
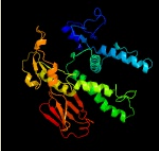






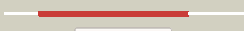








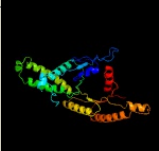





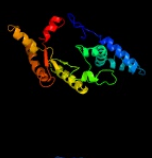



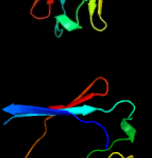


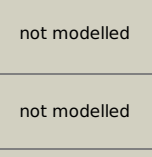


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2184c (-) _2445815_2446954
Date	Mon Aug 5 13:25:31 BST 2019
Unique Job ID	c4a8ebb57cc71b7a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3igfB_</a>	 Alignment		100.0	25	<b>PDB header:</b> atp binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> all4481 protein; <b>PDBTitle:</b> crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
2	<a href="#">c5zmfA_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> atpase arsa1; <b>PDBTitle:</b> amppnp complex of c. reinhardtii arsa1
3	<a href="#">c1ii0A_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> arsenical pump-driving atpase; <b>PDBTitle:</b> crystal structure of the escherichia coli arsenite-translocating2 atpase
4	<a href="#">c6bs5B_</a>	 Alignment		100.0	23	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> anion transporter; <b>PDBTitle:</b> crystal structure of amp-pnp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
5	<a href="#">c3ug7D_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> arsenical pump-driving atpase; <b>PDBTitle:</b> crystal structure of get3 from methanocaldococcus jannaschii
6	<a href="#">c3zq6D_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> putative arsenical pump-driving atpase; <b>PDBTitle:</b> adp-alf4 complex of m. therm. trc40
7	<a href="#">c2wo0C_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> atpase get3; <b>PDBTitle:</b> nucleotide-free form of s. pombe get3
8	<a href="#">c6bs3A_</a>	 Alignment		100.0	18	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative atpase rv3679; <b>PDBTitle:</b> crystal structure of adp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
9	<a href="#">c3ibgF_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> atpase, subunit of the get complex; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus get3 with bound2 adp
10	<a href="#">c2wojD_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> atpase get3; <b>PDBTitle:</b> adp-alf4 complex of s. cerevisiae get3
11	<a href="#">c5bwkA_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase/transport <b>Chain:</b> A; <b>PDB Molecule:</b> atpase get3; <b>PDBTitle:</b> 6.0 a crystal structure of a get3-get4-get5 intermediate complex from2 s.cerevisiae

12	<a href="#">d1ihua1</a>	Alignment		100.0	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
13	<a href="#">d1ihua2</a>	Alignment		99.8	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
14	<a href="#">c3io3A</a>	Alignment		99.8	29	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> deha2d07832p; <b>PDBTitle:</b> get3 with adp from d. hansenii in closed form
15	<a href="#">c3kjbB</a>	Alignment		98.3	20	<b>PDB header:</b> hydrolase, metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> co dehydrogenase/acetyl-coa synthase complex, accessory <b>PDBTitle:</b> adp-bound state of cooc1
16	<a href="#">c4rzka</a>	Alignment		98.3	10	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> small heat shock protein hsp20 family; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus hsp20.1 acd
17	<a href="#">c5mb8L</a>	Alignment		98.2	16	<b>PDB header:</b> chaperone <b>Chain:</b> L: <b>PDB Molecule:</b> 25.3 kda heat shock protein, chloroplastic; <b>PDBTitle:</b> hsp21 dodecamer, structural model based on cryo-em and homology2 modelling
18	<a href="#">c4zjdf</a>	Alignment		98.2	19	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> aggregation suppressing protein; <b>PDBTitle:</b> small heat shock protein agsa from salmonella typhimurium: truncations2 at n- and c- termini
19	<a href="#">c3w1zA</a>	Alignment		98.2	12	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 16; <b>PDBTitle:</b> heat shock protein 16.0 from schizosaccharomyces pombe
20	<a href="#">c3glaA</a>	Alignment		98.2	22	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight heat shock protein; <b>PDBTitle:</b> crystal structure of the hspa from xanthomonas axonopodis
21	<a href="#">c3w1zD</a>	Alignment	not modelled	98.2	14	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> heat shock protein 16; <b>PDBTitle:</b> heat shock protein 16.0 from schizosaccharomyces pombe
22	<a href="#">d1shsa</a>	Alignment	not modelled	98.1	17	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> HSP20
23	<a href="#">c1shsD</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> heat shock protein <b>Chain:</b> D: <b>PDB Molecule:</b> small heat shock protein; <b>PDBTitle:</b> small heat shock protein from methanococcus jannaschii
24	<a href="#">c5mb8J</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> chaperone <b>Chain:</b> J: <b>PDB Molecule:</b> 25.3 kda heat shock protein, chloroplastic; <b>PDBTitle:</b> hsp21 dodecamer, structural model based on cryo-em and homology2 modelling
25	<a href="#">c4feiA</a>	Alignment	not modelled	98.1	34	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein-related protein; <b>PDBTitle:</b> hsp17.7 from deinococcus radiodurans
26	<a href="#">d1gmea</a>	Alignment	not modelled	98.1	20	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> HSP20
27	<a href="#">d2h50a1</a>	Alignment	not modelled	98.0	28	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> HSP20
28	<a href="#">c4pbdA</a>	Alignment	not modelled	98.0	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein shq1 homolog; <b>PDBTitle:</b> crystal structure of the n-terminal cs domain of human shq1
29	<a href="#">c5dc1B</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> 17.1 kda class ii heat shock protein;

29	<a href="#">c0u5tB</a>	Alignment	not modelled	97.9	20	<b>PDBTitle:</b> core domain of the class ii small heat-shock protein hsp 17.7 from2 pisum sativum <b>PDB header:</b> chaperone
30	<a href="#">c2ygdV</a>	Alignment	not modelled	97.9	19	<b>Chain:</b> V: <b>PDB Molecule:</b> <b>PDBTitle:</b> molecular architectures of the 24meric eye lens chaperone alphab-2 crystallin elucidated by a triple hybrid approach
31	<a href="#">c3aabA</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein st1653; <b>PDBTitle:</b> small heat shock protein hsp14.0 with the mutations of i120f and i122f2 in the form i crystal
32	<a href="#">d1gmeb</a>	Alignment	not modelled	97.9	23	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> HSP20
33	<a href="#">c2wj5A</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein beta-6; <b>PDBTitle:</b> rat alpha crystallin domain
34	<a href="#">c5ltwK</a>	Alignment	not modelled	97.8	21	<b>PDB header:</b> protein binding <b>Chain:</b> K: <b>PDB Molecule:</b> heat shock protein beta-6; <b>PDBTitle:</b> complex of human 14-3-3 sigma clu1 mutant with phosphorylated heat2 shock protein b6
35	<a href="#">c2bolA</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> heat shock protein <b>Chain:</b> A: <b>PDB Molecule:</b> small heat shock protein; <b>PDBTitle:</b> crystal structure and assembly of tsp36, a metazoan small heat shock2 protein
36	<a href="#">c2n3jA</a>	Alignment	not modelled	97.8	23	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein beta-1; <b>PDBTitle:</b> solution structure of the alpha-crystallin domain from the redox-2 sensitive chaperone, hspb1
37	<a href="#">c4ydzA</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> stress-induced protein 1; <b>PDBTitle:</b> stress-induced protein 1 from caenorhabditis elegans
38	<a href="#">c3l1eA</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-crystallin a chain; <b>PDBTitle:</b> bovine alphaa crystallin zinc bound
39	<a href="#">c4ylcF</a>	Alignment	not modelled	97.6	12	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> heat shock protein hsp20; <b>PDBTitle:</b> crystal structure of del-c4 mutant of hsp14.1 from sulfobolbus2 solfatataricus p2
40	<a href="#">c3q9qB</a>	Alignment	not modelled	97.6	27	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock protein beta-1; <b>PDBTitle:</b> hspb1 fragment second crystal form
41	<a href="#">c6ewnA</a>	Alignment	not modelled	97.6	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hspa; <b>PDBTitle:</b> hspa from thermosynechococcus vulcanus in the presence of 2m urea with2 initial stages of denaturation
42	<a href="#">c6f2rK</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> chaperone <b>Chain:</b> K: <b>PDB Molecule:</b> hspb2,heat shock protein beta-2,heat shock protein beta-2, <b>PDBTitle:</b> a hetrotetramer of human hspb2 and hspb3
43	<a href="#">c3la6P</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> transferase <b>Chain:</b> P: <b>PDB Molecule:</b> tyrosine-protein kinase wzc; <b>PDBTitle:</b> octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
44	<a href="#">c6dv5T</a>	Alignment	not modelled	97.5	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
45	<a href="#">c2wj7D</a>	Alignment	not modelled	97.4	23	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-crystallin b chain; <b>PDBTitle:</b> human alphab crystallin
46	<a href="#">c2klrA</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-crystallin b chain; <b>PDBTitle:</b> solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers
47	<a href="#">c3cioA</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> signaling protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase etk; <b>PDBTitle:</b> the kinase domain of escherichia coli tyrosine kinase etk
48	<a href="#">c6f2rI</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> chaperone <b>Chain:</b> I: <b>PDB Molecule:</b> hspb2,heat shock protein beta-2,heat shock protein beta-2, <b>PDBTitle:</b> a hetrotetramer of human hspb2 and hspb3
49	<a href="#">c6f2rE</a>	Alignment	not modelled	97.3	21	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> hspb2,heat shock protein beta-2,heat shock protein beta-2, <b>PDBTitle:</b> a hetrotetramer of human hspb2 and hspb3
50	<a href="#">c6f2rT</a>	Alignment	not modelled	97.3	26	<b>PDB header:</b> chaperone <b>Chain:</b> T: <b>PDB Molecule:</b> heat shock protein beta-3,heat shock protein beta-3,heat shock protein beta-3, <b>PDBTitle:</b> a hetrotetramer of human hspb2 and hspb3
51	<a href="#">c6nonB</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> coobyric acid ac-diamide synthase; <b>PDBTitle:</b> structure of cyanthece apo mcda
52	<a href="#">c6g2gA</a>	Alignment	not modelled	97.2	25	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytosolic fe-s cluster assembly factor cfd1; <b>PDBTitle:</b> fe-s assembly cfd1
53	<a href="#">c2qmoA</a>	Alignment	not modelled	97.2	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
54	<a href="#">c6iucC</a>	Alignment	not modelled	97.1	17	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> spooj regulator (soj); <b>PDBTitle:</b> structure of helicobacter pylori soj-atp complex bound to dna
55	<a href="#">c6f2rA</a>	Alignment	not modelled	97.0	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hspb2,heat shock protein beta-2,heat shock protein beta-2, <b>PDBTitle:</b> a hetrotetramer of human hspb2 and hspb3

56	<a href="#">c4pfsA</a>	Alignment	not modelled	96.9	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> cobyrinic acid a,c-diamide synthase; <b>PDBTitle:</b> crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
57	<a href="#">c6gxzD</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> pih1 domain-containing protein 1; <b>PDBTitle:</b> crystal structure of the human rpap3(tp2)-pih1d1(cs) complex
58	<a href="#">c5zulB</a>	Alignment	not modelled	96.7	22	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> small heat shock protein; <b>PDBTitle:</b> small heat shock protein from mycobacterium marinum m : form-3
59	<a href="#">c3fmfA</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
60	<a href="#">c5lj1A</a>	Alignment	not modelled	96.7	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> structure of flen-ampnp complex
61	<a href="#">c2vedA</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> membrane protein capa1, protein tyrosine kinase; <b>PDBTitle:</b> crystal structure of the chimerical mutant capabk55m2 protein
62	<a href="#">c2ph1A</a>	Alignment	not modelled	96.6	17	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotide-binding protein; <b>PDBTitle:</b> crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
63	<a href="#">c2ozeA</a>	Alignment	not modelled	96.6	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> orf delta'; <b>PDBTitle:</b> the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
64	<a href="#">c3pg5A</a>	Alignment	not modelled	96.5	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein dip2308 from corynebacterium diphtheriae,2 northeast structural genomics consortium target cdr78
65	<a href="#">c3endA</a>	Alignment	not modelled	96.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase <b>PDBTitle:</b> crystal structure of the I protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
66	<a href="#">c3fkqA</a>	Alignment	not modelled	96.4	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ntrc-like two-domain protein; <b>PDBTitle:</b> crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
67	<a href="#">c3k9gA</a>	Alignment	not modelled	96.4	25	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> pf-32 protein; <b>PDBTitle:</b> crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
68	<a href="#">d1g3qa</a>	Alignment	not modelled	96.3	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
69	<a href="#">c3vx3A</a>	Alignment	not modelled	96.3	25	<b>PDB header:</b> adp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> atpase involved in chromosome partitioning, para/mind <b>PDBTitle:</b> crystal structure of [nife] hydrogenase maturation protein hypb from2 thermococcus kodakarensis kod1
70	<a href="#">c3ez6B</a>	Alignment	not modelled	96.2	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> plasmid partition protein a; <b>PDBTitle:</b> structure of para-adp complex:tetragonal form
71	<a href="#">d1iona</a>	Alignment	not modelled	96.2	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
72	<a href="#">c4v02B</a>	Alignment	not modelled	96.0	22	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> minc:mind cell division protein complex, aquifex aeolicus
73	<a href="#">d2afhe1</a>	Alignment	not modelled	95.9	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
74	<a href="#">c3ea0B</a>	Alignment	not modelled	95.7	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atpase, para family; <b>PDBTitle:</b> crystal structure of para family atpase from chlorobium tepidum t1s
75	<a href="#">c4rz3B</a>	Alignment	not modelled	95.6	26	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> crystal structure of the mind-like atpase filhg
76	<a href="#">c4ru8C</a>	Alignment	not modelled	95.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of pnob8 para with ampnp
77	<a href="#">c3q9lB</a>	Alignment	not modelled	94.9	39	<b>PDB header:</b> cell cycle, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> septum site-determining protein mind; <b>PDBTitle:</b> the structure of the dimeric e.coli mind-atp complex
78	<a href="#">d1byia</a>	Alignment	not modelled	94.8	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
79	<a href="#">c3of5A</a>	Alignment	not modelled	94.7	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
80	<a href="#">d1cp2a</a>	Alignment	not modelled	94.6	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like

81	<a href="#">c3ezfA</a>	Alignment	not modelled	93.0	38	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> para; <b>PDBTitle:</b> partition protein
82	<a href="#">c2bekB</a>	Alignment	not modelled	93.0	22	<b>PDB header:</b> chromosome segregation <b>Chain:</b> B: <b>PDB Molecule:</b> segregation protein; <b>PDBTitle:</b> structure of the bacterial chromosome segregation protein soj
83	<a href="#">c3cwqB</a>	Alignment	not modelled	92.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> para family chromosome partitioning protein; <b>PDBTitle:</b> crystal structure of chromosome partitioning protein (para) in complex2 with adp from synechocystis sp. northeast structural genomics3 consortium target sgr89
84	<a href="#">c1hyqA</a>	Alignment	not modelled	92.6	18	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division inhibitor (mind-1); <b>PDBTitle:</b> mind bacterial cell division regulator from a. fulgidus
85	<a href="#">d1hyqa</a>	Alignment	not modelled	92.6	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
86	<a href="#">c4dzzB</a>	Alignment	not modelled	91.4	13	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> plasmid partitioning protein parf; <b>PDBTitle:</b> structure of parf-adp, crystal form 1
87	<a href="#">c2og2A</a>	Alignment	not modelled	86.0	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal recognition particle receptor; <b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2 thaliana
88	<a href="#">c5l3qB</a>	Alignment	not modelled	85.5	22	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor subunit alpha; <b>PDBTitle:</b> structure of the gtpase heterodimer of human srp54 and sralpha
89	<a href="#">c3b9qA</a>	Alignment	not modelled	85.0	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloroplast srp receptor homolog, alpha subunit <b>PDBTitle:</b> the crystal structure of cpftsyt from arabidopsis thaliana
90	<a href="#">c4a0rB</a>	Alignment	not modelled	80.1	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate <b>PDBTitle:</b> structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana bound to dethiobiotin (dtb).
91	<a href="#">c4a0gC</a>	Alignment	not modelled	77.6	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate <b>PDBTitle:</b> structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana in its apo form.
92	<a href="#">c2cnwF</a>	Alignment	not modelled	76.7	23	<b>PDB header:</b> signal recognition <b>Chain:</b> F: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> gdpalf4 complex of the srp gtpases ffh and ftsy
93	<a href="#">c2qy9A</a>	Alignment	not modelled	75.5	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy
94	<a href="#">c2yhsA</a>	Alignment	not modelled	72.4	24	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the e. coli srp receptor ftsy
95	<a href="#">c2xj9B</a>	Alignment	not modelled	70.7	29	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> mipz; <b>PDBTitle:</b> dimer structure of the bacterial cell division regulator mipz
96	<a href="#">c2iy3A</a>	Alignment	not modelled	70.2	24	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein,signal recognition <b>PDBTitle:</b> structure of the e. coli signal recognition particle
97	<a href="#">c1qzwC</a>	Alignment	not modelled	70.1	15	<b>PDB header:</b> signaling protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
98	<a href="#">c5l3rC</a>	Alignment	not modelled	68.3	10	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle 54 kda protein, chloroplastic; <b>PDBTitle:</b> structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
99	<a href="#">c2j7pA</a>	Alignment	not modelled	64.4	30	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
100	<a href="#">c2q9cA</a>	Alignment	not modelled	63.4	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of ftsy:gmppnp with mgcl complex
101	<a href="#">c3dm5A</a>	Alignment	not modelled	61.8	21	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
102	<a href="#">c5l3sF</a>	Alignment	not modelled	60.5	16	<b>PDB header:</b> protein transport <b>Chain:</b> F: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
103	<a href="#">c2j37W</a>	Alignment	not modelled	58.3	21	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein (srp54); <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
104	<a href="#">c1zu4A</a>	Alignment	not modelled	56.6	15	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsyt; <b>PDBTitle:</b> crystal structure of ftsy from mycoplasma mycoides-space2 group p21212

105	<a href="#">c5gafi_</a>	Alignment	not modelled	52.0	17	<b>PDB header:</b> ribosome <b>Chain:</b> I; <b>PDB Molecule:</b> 50s ribosomal protein l10; <b>PDBTitle:</b> rnc in complex with srp
106	<a href="#">d1g5ta_</a>	Alignment	not modelled	49.9	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
107	<a href="#">d1g64b_</a>	Alignment	not modelled	49.5	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
108	<a href="#">c2j289_</a>	Alignment	not modelled	47.7	14	<b>PDB header:</b> ribosome <b>Chain:</b> 9; <b>PDB Molecule:</b> signal recognition particle 54; <b>PDBTitle:</b> model of e. coli srp bound to 70s rncs
109	<a href="#">c1vmaA_</a>	Alignment	not modelled	47.5	24	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
110	<a href="#">d1rl1a_</a>	Alignment	not modelled	45.8	10	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> GS domain
111	<a href="#">c3dmdA_</a>	Alignment	not modelled	41.7	25	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> signal recognition particle receptor; <b>PDBTitle:</b> structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
112	<a href="#">c3c0kB_</a>	Alignment	not modelled	34.2	17	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> upf0064 protein yccw; <b>PDBTitle:</b> crystal structure of a ribosomal rna methyltransferase
113	<a href="#">c1wb1C_</a>	Alignment	not modelled	32.4	12	<b>PDB header:</b> protein synthesis <b>Chain:</b> C; <b>PDB Molecule:</b> translation elongation factor selb; <b>PDBTitle:</b> crystal structure of translation elongation factor selb2 from methanococcus maripaludis in complex with gdp
114	<a href="#">c6cy1B_</a>	Alignment	not modelled	31.7	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
115	<a href="#">c2jkiS_</a>	Alignment	not modelled	31.2	8	<b>PDB header:</b> chaperone <b>Chain:</b> S; <b>PDB Molecule:</b> sgt1-like protein; <b>PDBTitle:</b> complex of hsp90 n-terminal and sgt1 cs domain
116	<a href="#">d1j8yf2</a>	Alignment	not modelled	28.7	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
117	<a href="#">c2as0A_</a>	Alignment	not modelled	28.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein ph1915; <b>PDBTitle:</b> crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase
118	<a href="#">c2cmgA_</a>	Alignment	not modelled	26.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> crystal structure of spermidine synthase from helicobacter2 pylori
119	<a href="#">d1lhpa_</a>	Alignment	not modelled	25.5	21	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> PfkB-like kinase
120	<a href="#">d1ju2a1</a>	Alignment	not modelled	25.4	16	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain