

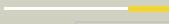
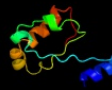











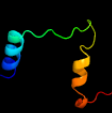

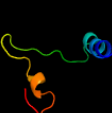



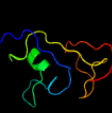
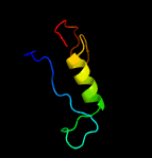
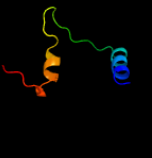
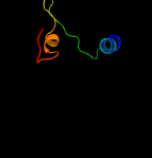
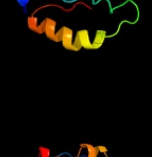
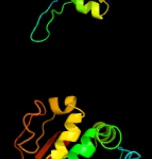
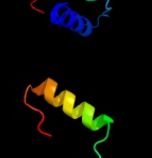
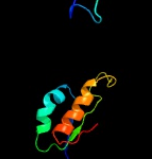

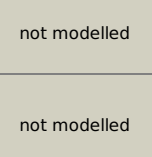


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2734 (- )_3046831_3047685
Date	Wed Aug 7 12:50:39 BST 2019
Unique Job ID	ea2397f7b55e5698

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4fheA_</a>	 Alignment		98.1	15	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> spore photoproduct lyase; <b>PDBTitle:</b> spore photoproduct lyase c140a mutant
2	<a href="#">c2ad5B_</a>	 Alignment		70.8	13	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
3	<a href="#">c2ywdA_</a>	 Alignment		69.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> crystal structure of glutamine amidotransferase
4	<a href="#">d2a9va1</a>	 Alignment		64.7	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
5	<a href="#">d1izca_</a>	 Alignment		57.5	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> HpcH/Hpal aldolase
6	<a href="#">c1izcA_</a>	 Alignment		57.5	18	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> macrophomate synthase intermolecular diels-alderase; <b>PDBTitle:</b> crystal structure analysis of macrophomate synthase
7	<a href="#">c5h7dl_</a>	 Alignment		47.5	23	<b>PDB header:</b> transferase, immune system/metal binding <b>Chain:</b> I; <b>PDB Molecule:</b> putrescine aminotransferase,immunoglobulin g-binding <b>PDBTitle:</b> crystal structure of the ygjg-protein a-zpa963-calmodulin complex
8	<a href="#">d1qkia2</a>	 Alignment		47.2	10	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Glucose 6-phosphate dehydrogenase-like
9	<a href="#">c1h9aA_</a>	 Alignment		41.3	28	<b>PDB header:</b> oxidoreductase (choh(d) - nad(p)) <b>Chain:</b> A; <b>PDB Molecule:</b> glucose 6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from I. mesenteroides with coenzyme nadp
10	<a href="#">c2zuuA_</a>	 Alignment		40.8	32	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> lacto-n-biose phosphorylase; <b>PDBTitle:</b> crystal structure of galacto-n-biose/lacto-n-biose i phosphorylase in2 complex with glcnac
11	<a href="#">c3imkA_</a>	 Alignment		40.4	29	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative molybdenum carrier protein; <b>PDBTitle:</b> crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution

12	<a href="#">d1gk8a1</a>	Alignment		40.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
13	<a href="#">c2bhbB</a>	Alignment		39.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> x-ray structure of human glucose-6-phosphate dehydrogenase (deletion2 variant) complexed with glucose-6-phosphate
14	<a href="#">d1h9aa2</a>	Alignment		38.6	26	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Glucose 6-phosphate dehydrogenase-like
15	<a href="#">c3n5mD</a>	Alignment		38.3	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate aminotransferase; <b>PDBTitle:</b> crystals structure of a bacillus anthracis aminotransferase
16	<a href="#">d1gsoa2</a>	Alignment		38.0	39	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
17	<a href="#">c3fseB</a>	Alignment		37.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> two-domain protein containing dj-1/thij/pfpi-like and <b>PDBTitle:</b> crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
18	<a href="#">c5ddwD</a>	Alignment		34.9	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> crmg; <b>PDBTitle:</b> crystal structure of aminotransferase crmg from actinoalloteichus sp.2 wh1-2216-6 in complex with the pmp external aldimine adduct with3 caerulomycin m
19	<a href="#">c2vwtA</a>	Alignment		34.3	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> yfau, 2-keto-3-deoxy sugar aldolase; <b>PDBTitle:</b> crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
20	<a href="#">c3qz6A</a>	Alignment		34.3	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hpch/hpai aldolase; <b>PDBTitle:</b> the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
21	<a href="#">c4e9iB</a>	Alignment	not modelled	33.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> glucose-6-p dehydrogenase (apo form) from trypanosoma cruzi
22	<a href="#">c3r5wO</a>	Alignment	not modelled	32.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> deazaflavin-dependent nitroreductase; <b>PDBTitle:</b> structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420
23	<a href="#">c2yqeA</a>	Alignment	not modelled	31.9	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> jumonjii/arid domain-containing protein 1d; <b>PDBTitle:</b> solution structure of the arid domain of jarid1d protein
24	<a href="#">d1to3a</a>	Alignment	not modelled	30.9	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
25	<a href="#">d1dxea</a>	Alignment	not modelled	30.7	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> HpCH/Hpal aldolase
26	<a href="#">c1qkiE</a>	Alignment	not modelled	28.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> x-ray structure of human glucose 6-phosphate dehydrogenase (variant2 canton r459l) complexed with structural nadp+
27	<a href="#">c3pdiB</a>	Alignment	not modelled	27.4	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nifn; <b>PDBTitle:</b> precursor bound nifen
28	<a href="#">c5u03C</a>	Alignment	not modelled	27.2	16	<b>PDB header:</b> ligase, protein fibril <b>Chain:</b> C: <b>PDB Molecule:</b> ctp synthase 1; <b>PDBTitle:</b> cryo-em structure of the human ctp synthase filament

29	<a href="#">c3r5zB_</a>	Alignment	not modelled	27.0	23	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
30	<a href="#">c2issF_</a>	Alignment	not modelled	26.7	18	<b>PDB header:</b> lyase, transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> structure of the plp synthase holoenzyme from thermotoga maritima
31	<a href="#">c5n6yE_</a>	Alignment	not modelled	26.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nitrogenase vanadium-iron protein beta chain; <b>PDBTitle:</b> azotobacter vinelandii vanadium nitrogenase
32	<a href="#">c4tv6A_</a>	Alignment	not modelled	26.3	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyglucarate aldolase; <b>PDBTitle:</b> crystal structure of citrate synthase variant sbng e151q
33	<a href="#">c4e77A_</a>	Alignment	not modelled	24.7	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-1-semialdehyde 2,1-aminomutase; <b>PDBTitle:</b> 2.0a crystal structure of a glutamate-1-semialdehyde aminotransferase2 from yersinia pestis co92
34	<a href="#">c3h96B_</a>	Alignment	not modelled	24.0	14	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> f420-h2 dependent reductase a; <b>PDBTitle:</b> msmeg_3358 f420 reductase
35	<a href="#">c3cneD_</a>	Alignment	not modelled	23.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative protease i; <b>PDBTitle:</b> crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
36	<a href="#">c4a0rB_</a>	Alignment	not modelled	23.2	23	<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).
37	<a href="#">c2zw3B_</a>	Alignment	not modelled	22.5	50	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> gap junction beta-2 protein; <b>PDBTitle:</b> structure of the connexin-26 gap junction channel at 3.52 angstrom resolution
38	<a href="#">c3bs8A_</a>	Alignment	not modelled	21.8	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-1-semialdehyde 2,1-aminomutase; <b>PDBTitle:</b> crystal structure of glutamate 1-semialdehyde aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
39	<a href="#">d1qh8a_</a>	Alignment	not modelled	21.3	13	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
40	<a href="#">c2ywjA_</a>	Alignment	not modelled	20.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
41	<a href="#">d1iloa_</a>	Alignment	not modelled	20.4	27	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
42	<a href="#">c6mhqE_</a>	Alignment	not modelled	20.2	50	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> gap junction alpha-3 protein, connexin-46; <b>PDBTitle:</b> structure of connexin-46 intercellular gap junction channel at 3.42 angstrom resolution by cryoem
43	<a href="#">c3on1A_</a>	Alignment	not modelled	19.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2414 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from bacillus2 halodurans c
44	<a href="#">c5v1tA_</a>	Alignment	not modelled	19.5	29	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> radical sam; <b>PDBTitle:</b> crystal structure of streptococcus suis suib bound to precursor2 peptide sua
45	<a href="#">d1jqna_</a>	Alignment	not modelled	19.4	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate carboxylase
46	<a href="#">c4zdiE_</a>	Alignment	not modelled	19.3	16	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
47	<a href="#">d1b8ta4</a>	Alignment	not modelled	19.3	32	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
48	<a href="#">d1wv2a_</a>	Alignment	not modelled	19.2	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
49	<a href="#">c4y9iA_</a>	Alignment	not modelled	19.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mycobacterium tuberculosis paralogous family 11; <b>PDBTitle:</b> structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
50	<a href="#">c3jrkG_</a>	Alignment	not modelled	18.2	32	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> tagatose 1,6-diphosphate aldolase 2; <b>PDBTitle:</b> a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
51	<a href="#">d2nv0a1</a>	Alignment	not modelled	18.2	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
52	<a href="#">d1m1na_</a>	Alignment	not modelled	18.1	15	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
53	<a href="#">c2lbwA_</a>	Alignment	not modelled	17.8	32	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> h/aca ribonucleoprotein complex subunit 2; <b>PDBTitle:</b> solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant

54	<a href="#">c1hyuA</a>	Alignment	not modelled	17.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> crystal structure of intact ahpf
55	<a href="#">c3p2aB</a>	Alignment	not modelled	17.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative thioredoxin-like protein; <b>PDBTitle:</b> crystal structure of thioredoxin 2 from yersinia pestis
56	<a href="#">d1jqoa</a>	Alignment	not modelled	17.3	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate carboxylase
57	<a href="#">c1jqoA</a>	Alignment	not modelled	17.3	35	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate carboxylase; <b>PDBTitle:</b> crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
58	<a href="#">c4b5sB</a>	Alignment	not modelled	17.3	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-2-oxo-heptane-1,7-dioate aldolase; <b>PDBTitle:</b> crystal structures of divalent metal dependent pyruvate aldolase,2 hpai, in complex with pyruvate
59	<a href="#">c2v5jB</a>	Alignment	not modelled	16.9	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; <b>PDBTitle:</b> apo class ii aldolase hpch
60	<a href="#">d2pv7a2</a>	Alignment	not modelled	16.8	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
61	<a href="#">c3hmuA</a>	Alignment	not modelled	16.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase, class iii; <b>PDBTitle:</b> crystal structure of a class iii aminotransferase from silicibacter2 pomeroyi
62	<a href="#">d1un2a</a>	Alignment	not modelled	16.5	56	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
63	<a href="#">c3l44A</a>	Alignment	not modelled	15.9	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-1-semialdehyde 2,1-aminomutase 1; <b>PDBTitle:</b> crystal structure of bacillus anthracis hemI-1, glutamate semialdehyde2 aminotransferase
64	<a href="#">d1qh8b</a>	Alignment	not modelled	15.8	11	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
65	<a href="#">d1miob</a>	Alignment	not modelled	15.4	19	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
66	<a href="#">c2eqyA</a>	Alignment	not modelled	15.2	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> jumonji, at rich interactive domain 1b; <b>PDBTitle:</b> solution structure of the arid domain of jarid1b protein
67	<a href="#">c4nn7A</a>	Alignment	not modelled	15.1	40	<b>PDB header:</b> cytokine/cytokine receptor <b>Chain:</b> A: <b>PDB Molecule:</b> thymic stromal lymphopoietin; <b>PDBTitle:</b> cytokine receptor complex - crystal form 2
68	<a href="#">d1xb4a1</a>	Alignment	not modelled	15.1	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Vacuolar sorting protein domain
69	<a href="#">c1vcnA</a>	Alignment	not modelled	14.9	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp synthetase; <b>PDBTitle:</b> crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
70	<a href="#">d1xi3a</a>	Alignment	not modelled	14.8	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
71	<a href="#">d1q7ra</a>	Alignment	not modelled	14.7	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
72	<a href="#">c1vw4W</a>	Alignment	not modelled	14.6	29	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 54s ribosomal protein l32, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
73	<a href="#">c3r5yC</a>	Alignment	not modelled	14.5	18	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420
74	<a href="#">d1vlia2</a>	Alignment	not modelled	14.2	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
75	<a href="#">c2ordA</a>	Alignment	not modelled	14.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution
76	<a href="#">c3aerB</a>	Alignment	not modelled	14.1	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
77	<a href="#">c3graA</a>	Alignment	not modelled	13.8	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, arac family; <b>PDBTitle:</b> crystal structure of arac family transcriptional regulator from2 pseudomonas putida
78	<a href="#">d1mnda2</a>	Alignment	not modelled	13.5	40	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Motor proteins
79	<a href="#">c3dtpA</a>	Alianment	not modelled	13.4	40	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain chimera of smooth and cardiac muscle;

						<b>PDBTitle:</b> tarantula heavy meromyosin obtained by flexible docking to tarantula2 muscle thick filament cryo-em 3d-map
80	<a href="#">c3jbbA_</a>	Alignment	not modelled	13.3	40	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain striated muscle; <b>PDBTitle:</b> two heavy meromyosin interacting-heads motifs flexible docked into2 tarantula thick filament 3d-map allows in depth study of intra- and3 intermolecular interactions
81	<a href="#">c1ni5A_</a>	Alignment	not modelled	13.2	20	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell cycle protein mesj; <b>PDBTitle:</b> structure of the mesj pp-atpase from escherichia coli
82	<a href="#">c4rjfB_</a>	Alignment	not modelled	12.7	56	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> cyclin-dependent kinase inhibitor 1; <b>PDBTitle:</b> crystal structure of the human sliding clamp at 2.0 angstrom2 resolution
83	<a href="#">c1nj3A_</a>	Alignment	not modelled	12.7	33	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> npl4; <b>PDBTitle:</b> structure and ubiquitin interactions of the conserved nzf domain of2 npl4
84	<a href="#">c4rjfD_</a>	Alignment	not modelled	12.6	56	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> cyclin-dependent kinase inhibitor 1; <b>PDBTitle:</b> crystal structure of the human sliding clamp at 2.0 angstrom2 resolution
85	<a href="#">c4atpD_</a>	Alignment	not modelled	12.6	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-aminobutyrate transaminase; <b>PDBTitle:</b> structure of gaba-transaminase a1r958 from arthrobacter aurescens in2 complex with plp
86	<a href="#">c3ewnA_</a>	Alignment	not modelled	12.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> crystal structure of a thij/pfpi family protein from pseudomonas2 syringae
87	<a href="#">d1br2a2</a>	Alignment	not modelled	12.5	40	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Motor proteins
88	<a href="#">d1fa2a_</a>	Alignment	not modelled	12.4	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
89	<a href="#">c1oe9A_</a>	Alignment	not modelled	12.3	50	<b>PDB header:</b> atpase/myosin <b>Chain:</b> A: <b>PDB Molecule:</b> myosin va; <b>PDBTitle:</b> crystal structure of myosin v motor with essential light2 chain - nucleotide-free
90	<a href="#">c4qbdC_</a>	Alignment	not modelled	12.3	40	<b>PDB header:</b> motor protein <b>Chain:</b> C: <b>PDB Molecule:</b> myosin heavy chain, muscle; <b>PDBTitle:</b> the first x-ray crystal structure of an insect muscle myosin.2 drosophila melanogaster, skeletal muscle myosin ii, an embryonic3 isoform, subfragment-1
91	<a href="#">c2cy8A_</a>	Alignment	not modelled	12.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-phenylglycine aminotransferase; <b>PDBTitle:</b> crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201
92	<a href="#">c4byfA_</a>	Alignment	not modelled	12.0	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> unconventional myosin-ic; <b>PDBTitle:</b> crystal structure of human myosin 1c in complex with2 calmodulin in the pre-power stroke state
93	<a href="#">c6nvoA_</a>	Alignment	not modelled	12.0	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclease mpe; <b>PDBTitle:</b> crystal structure of pseudomonas putida nuclease mpe
94	<a href="#">c1ldbA_</a>	Alignment	not modelled	12.0	16	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> apo-l-lactate dehydrogenase; <b>PDBTitle:</b> structure determination and refinement of bacillus2 stearothermophilus lactate dehydrogenase
95	<a href="#">c6dueA_</a>	Alignment	not modelled	12.0	50	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin a; <b>PDBTitle:</b> toxoplasma gondii myoa, a class-xiv myosin, in the pre-powerstroke2 state
96	<a href="#">d1qdlb_</a>	Alignment	not modelled	11.9	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
97	<a href="#">c1w9iA_</a>	Alignment	not modelled	11.8	40	<b>PDB header:</b> myosin <b>Chain:</b> A: <b>PDB Molecule:</b> myosin ii heavy chain; <b>PDBTitle:</b> myosin ii dictyostelium discoideum motor domain s456y bound2 with mgadp-befx
98	<a href="#">c2r5rA_</a>	Alignment	not modelled	11.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0343 protein ne1163; <b>PDBTitle:</b> the crystal structure of duf198 from nitrosomonas europaea2 atcc 19718
99	<a href="#">d1w7ja2</a>	Alignment	not modelled	11.7	50	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Motor proteins