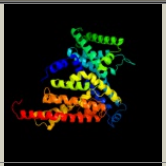
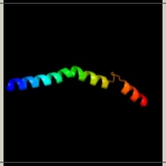
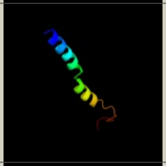
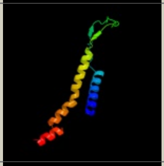
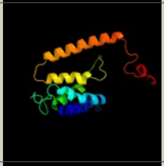
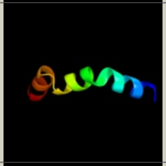
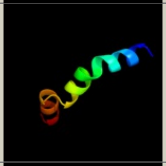
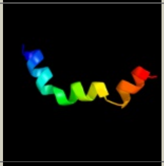
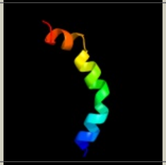
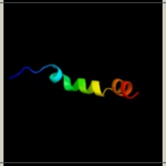
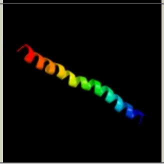
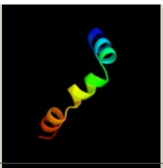
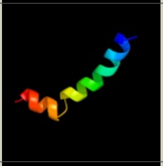
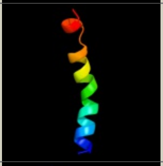
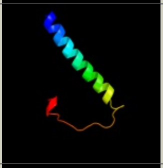
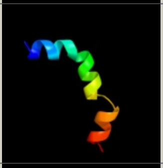
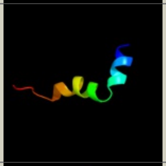
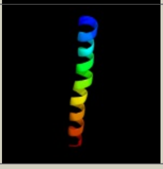
Phyre^{2}

Email	l.a.kelley@imperial.ac.uk
Description	P17334
Date	Thu Jan 5 11:36:06 GMT 2012
Unique Job ID	1d0a5490fece6ac1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qnqD_	Alignment		100.0	32	**PDB header:** membrane protein, transport protein **Chain:** D: **PDB Molecule:** pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
2	d2oara1	Alignment		83.2	19	**Fold:** Gated mechanosensitive channel **Superfamily:** Gated mechanosensitive channel **Family:** Gated mechanosensitive channel
3	c2kncA_	Alignment		64.0	24	**PDB header:** cell adhesion **Chain:** A: **PDB Molecule:** integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
4	c2oarA_	Alignment		61.5	16	**PDB header:** membrane protein **Chain:** A: **PDB Molecule:** large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
5	c3b9yA_	Alignment		49.0	16	**PDB header:** transport protein **Chain:** A: **PDB Molecule:** ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
6	d1to9a_	Alignment		40.6	14	**Fold:** Heme oxygenase-like **Superfamily:** Heme oxygenase-like **Family:** TENA/THI-4
7	c1to9A_	Alignment		40.6	14	**PDB header:** biosynthetic protein **Chain:** A: **PDB Molecule:** thi-4 protein; **PDBTitle:** crystal structure of thi-4 protein from bacillus subtilis
8	c2qcxA_	Alignment		30.0	14	**PDB header:** hydrolase **Chain:** A: **PDB Molecule:** transcriptional activator tena; **PDBTitle:** crystal structure of bacillus subtilis tena y112f mutant complexed2 with formyl aminomethyl pyrimidine
9	c2rd3A_	Alignment		29.0	21	**PDB header:** hydrolase **Chain:** A: **PDB Molecule:** transcriptional regulator; **PDBTitle:** crystal structure of tena homologue (hp1287) from2 helicobacter pylori
10	d1udda_	Alignment		25.3	21	**Fold:** Heme oxygenase-like **Superfamily:** Heme oxygenase-like **Family:** TENA/THI-4
11	c2kncB_	Alignment		23.5	18	**PDB header:** cell adhesion **Chain:** B: **PDB Molecule:** integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex

12	c3mvuA_	Alignment		22.9	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tena family transcriptional regulator; **PDBTitle:** crystal structure of a tena family transcription regulator2 (tm1040_3656) from silicibacter sp. tm1040 at 1.80 a resolution
13	c3no6B_	Alignment		19.2	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcriptional activator tena; **PDBTitle:** crystal structure of a putative thiaminase ii (se1693) from2 staphylococcus epidermidis atcc 12228 at 1.65 a resolution
14	d1rtwa_	Alignment		17.0	7	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**TENA/THI-4
15	d1z72a1	Alignment		14.4	14	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**TENA/THI-4
16	c3oqlA_	Alignment		12.2	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tena homolog; **PDBTitle:** crystal structure of a tena homolog (pspto1738) from pseudomonas2 syringae pv. tomato str. dc3000 at 2.54 a resolution
17	d3dtub2	Alignment		11.8	9	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
18	d2gm8a1	Alignment		11.7	21	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**TENA/THI-4
19	c2qzcB_	Alignment		11.5	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**transcriptional activator tena-1; **PDBTitle:** crystal structure of a putative tena-like thiaminase (tena-1, sso2206)2 from sulfolobus solfataricus p2 at 1.50 a resolution
20	c2rddB_	Alignment		10.4	13	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
21	c1unyA_	Alignment	not modelled	10.4	27	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
22	c1u9hB_	Alignment	not modelled	9.6	27	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of e(22)l(23)
23	d1rzsa_	Alignment	not modelled	9.4	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
24	c1hgvA_	Alignment	not modelled	9.0	11	**PDB header:**virus **Chain:** A: **PDB Molecule:**ph75 inovirus major coat protein; **PDBTitle:** filamentous bacteriophage ph75
25	c2ccfA_	Alignment	not modelled	8.8	29	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel configuration of pli e20s
26	c1unwB_	Alignment	not modelled	8.5	29	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
27	c1unyB_	Alignment	not modelled	8.5	29	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
28	c1uo0B_	Alignment	not modelled	8.4	29	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
						PDB header:four helix bundle

29	c1uo0A_	Alignment	not modelled	8.4	29	**Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
30	c1uo1A_	Alignment	not modelled	8.4	29	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
31	c1uo1B_	Alignment	not modelled	8.4	29	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
32	c1unxA_	Alignment	not modelled	8.4	29	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
33	c1gclD_	Alignment	not modelled	8.4	29	**PDB header:**leucine zipper **Chain:** D: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
34	c1gclA_	Alignment	not modelled	8.4	29	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
35	c1gclC_	Alignment	not modelled	8.4	29	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
36	c2cceA_	Alignment	not modelled	8.4	29	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** parallel configuration of pli e20s
37	c2cceB_	Alignment	not modelled	8.4	29	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** parallel configuration of pli e20s
38	c1u9hA_	Alignment	not modelled	8.3	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of e(22)l(23)
39	c3ddeB_	Alignment	not modelled	8.3	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**tena/thi-4 protein, domain of unknown function with a heme **PDBTitle:** crystal structure of a domain of unknown function with a heme2 oxygenase-like fold (sden_3740) from shewanella denitrificans os2173 at 2.30 a resolution
40	c2wwbA_	Alignment	not modelled	8.1	13	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**protein transport protein sec61 subunit alpha isoform 1; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
41	c1rkcB_	Alignment	not modelled	8.0	14	**PDB header:**cell adhesion, structural protein **Chain:** B: **PDB Molecule:**talin; **PDBTitle:** human vinculin head (1-258) in complex with talin's2 vinculin binding site 3 (residues 1944-1969)
42	c3hd6A_	Alignment	not modelled	7.9	11	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
43	d3ehbb2	Alignment	not modelled	7.9	9	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
44	c3s90D_	Alignment	not modelled	7.9	30	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**talin-1; **PDBTitle:** human vinculin head domain vh1 (residues 1-252) in complex with murine2 talin (vbs33; residues 1512-1546)
45	c1w5iA_	Alignment	not modelled	7.8	29	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** aba does not affect topology of pli.
46	c1uo2A_	Alignment	not modelled	7.8	29	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
47	c2w8aC_	Alignment	not modelled	7.8	7	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
48	c1unxB_	Alignment	not modelled	7.7	29	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
49	c1w5iB_	Alignment	not modelled	7.7	29	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** aba does not affect topology of pli.
50	c1uo2B_	Alignment	not modelled	7.7	29	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
51	c1u9fA_	Alignment	not modelled	7.7	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
52	c1ij1C_	Alignment	not modelled	7.6	20	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvlt coiled-coil trimer with threonine at the d(12)2 position
53	c1ij1B_	Alignment	not modelled	7.6	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvlt coiled-coil trimer with threonine at the d(12)2 position
						PDB header:transcription

54	c1ij1A_	Alignment	not modelled	7.6	20	**Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvlt coiled-coil trimer with threonine at the d(12)2 position
55	c1w5kC_	Alignment	not modelled	7.6	29	**PDB header:**four helix bundle **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
56	c1w5kB_	Alignment	not modelled	7.6	29	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
57	c1w5kD_	Alignment	not modelled	7.6	29	**PDB header:**four helix bundle **Chain:** D: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
58	c1w5kA_	Alignment	not modelled	7.6	29	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
59	c1piqA_	Alignment	not modelled	7.4	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein (general control protein gcn4-piq); **PDBTitle:** crystal structure of gcn4-piq, a trimeric coiled coil with buried2 polar residues
60	c1w5jC_	Alignment	not modelled	7.4	29	**PDB header:**four helix bundle **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
61	c1w5jD_	Alignment	not modelled	7.4	29	**PDB header:**four helix bundle **Chain:** D: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
62	c1w5jA_	Alignment	not modelled	7.4	29	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
63	c1w5jB_	Alignment	not modelled	7.4	29	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
64	c3oqlB_	Alignment	not modelled	7.3	7	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tena homolog; **PDBTitle:** crystal structure of a tena homolog (pspto1738) from pseudomonas2 syringae pv. tomato str. dc3000 at 2.54 a resolution
65	c1gcmA_	Alignment	not modelled	7.2	20	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
66	c3lo0A_	Alignment	not modelled	7.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic pyrophosphatase from2 ehrlichia chaffeensis
67	c1u9fB_	Alignment	not modelled	7.2	31	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
68	c1u9fC_	Alignment	not modelled	7.2	31	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
69	c1u9fD_	Alignment	not modelled	7.1	31	**PDB header:**transcription **Chain:** D: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
70	c1gclB_	Alignment	not modelled	7.0	29	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
71	c1ij0B_	Alignment	not modelled	6.9	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** coiled coil trimer gcn4-pvls ser at buried d position
72	c1ij0A_	Alignment	not modelled	6.9	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** coiled coil trimer gcn4-pvls ser at buried d position
73	c1ij0C_	Alignment	not modelled	6.9	20	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** coiled coil trimer gcn4-pvls ser at buried d position
74	d1pv7a_	Alignment	not modelled	6.8	6	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
75	d1h3ga1	Alignment	not modelled	6.8	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
76	c1gcmB_	Alignment	not modelled	6.8	20	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
77	c1gcmC_	Alignment	not modelled	6.7	20	**PDB header:**transcription regulation **Chain:** C: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
78	d1j9ia_	Alignment	not modelled	6.5	17	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
79	c2jo1A_	Alignment	not modelled	6.5	20	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
80	c2a45J_	Alignment	not modelled	6.4	14	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** J: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of the complex between thrombin and the central "e"2 region of fibrin

81	c2b2hA_	Alignment	not modelled	6.4	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
82	d2nr9a1	Alignment	not modelled	6.3	24	**Fold:**Rhomboid-like **Superfamily:**Rhomboid-like **Family:**Rhomboid-like
83	c3hd7A_	Alignment	not modelled	6.2	10	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
84	c1f3mB_	Alignment	not modelled	6.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** crystal structure of human serine/threonine kinase pak1
85	c3hzqA_	Alignment	not modelled	6.1	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** structure of a tetrameric mscl in an expanded intermediate2 state
86	c2wpzA_	Alignment	not modelled	6.1	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
87	c3dzvB_	Alignment	not modelled	6.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-methyl-5-(beta-hydroxyethyl)thiazole kinase; **PDBTitle:** crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution
88	c2k9pA_	Alignment	not modelled	5.9	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**pheromone alpha factor receptor; **PDBTitle:** structure of tm1_tm2 in lppg micelles
89	c3iz5d_	Alignment	not modelled	5.8	19	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**60s ribosomal protein l4 (l4p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
90	c2q9kA_	Alignment	not modelled	5.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution
91	c2wpzB_	Alignment	not modelled	5.7	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
92	c1ld4E_	Alignment	not modelled	5.7	21	**PDB header:**virus **Chain:** E: **PDB Molecule:**general control protein gcn4; **PDBTitle:** placement of the structural proteins in sindbis virus
93	c2o60B_	Alignment	not modelled	5.7	44	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**peptide corresponding to calmodulin binding domain of **PDBTitle:** calmodulin bound to peptide from neuronal nitric oxide synthase
94	c1rb4C_	Alignment	not modelled	5.7	21	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution
95	c2wpzC_	Alignment	not modelled	5.6	21	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
96	c1ziiA_	Alignment	not modelled	5.6	21	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the dimeric2 state
97	c1ziiB_	Alignment	not modelled	5.6	21	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the dimeric2 state
98	c2wpyA_	Alignment	not modelled	5.6	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with one vxxnxxx motif2 coordinating chloride
99	c1swiB_	Alignment	not modelled	5.6	21	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene