6	27	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ethanolamine utilization protein eutk; <b>PDBTitle:</b> ethanolamine utilization microcompartment shell subunit, eutk c-2 terminal domain
83	<a href="#">c2ka6B_</a>	Alignment	not modelled	12.6	35	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> nmr structure of the cbp-taz2/stat1-tad complex
84	<a href="#">c5a6eB_</a>	Alignment	not modelled	12.6	25	<b>PDB header:</b> transport <b>Chain:</b> B: <b>PDB Molecule:</b> pore domain of potassium channel subfamily t member 1; <b>PDBTitle:</b> cryo-em structure of the slo2.2 na-activated k channel
85	<a href="#">c1oftC_</a>	Alignment	not modelled	12.4	14	<b>PDB header:</b> bacterial cell division inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein pa3008; <b>PDBTitle:</b> crystal structure of sula from pseudomonas aeruginosa
86	<a href="#">d1eaka1</a>	Alignment	not modelled	12.3	50	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> MMP N-terminal domain
87	<a href="#">d1l6ja1</a>	Alignment	not modelled	12.2	50	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> MMP N-terminal domain
88	<a href="#">c1m8pB_</a>	Alignment	not modelled	12.2	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate adenylyltransferase; <b>PDBTitle:</b> crystal structure of p. chrysogenum atp sulfurylase in the t-state
89	<a href="#">d1s0pa_</a>	Alignment	not modelled	12.0	29	<b>Fold:</b> N-terminal domain of adenylylcyclase associated protein, CAP <b>Superfamily:</b> N-terminal domain of adenylylcyclase associated protein, CAP <b>Family:</b> N-terminal domain of adenylylcyclase associated protein, CAP
90	<a href="#">c6f5dl_</a>	Alignment	not modelled	11.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> atp synthase subunit epsilon, mitochondrial; <b>PDBTitle:</b> trypanosoma brucei f1-atpase
91	<a href="#">d1ofux_</a>	Alignment	not modelled	11.9	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Bacterial cell division inhibitor SulA
92	<a href="#">c5ibwC_</a>	Alignment	not modelled	11.7	13	<b>PDB header:</b> motor protein <b>Chain:</b> C: <b>PDB Molecule:</b> myosin ic heavy chain; <b>PDBTitle:</b> complex of mlcc bound to the tandem iq motif of myoc
93	<a href="#">d3bmva3</a>	Alignment	not modelled	11.6	47	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
94	<a href="#">c2d6fD_</a>	Alignment	not modelled	11.5	22	<b>PDB header:</b> ligase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit e; <b>PDBTitle:</b> crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
95	<a href="#">d1kona_</a>	Alignment	not modelled	11.5	60	<b>Fold:</b> YebC-like <b>Superfamily:</b> YebC-like <b>Family:</b> YebC-like
96	<a href="#">c3kwpA_</a>	Alignment	not modelled	11.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from lactobacillus2 brevis
97	<a href="#">c1bm4A_</a>	Alignment	not modelled	11.4	20	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (moloney murine leukemia virus capsid); <b>PDBTitle:</b> momlv capsid protein major homology region peptide analog
98	<a href="#">c5a08A_</a>	Alignment	not modelled	11.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable mannosyltransferase ktr4; <b>PDBTitle:</b> x-ray structure of the mannosyltransferase ktr4p from s. cerevisiae
99	<a href="#">d1ewna_</a>	Alignment	not modelled	11.4	16	<b>Fold:</b> FMT C-terminal domain-like <b>Superfamily:</b> FMT C-terminal domain-like <b>Family:</b> 3-methyladenine DNA glycosylase (AAG, ANPG, MPG)