






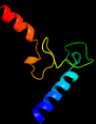

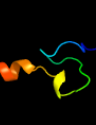
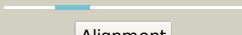

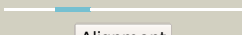





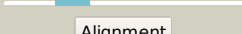

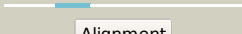
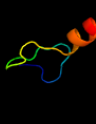

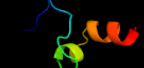






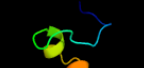


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2080_(lpp)_2337314_2337877
Date	Mon Aug 5 13:25:19 BST 2019
Unique Job ID	fabf5d9b4a137734

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1q8ra_</a>	 Alignment		59.5	17	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Holliday junction resolvase RusA <b>Family:</b> Holliday junction resolvase RusA
2	<a href="#">d2ag4a1</a>	 Alignment		44.8	22	<b>Fold:</b> Ganglioside M2 (gm2) activator <b>Superfamily:</b> Ganglioside M2 (gm2) activator <b>Family:</b> Ganglioside M2 (gm2) activator
3	<a href="#">c1zzgB_</a>	 Alignment		36.8	28	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
4	<a href="#">c2q8nB_</a>	 Alignment		34.9	32	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of glucose-6-phosphate isomerase (ec 5.3.1.9)2 (tm1385) from thermotoga maritima at 1.82 a resolution
5	<a href="#">c3pr3B_</a>	 Alignment		34.1	28	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
6	<a href="#">c1t10A_</a>	 Alignment		33.7	28	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
7	<a href="#">c6bzcA_</a>	 Alignment		33.2	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of glucose-6-phosphate isomerase from2 elizabethkingia anophelis with bound glucose-6-phosphate
8	<a href="#">c2o2cB_</a>	 Alignment		32.9	22	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase, glycosomal; <b>PDBTitle:</b> crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
9	<a href="#">d1hm5a_</a>	 Alignment		31.8	33	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
10	<a href="#">c2wu8A_</a>	 Alignment		31.6	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
11	<a href="#">d1u0fa_</a>	 Alignment		31.4	33	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI

12	<a href="#">c4qfhA_</a>	Alignment		30.8	28	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> structure of a glucose-6-phosphate isomerase from trypanosoma cruzi
13	<a href="#">c3ljkA_</a>	Alignment		30.7	28	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> glucose-6-phosphate isomerase from francisella tularensis.
14	<a href="#">d1c7qa_</a>	Alignment		30.5	33	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
15	<a href="#">c4em6D_</a>	Alignment		30.5	28	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> the structure of glucose-6-phosphate isomerase (gpi) from brucella2 melitensis
16	<a href="#">c3hjbA_</a>	Alignment		29.8	28	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
17	<a href="#">d1gzda_</a>	Alignment		29.6	33	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
18	<a href="#">d1q50a_</a>	Alignment		29.1	28	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
19	<a href="#">c3nbuC_</a>	Alignment		29.1	28	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of pgi glucosephosphate isomerase
20	<a href="#">c3ujhB_</a>	Alignment		28.9	28	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
21	<a href="#">d1iata_</a>	Alignment	not modelled	27.6	33	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
22	<a href="#">c6otuA_</a>	Alignment	not modelled	26.3	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of a glucose-6-phosphate isomerase from chlamydia2 trachomatis d/uw-3/cx
23	<a href="#">c4hzbA_</a>	Alignment	not modelled	25.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
24	<a href="#">c3ff1B_</a>	Alignment	not modelled	24.2	22	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> structure of glucose 6-phosphate isomerase from staphylococcus aureus
25	<a href="#">c2l25A_</a>	Alignment	not modelled	23.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> np_888769.1
26	<a href="#">c4r3zB_</a>	Alignment	not modelled	21.9	24	<b>PDB header:</b> protein binding/ligase <b>Chain:</b> B: <b>PDB Molecule:</b> arginine--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of human arggrs-glnrs-aimp1 complex
27	<a href="#">d1xrsb2</a>	Alignment	not modelled	20.1	20	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain <b>Family:</b> D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
28	<a href="#">c3ljrF_</a>	Alignment	not modelled	19.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of a short

						chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
29	<a href="#">d1nzea_</a>	Alignment	not modelled	16.8	19	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Oxygen-evolving enhancer protein 3, <b>Family:</b> Oxygen-evolving enhancer protein 3,
30	<a href="#">c1nzeA_</a>	Alignment	not modelled	16.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxygen-evolving enhancer protein 3; <b>PDBTitle:</b> crystal structure of psbq polypeptide of photosystem ii2 from higher plants
31	<a href="#">c3koxA_</a>	Alignment	not modelled	15.4	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-ornithine aminomutase e component; <b>PDBTitle:</b> crystal structure of ornithine 4,5 aminomutase in complex with 2,4-2 diaminobutyrate (anaerobic)
32	<a href="#">c3mkxC_</a>	Alignment	not modelled	15.2	63	<b>PDB header:</b> antiviral protein <b>Chain:</b> C: <b>PDB Molecule:</b> bone marrow stromal antigen 2; <b>PDBTitle:</b> crystal structure of bst2/tetherin
33	<a href="#">c5twaA_</a>	Alignment	not modelled	14.8	14	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-x homologous protein, bhp2; <b>PDBTitle:</b> crystal structure of geodia cydonium bhp2 in complex with lubomirskia2 baicalensis bak-2
34	<a href="#">d1wjfa_</a>	Alignment	not modelled	14.7	57	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> N-terminal Zn binding domain of HIV integrase <b>Family:</b> N-terminal Zn binding domain of HIV integrase
35	<a href="#">c3ni0A_</a>	Alignment	not modelled	14.6	75	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> bone marrow stromal antigen 2; <b>PDBTitle:</b> crystal structure of mouse bst-2/tetherin ectodomain
36	<a href="#">d1mxaa3</a>	Alignment	not modelled	13.7	19	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
37	<a href="#">d2b4ya1</a>	Alignment	not modelled	13.3	27	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
38	<a href="#">c2nx8A_</a>	Alignment	not modelled	13.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-specific adenosine deaminase; <b>PDBTitle:</b> the crystal structure of the trna-specific adenosine deaminase from2 streptococcus pyogenes
39	<a href="#">d2higa1</a>	Alignment	not modelled	12.4	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Hypothetical protein YdhR
40	<a href="#">d1z3aa1</a>	Alignment	not modelled	11.4	16	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
41	<a href="#">c4ce4S_</a>	Alignment	not modelled	11.4	15	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> mrpl18; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
42	<a href="#">c2mwqA_</a>	Alignment	not modelled	10.8	20	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> oxygen-evolving enhancer protein 3, chloroplastic; <b>PDBTitle:</b> solution structure of psbq from spinacia oleracea
43	<a href="#">d1oisa_</a>	Alignment	not modelled	10.8	32	<b>Fold:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment <b>Superfamily:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment <b>Family:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
44	<a href="#">d1k4ta3</a>	Alignment	not modelled	10.7	32	<b>Fold:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment <b>Superfamily:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment <b>Family:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
45	<a href="#">d2o3bb1</a>	Alignment	not modelled	10.4	21	<b>Fold:</b> Nuclease A inhibitor (NuiA) <b>Superfamily:</b> Nuclease A inhibitor (NuiA) <b>Family:</b> Nuclease A inhibitor (NuiA)
46	<a href="#">d1rbli_</a>	Alignment	not modelled	10.4	50	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
47	<a href="#">c3ddcB_</a>	Alignment	not modelled	10.1	20	<b>PDB header:</b> hydrolase/apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> ras association domain-containing family protein 5; <b>PDBTitle:</b> crystal structure of nore1a in complex with ras
48	<a href="#">d1p1ja1</a>	Alignment	not modelled	10.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	<a href="#">c3uc7E_</a>	Alignment	not modelled	9.9	40	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form
50	<a href="#">c2i18S_</a>	Alignment	not modelled	9.7	31	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 50s ribosomal protein l18; <b>PDBTitle:</b> insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
51	<a href="#">c2m9xA_</a>	Alignment	not modelled	9.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> microtubule-associated serine/threonine-protein kinase 1; <b>PDBTitle:</b> solution nmr structure of microtubule-associated serine/threonine-2 protein kinase 1 from homo sapiens, northeast structural genomics3 consortium (nesg) target hr9151a
52	<a href="#">c3uc7F_</a>	Alignment	not modelled	9.3	40	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form
						<b>PDB header:</b> de novo protein

53	<a href="#">c3uc8B_</a>	Alignment	not modelled	9.3	40	<b>Chain:</b> B: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - tetragonal crystal form
54	<a href="#">c3uc7D_</a>	Alignment	not modelled	9.3	40	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form
55	<a href="#">c3uc8A_</a>	Alignment	not modelled	9.3	40	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - tetragonal crystal form
56	<a href="#">c3uc7A_</a>	Alignment	not modelled	9.3	40	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form
57	<a href="#">c3uc8C_</a>	Alignment	not modelled	9.3	40	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - tetragonal crystal form
58	<a href="#">c2ll5A_</a>	Alignment	not modelled	9.2	40	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> cyclo-tc1 trp-cage
59	<a href="#">c5mz2l_</a>	Alignment	not modelled	9.2	50	<b>PDB header:</b> photosynthesis <b>Chain:</b> I: <b>PDB Molecule:</b> rubisco small subunit; <b>PDBTitle:</b> rubisco from thalassiosira antarctica
60	<a href="#">c3uc7B_</a>	Alignment	not modelled	9.2	40	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form
61	<a href="#">c3uc7C_</a>	Alignment	not modelled	9.2	40	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> cyclo-tc1; <b>PDBTitle:</b> trp-cage cyclo-tc1 - monoclinic crystal form
62	<a href="#">c2ahqA_</a>	Alignment	not modelled	9.1	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
63	<a href="#">d1gk8i_</a>	Alignment	not modelled	9.0	67	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
64	<a href="#">d1vkoa1</a>	Alignment	not modelled	8.7	39	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
65	<a href="#">d1svdm1</a>	Alignment	not modelled	8.6	25	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
66	<a href="#">c3rv2B_</a>	Alignment	not modelled	8.6	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosylmethionine synthase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
67	<a href="#">c3civA_</a>	Alignment	not modelled	8.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,4-mannanase; <b>PDBTitle:</b> crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius
68	<a href="#">d2j01s1</a>	Alignment	not modelled	8.5	31	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
69	<a href="#">c4obyA_</a>	Alignment	not modelled	8.4	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginine--trna ligase; <b>PDBTitle:</b> crystal structure of e.coli arginyl-trna synthetase and ligand binding2 studies revealed key residues in arginine recognition
70	<a href="#">c3imlB_</a>	Alignment	not modelled	8.4	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
71	<a href="#">c2ns2B_</a>	Alignment	not modelled	8.4	37	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> spindlin-1; <b>PDBTitle:</b> crystal structure of spindlin1
72	<a href="#">d1qm4a1</a>	Alignment	not modelled	8.2	19	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
73	<a href="#">c4odjA_</a>	Alignment	not modelled	8.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine synthase; <b>PDBTitle:</b> crystal structure of a putative s-adenosylmethionine synthetase from2 cryptosporidium hominis in complex with s-adenosyl-methionine
74	<a href="#">c4er8A_</a>	Alignment	not modelled	8.1	10	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> tnparep for protein; <b>PDBTitle:</b> structure of the rep associates tyrosine transposase bound to a rep2 hairpin
75	<a href="#">d1qm4a3</a>	Alignment	not modelled	8.1	13	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
76	<a href="#">c3o2lB_</a>	Alignment	not modelled	7.9	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein from2 leptospirillum sp. group ii uba
77	<a href="#">c1jloA_</a>	Alignment	not modelled	7.8	67	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> psi-conotoxin piiie; <b>PDBTitle:</b> solution structure of the noncompetitive skeletal muscle nicotinic2 acetylcholine receptor antagonist psi-conotoxin piiie
78	<a href="#">d1ylxa1</a>	Alignment	not modelled	7.8	22	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GK1464-like <b>Family:</b> GK1464-like
79	<a href="#">d1lou8a_</a>	Alignment	not modelled	7.6	25	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB

80	<a href="#">c2ybvN</a>	Alignment	not modelled	7.6	42	<b>PDB header:</b> lyase <b>Chain:</b> N: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase small subunit; <b>PDBTitle:</b> structure of rubisco from thermosynechococcus elongatus
81	<a href="#">c1y80A</a>	Alignment	not modelled	7.5	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted cobalamin binding protein; <b>PDBTitle:</b> structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
82	<a href="#">c2ns2A</a>	Alignment	not modelled	7.4	37	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> spindlin-1; <b>PDBTitle:</b> crystal structure of spindlin1
83	<a href="#">d1w6ga2</a>	Alignment	not modelled	7.4	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
84	<a href="#">c5y4gA</a>	Alignment	not modelled	7.4	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ampb3; <b>PDBTitle:</b> apo structure of ampb3
85	<a href="#">c1jlpA</a>	Alignment	not modelled	7.3	67	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> psi-conotoxin piiif; <b>PDBTitle:</b> solution structure of the noncompetitive skeletal muscle2 nicotinic acetylcholine receptor antagonist psi-conotoxin3 piiif
86	<a href="#">d1wdds</a>	Alignment	not modelled	7.3	33	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
87	<a href="#">c1as5A</a>	Alignment	not modelled	7.1	67	<b>PDB header:</b> neurotoxin <b>Chain:</b> A: <b>PDB Molecule:</b> conotoxin y-piiee; <b>PDBTitle:</b> solution structure of conotoxin y-piiee from conus2 purpurascens, nmr, 14 structures
88	<a href="#">c5o60P</a>	Alignment	not modelled	7.1	21	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 50s ribosomal protein l18; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
89	<a href="#">d1bwvs</a>	Alignment	not modelled	7.0	42	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
90	<a href="#">c3fhaD</a>	Alignment	not modelled	7.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> endo-beta-n-acetylglucosaminidase; <b>PDBTitle:</b> structure of endo-beta-n-acetylglucosaminidase a
91	<a href="#">d2p02a3</a>	Alignment	not modelled	6.9	13	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
92	<a href="#">c4ee7A</a>	Alignment	not modelled	6.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> prenyltransferase; <b>PDBTitle:</b> crystal structure of the novel phenazine prenyltransferase epzp in2 complex with s-thiolodiphosphate (methylated)
93	<a href="#">c2o8kA</a>	Alignment	not modelled	6.8	27	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
94	<a href="#">d1xuba2</a>	Alignment	not modelled	6.8	12	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
95	<a href="#">c2b9sA</a>	Alignment	not modelled	6.6	26	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase i-like protein; <b>PDBTitle:</b> crystal structure of heterodimeric I. donovani topoisomerase i-2 vanadate-dna complex
96	<a href="#">d2p02a1</a>	Alignment	not modelled	6.6	19	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
97	<a href="#">c4ndvB</a>	Alignment	not modelled	6.6	24	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-galactosyl-binding lectin; <b>PDBTitle:</b> crystal structure of I. decastes alpha-galactosyl-binding lectin in2 complex with globotriose
98	<a href="#">d1bxni</a>	Alignment	not modelled	6.5	42	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
99	<a href="#">c4le5A</a>	Alignment	not modelled	6.5	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> structure of an unusual s-adenosylmethionine synthetase from2 campylobacter jejuni