


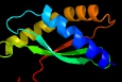

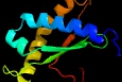







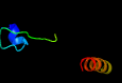

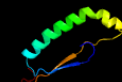








# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD2838c\_(rbfA)\_3144630\_3145181  
 Date Wed Aug 7 12:50:50 BST 2019  
 Unique Job ID c543d8e37fc1ed91

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1kkga_</a>	 Alignment		100.0	32	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Ribosome-binding factor A, RbfA <b>Family:</b> Ribosome-binding factor A, RbfA
2	<a href="#">d1josa_</a>	 Alignment		100.0	29	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Ribosome-binding factor A, RbfA <b>Family:</b> Ribosome-binding factor A, RbfA
3	<a href="#">c2kzfA_</a>	 Alignment		100.0	25	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribosome-binding factor a; <b>PDBTitle:</b> solution nmr structure of the thermotoga maritima protein tm0855 a2 putative ribosome binding factor a
4	<a href="#">d2e7ga1</a>	 Alignment		100.0	23	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Ribosome-binding factor A, RbfA <b>Family:</b> Ribosome-binding factor A, RbfA
5	<a href="#">d1pa4a_</a>	 Alignment		100.0	22	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Ribosome-binding factor A, RbfA <b>Family:</b> Ribosome-binding factor A, RbfA
6	<a href="#">d2dyja1</a>	 Alignment		99.9	25	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Ribosome-binding factor A, RbfA <b>Family:</b> Ribosome-binding factor A, RbfA
7	<a href="#">c2qsiB_</a>	 Alignment		49.7	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative hydrogenase expression/formation protein hupg; <b>PDBTitle:</b> crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
8	<a href="#">c5nkmE_</a>	 Alignment		46.5	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> protein smg-8; <b>PDBTitle:</b> smg8-smg9 complex
9	<a href="#">c1rb6C_</a>	 Alignment		40.1	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal form
10	<a href="#">c3k7zA_</a>	 Alignment		40.1	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
11	<a href="#">c1swiA_</a>	 Alignment		40.1	27	<b>PDB header:</b> leucine zipper <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4p1; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a complexed with benzene

12	<a href="#">c3k7zB_</a>	Alignment		40.1	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
13	<a href="#">c1rb1B_</a>	Alignment		40.1	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
14	<a href="#">c1rb1A_</a>	Alignment		40.1	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
15	<a href="#">c1rb1C_</a>	Alignment		39.1	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
16	<a href="#">c3k7zC_</a>	Alignment		39.1	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
17	<a href="#">c1rb4C_</a>	Alignment		38.4	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal automatic solution
18	<a href="#">c1swiB_</a>	Alignment		37.5	30	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> gcn4p1; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a complexed with benzene
19	<a href="#">c1rb4A_</a>	Alignment		37.5	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal automatic solution
20	<a href="#">c1rb5C_</a>	Alignment		35.9	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 trigonal form
21	<a href="#">c1rb6B_</a>	Alignment	not modelled	35.9	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal form
22	<a href="#">c1rb4B_</a>	Alignment	not modelled	35.9	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal automatic solution
23	<a href="#">c1rb5B_</a>	Alignment	not modelled	34.9	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 trigonal form
24	<a href="#">c1rb6A_</a>	Alignment	not modelled	34.9	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal form
25	<a href="#">c1rb5A_</a>	Alignment	not modelled	34.9	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 trigonal form
26	<a href="#">c6qt9Y_</a>	Alignment	not modelled	29.2	50	<b>PDB header:</b> virus <b>Chain:</b> Y: <b>PDB Molecule:</b> orf 31; <b>PDBTitle:</b> cryo-em structure of sh1 full particle.
27	<a href="#">c1ij3B_</a>	Alignment	not modelled	28.7	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
28	<a href="#">c1ij3C_</a>	Alignment	not modelled	28.7	23	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c3hd5A</a>	Alignment	not modelled	28.3	17	<b>Chain:</b> A; <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
30	<a href="#">c1swiC</a>	Alignment	not modelled	27.5	32	<b>PDB header:</b> leucine zipper <b>Chain:</b> C; <b>PDB Molecule:</b> gcn4p1; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a complexed with benzene
31	<a href="#">c1ij2C</a>	Alignment	not modelled	26.9	23	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
32	<a href="#">c2wpyA</a>	Alignment	not modelled	25.6	25	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper mutant with one vxxnxxx motif2 coordinating chloride
33	<a href="#">c5irdA</a>	Alignment	not modelled	25.2	15	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of rv1466 from mycobacterium tuberculosis, a2 protein associated with [fe-s] complex assembly and repair - seattle3 structural genomics center for infectious disease target4 mytud.17486.a
34	<a href="#">c1ij2B</a>	Alignment	not modelled	25.0	23	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
35	<a href="#">c4g7xB</a>	Alignment	not modelled	24.9	16	<b>PDB header:</b> protein binding/protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> tola protein; <b>PDBTitle:</b> crystal structure of a complex between the ctxphi piiii n-terminal2 domain and the vibrio cholerae tola c-terminal domain
36	<a href="#">c6h9cb</a>	Alignment	not modelled	22.2	38	<b>PDB header:</b> virus <b>Chain:</b> B; <b>PDB Molecule:</b> vp4; <b>PDBTitle:</b> cryo-em structure of archaeal extremophilic internal membrane-2 containing haloarcula californiae icosahedral virus 1 (hciv-1) at3 3.74 angstroms resolution.
37	<a href="#">c2o7hF</a>	Alignment	not modelled	21.5	23	<b>PDB header:</b> transcription <b>Chain:</b> F; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> crystal structure of trimeric coiled coil gcn4 leucine zipper
38	<a href="#">c1ce0B</a>	Alignment	not modelled	21.2	24	<b>PDB header:</b> hiv-1 envelope protein <b>Chain:</b> B; <b>PDB Molecule:</b> protein (leucine zipper model h38-p1); <b>PDBTitle:</b> trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
39	<a href="#">c2mxnA</a>	Alignment	not modelled	21.1	18	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> mono-cysteine glutaredoxin; <b>PDBTitle:</b> nmr structure of the mature form of trypanosoma brucei 1cgrx1
40	<a href="#">c1gcmA</a>	Alignment	not modelled	19.6	20	<b>PDB header:</b> transcription regulation <b>Chain:</b> A; <b>PDB Molecule:</b> gcn4p-ii; <b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li
41	<a href="#">c5j7dG</a>	Alignment	not modelled	19.4	20	<b>PDB header:</b> de novo protein <b>Chain:</b> G; <b>PDB Molecule:</b> designed thioredoxin df106; <b>PDBTitle:</b> computationally designed thioredoxin df106
42	<a href="#">c1decA</a>	Alignment	not modelled	19.2	75	<b>PDB header:</b> blood coagulation <b>Chain:</b> A; <b>PDB Molecule:</b> decorsin; <b>PDBTitle:</b> structure of the rgd protein decorsin: conserved motif and distinct2 function in leech proteins that affect blood clotting
43	<a href="#">d1deca</a>	Alignment	not modelled	19.2	75	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Leech antihemostatic proteins <b>Family:</b> Hirudin-like
44	<a href="#">c1ztaA</a>	Alignment	not modelled	18.7	23	<b>PDB header:</b> dna-binding motif <b>Chain:</b> A; <b>PDB Molecule:</b> leucine zipper monomer; <b>PDBTitle:</b> the solution structure of a leucine-zipper motif peptide
45	<a href="#">c1u6tA</a>	Alignment	not modelled	18.5	17	<b>PDB header:</b> protein binding, signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> sh3 domain-binding glutamic acid-rich-like <b>PDBTitle:</b> crystal structure of the human sh3 binding glutamic-rich2 protein like
46	<a href="#">c1w5kC</a>	Alignment	not modelled	18.4	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> C; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
47	<a href="#">c1w5kD</a>	Alignment	not modelled	18.4	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> D; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
48	<a href="#">c1w5kA</a>	Alignment	not modelled	18.4	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> A; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
49	<a href="#">c1w5kB</a>	Alignment	not modelled	18.4	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> B; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
50	<a href="#">c1gcmB</a>	Alignment	not modelled	17.9	20	<b>PDB header:</b> transcription regulation <b>Chain:</b> B; <b>PDB Molecule:</b> gcn4p-ii; <b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li
51	<a href="#">c5appB</a>	Alignment	not modelled	17.6	21	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> general control protein gcn4, outer membrane protein 100; <b>PDBTitle:</b> actinobacillus actinomycetemcomitans omp100 residues 133-198 fused to2 gcn4 adaptors
52	<a href="#">c1gcmC</a>	Alignment	not modelled	17.2	20	<b>PDB header:</b> transcription regulation <b>Chain:</b> C; <b>PDB Molecule:</b> gcn4p-ii; <b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li
53	<a href="#">c4k2dA</a>	Alignment	not modelled	16.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> crystal structure of burkholderia pseudomallei dsba
54	<a href="#">c1ij3A</a>	Alignment	not modelled	15.9	25	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position

55	<a href="#">c3d5jB_</a>	Alignment	not modelled	15.7	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin-2, mitochondrial; <b>PDBTitle:</b> structure of yeast grx2-c30s mutant with glutathionyl mixed disulfide
56	<a href="#">d1lr0a_</a>	Alignment	not modelled	14.7	12	<b>Fold:</b> TolA/TonB C-terminal domain <b>Superfamily:</b> TolA/TonB C-terminal domain <b>Family:</b> TolA
57	<a href="#">c2ct6A_</a>	Alignment	not modelled	14.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sh3 domain-binding glutamic acid-rich-like <b>PDBTitle:</b> solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2
58	<a href="#">c3c1sA_</a>	Alignment	not modelled	14.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-1; <b>PDBTitle:</b> crystal structure of grx1 in glutathionylated form
59	<a href="#">c1ij2A_</a>	Alignment	not modelled	13.8	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
60	<a href="#">c1w5jD_</a>	Alignment	not modelled	13.5	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> D: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
61	<a href="#">c1w5jC_</a>	Alignment	not modelled	13.5	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
62	<a href="#">c1w5jB_</a>	Alignment	not modelled	13.5	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
63	<a href="#">c1w5jA_</a>	Alignment	not modelled	13.5	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
64	<a href="#">c2jacA_</a>	Alignment	not modelled	13.2	14	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-1; <b>PDBTitle:</b> glutaredoxin grx1p c30s mutant from yeast
65	<a href="#">d1l0wa2</a>	Alignment	not modelled	13.1	19	<b>Fold:</b> DCoH-like <b>Superfamily:</b> GAD domain-like <b>Family:</b> GAD domain
66	<a href="#">c3ipzA_</a>	Alignment	not modelled	13.0	13	<b>PDB header:</b> electron transport, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin-s14, chloroplastic; <b>PDBTitle:</b> crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
67	<a href="#">c6a42A_</a>	Alignment	not modelled	12.8	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-directed dna polymerase homolog (r1), polyubiquitin-c; <b>PDBTitle:</b> r1en(5-223)-ubiquitin fusion
68	<a href="#">c3fzaA_</a>	Alignment	not modelled	12.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol
69	<a href="#">d1t3ba1</a>	Alignment	not modelled	12.5	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
70	<a href="#">c1piqA_</a>	Alignment	not modelled	12.4	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (general control protein gcn4-piq); <b>PDBTitle:</b> crystal structure of gcn4-piq, a trimeric coiled coil with buried2 polar residues
71	<a href="#">c3kh0A_</a>	Alignment	not modelled	11.9	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ral guanine nucleotide dissociation stimulator; <b>PDBTitle:</b> crystal structure of the ras-association (ra) domain of ralgds
72	<a href="#">c4i2uA_</a>	Alignment	not modelled	11.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> crystal structure of the reduced glutaredoxin from chlorella2 sorokiniana t-89 in complex with glutathione
73	<a href="#">c5fmnB_</a>	Alignment	not modelled	11.0	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> inrs; <b>PDBTitle:</b> the nickel-responsive transcriptional regulator inrs
74	<a href="#">d2rgfa_</a>	Alignment	not modelled	11.0	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
75	<a href="#">c3d22A_</a>	Alignment	not modelled	11.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin h-type; <b>PDBTitle:</b> crystal structure of a poplar thioredoxin h mutant, ptxrh4c61s
76	<a href="#">c2wpzA_</a>	Alignment	not modelled	11.0	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
77	<a href="#">d1ep7a_</a>	Alignment	not modelled	11.0	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
78	<a href="#">c2remB_</a>	Alignment	not modelled	10.7	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> disulfide oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase dsba from xylella fastidiosa
79	<a href="#">c2vm2C_</a>	Alignment	not modelled	10.2	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin h isoform 1.; <b>PDBTitle:</b> crystal structure of barley thioredoxin h isoform 1 crystallized using2 peg as precipitant
80	<a href="#">c1ld4E_</a>	Alignment	not modelled	10.2	25	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> placement of the structural proteins in sindbis virus
81	<a href="#">c2wpzB_</a>	Alignment	not modelled	10.1	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;

81	<a href="#">c2wpzB</a>	Alignment	not modelled	10.1	20	<b>PDBTitle:</b> gcn4 leucine zipper mutant with two vxnxnxxx motifs2 coordinating chloride
82	<a href="#">c4oz1A</a>	Alignment	not modelled	10.1	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii; <b>PDBTitle:</b> glnk2 from haloferax mediterranei complexed with amp
83	<a href="#">d1wf3a2</a>	Alignment	not modelled	10.1	13	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
84	<a href="#">c6a8kA</a>	Alignment	not modelled	10.0	17	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> ice binding protein 1; <b>PDBTitle:</b> crystal structure of ice-binding protein from a sea-ice microalga
85	<a href="#">c2n6uA</a>	Alignment	not modelled	9.9	31	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> astexin2-dc4; <b>PDBTitle:</b> solution study of astexin2-dc4
86	<a href="#">c4p3yB</a>	Alignment	not modelled	9.9	13	<b>PDB header:</b> translation/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> crystal structure of acinetobacter baumannii dsba in complex with ef-2 tu
87	<a href="#">c1uo1B</a>	Alignment	not modelled	9.8	25	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles
88	<a href="#">c1uo1A</a>	Alignment	not modelled	9.8	25	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles
89	<a href="#">d1uxya2</a>	Alignment	not modelled	9.7	26	<b>Fold:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain <b>Superfamily:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain <b>Family:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
90	<a href="#">c2wpzC</a>	Alignment	not modelled	9.7	20	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper mutant with two vxnxnxxx motifs2 coordinating chloride
91	<a href="#">d2jdia1</a>	Alignment	not modelled	9.7	20	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
92	<a href="#">c1zilA</a>	Alignment	not modelled	9.6	25	<b>PDB header:</b> leucine zipper <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the dimeric2 state
93	<a href="#">c1zilB</a>	Alignment	not modelled	9.6	25	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the dimeric2 state
94	<a href="#">d1u5tb1</a>	Alignment	not modelled	9.5	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Vacuolar sorting protein domain
95	<a href="#">c2ztaB</a>	Alignment	not modelled	9.3	25	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> gcn4 leucine zipper; <b>PDBTitle:</b> x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil
96	<a href="#">c2ztaA</a>	Alignment	not modelled	9.3	25	<b>PDB header:</b> leucine zipper <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4 leucine zipper; <b>PDBTitle:</b> x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil
97	<a href="#">d1lfda</a>	Alignment	not modelled	9.2	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
98	<a href="#">d1gh2a</a>	Alignment	not modelled	9.0	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
99	<a href="#">c1jzdA</a>	Alignment	not modelled	8.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbc; <b>PDBTitle:</b> dsbc-dsbdalpha complex