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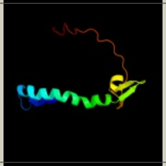
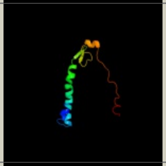
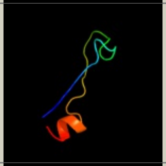
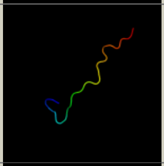
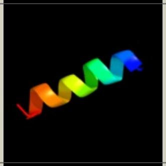
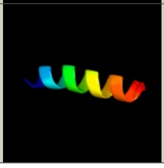
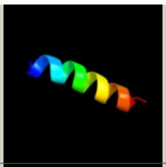
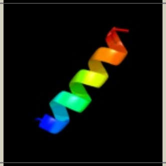
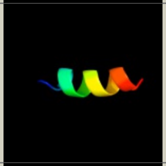
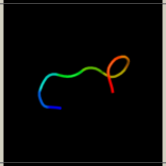
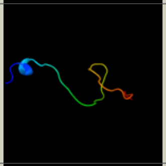
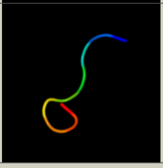
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1l6sa_	Alignment		48.1	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
2	c1yewF_	Alignment		26.0	30	**PDB header:**oxidoreductase, membrane protein **Chain:** F: **PDB Molecule:**particulate methane monooxygenase, a subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
3	c3chxF_	Alignment		25.3	24	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**pmoa; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
4	c3l4cB_	Alignment		20.0	39	**PDB header:**cell adhesion, cell invasion, apoptosis **Chain:** B: **PDB Molecule:**dedicator of cytokinesis protein 1; **PDBTitle:** structural basis of membrane-targeting by dock180
5	c1zikB_	Alignment		19.6	60	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16lys in the dimeric2 state
6	c1zikA_	Alignment		19.2	60	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16lys in the dimeric2 state
7	d1x6aa2	Alignment		18.9	35	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
8	c1wyyB_	Alignment		17.9	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
9	c2gohA_	Alignment		17.3	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles
10	c1pjeA_	Alignment		17.3	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** structure of the channel-forming trans-membrane domain of2 virus protein "u"(vpu) from hiv-1
11	c1pi8A_	Alignment		17.3	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1

12	c1pi7A_	Alignment		17.3	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
13	c2gofA_	Alignment		17.3	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles
14	c2vpvA_	Alignment		16.7	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
15	c1ziiB_	Alignment		14.8	57	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the dimeric2 state
16	c1ziiA_	Alignment		14.8	57	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the dimeric2 state
17	c3mhvC_	Alignment		14.6	67	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** crystal structure of vps4 and vta1
18	c1zijA_	Alignment		14.5	57	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
19	c1u24A_	Alignment		14.5	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**myo-inositol hexaphosphate phosphohydrolase; **PDBTitle:** crystal structure of selenomonas ruminantium phytase
20	c2dzoD_	Alignment		14.2	56	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**26s protease regulatory subunit 6b homolog; **PDBTitle:** crystal structure analysis of yeast nas6p complexed with2 the proteasome subunit, rpt3
21	c1no7A_	Alignment	not modelled	14.2	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major capsid protein; **PDBTitle:** structure of the large protease resistant upper domain of2 vp5, the major capsid protein of herpes simplex virus-1
22	d1no7a_	Alignment	not modelled	14.2	21	**Fold:**Major capsid protein VP5 **Superfamily:**Major capsid protein VP5 **Family:**Major capsid protein VP5
23	d1vh3a_	Alignment	not modelled	14.2	26	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
24	c1zijC_	Alignment	not modelled	14.1	57	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
25	c1zijB_	Alignment	not modelled	13.7	57	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
26	d1ou5a2	Alignment	not modelled	13.6	37	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
27	c1piqA_	Alignment	not modelled	13.3	47	**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
28	c2dvwB_	Alignment	not modelled	13.2	56	**PDB header:**cell cycle/protein-binding **Chain:** B: **PDB Molecule:**26s protease regulatory subunit 6b; **PDBTitle:** structure of the oncoprotein gankyrin in complex with s62 atpase of the 26s proteasome

29	c3nicA_	Alignment	not modelled	13.1	44	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**eco29kir; **PDBTitle:** dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
30	c3jycA_	Alignment	not modelled	13.0	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**inward-rectifier k+ channel kir2.2; **PDBTitle:** crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution
31	d1vfga2	Alignment	not modelled	12.8	37	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
32	d2r8ca1	Alignment	not modelled	12.8	25	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
33	c1w5jB_	Alignment	not modelled	12.7	47	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
34	c1w5jD_	Alignment	not modelled	12.7	47	**PDB header:**four helix bundle **Chain:** D: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
35	c1w5jA_	Alignment	not modelled	12.7	47	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
36	c1w5jC_	Alignment	not modelled	12.7	47	**PDB header:**four helix bundle **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
37	c2voyG_	Alignment	not modelled	12.6	38	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
38	d1vi7a2	Alignment	not modelled	11.9	50	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**YigZ C-terminal domain-like
39	c3hriF_	Alignment	not modelled	11.7	20	**PDB header:**ligase **Chain:** F: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase (apo) from trypanosoma brucei
40	d1kmma2	Alignment	not modelled	11.6	22	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
41	c1gclA_	Alignment	not modelled	11.5	47	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
42	c1gcmA_	Alignment	not modelled	11.5	47	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
43	d1bg3a2	Alignment	not modelled	11.3	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
44	c1uo3B_	Alignment	not modelled	11.2	47	**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
45	c1zilA_	Alignment	not modelled	11.2	53	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16gln in the dimeric2 state
46	d1ayra2	Alignment	not modelled	11.2	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
47	c1gclD_	Alignment	not modelled	11.1	47	**PDB header:**leucine zipper **Chain:** D: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
48	c1gclB_	Alignment	not modelled	11.1	47	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
49	c1gclC_	Alignment	not modelled	11.1	47	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
50	c1unuB_	Alignment	not modelled	11.1	47	**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	c1unuA_	Alignment	not modelled	11.1	47	**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
52	c1uo5A_	Alignment	not modelled	11.0	47	**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
53	c1uo5B_	Alignment	not modelled	11.0	47	**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
54	c1unxA_	Alignment	not modelled	11.0	47	**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
55	c1zimA_	Alignment	not modelled	10.9	53	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16gln in the

						trimeric2 state
56	c2ahpB_	Alignment	not modelled	10.8	53	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper, mutation of lys15 to epsilon-azido-lys
57	c1zilB_	Alignment	not modelled	10.8	53	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16gln in the dimeric2 state
58	c1gcmB_	Alignment	not modelled	10.8	47	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
59	d2pt0a1	Alignment	not modelled	10.7	34	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Myo-inositol hexaphosphate phosphohydrolase (phytase) PhyA
60	c1w5iA_	Alignment	not modelled	10.7	47	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** aba does not affect topology of pli.
61	c1uo2A_	Alignment	not modelled	10.7	47	**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
62	c1untA_	Alignment	not modelled	10.7	47	**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
63	c1ld4E_	Alignment	not modelled	10.6	53	**PDB header:**virus **Chain:** E: **PDB Molecule:**general control protein gcn4; **PDBTitle:** placement of the structural proteins in sindbis virus
64	c2ahpA_	Alignment	not modelled	10.6	53	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper, mutation of lys15 to epsilon-azido-lys
65	c3t47A_	Alignment	not modelled	10.5	53	**PDB header:**immune system **Chain:** A: **PDB Molecule:**scin-d; **PDBTitle:** crystal structure of truncated form of staphylococcal complement2 inhibitor d (scin-d) at 1.3 angstrom
66	c1gcmC_	Alignment	not modelled	10.5	47	**PDB header:**transcription regulation **Chain:** C: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
67	c1uo1B_	Alignment	not modelled	10.5	47	**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
68	c1uo1A_	Alignment	not modelled	10.5	47	**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
69	c1zimB_	Alignment	not modelled	10.5	53	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16gln in the trimeric2 state
70	c1zimC_	Alignment	not modelled	10.5	53	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16gln in the trimeric2 state
71	c1unwB_	Alignment	not modelled	10.4	47	**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
72	c1uo0A_	Alignment	not modelled	10.4	47	**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
73	c1uo0B_	Alignment	not modelled	10.4	47	**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
74	c1w5iB_	Alignment	not modelled	10.4	47	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** aba does not affect topology of pli.
75	c1uo2B_	Alignment	not modelled	10.4	47	**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
76	c1untB_	Alignment	not modelled	10.4	47	**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
77	d1ejxc1	Alignment	not modelled	10.4	25	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**alpha-Subunit of urease
78	c3m4wH_	Alignment	not modelled	10.4	100	**PDB header:**signaling protein/signaling protein **Chain:** H: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** structural basis for the negative regulation of bacterial stress2 response by rseb
79	c2hdlA_	Alignment	not modelled	10.3	42	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**small inducible cytokine b14; **PDBTitle:** solution structure of brak/cxcl14
80	c1unyB_	Alignment	not modelled	10.3	47	**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
81	d1tsfa_	Alignment	not modelled	10.2	33	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**RNase P subunit p29-like

82	c3iabA_	Alignment	not modelled	10.2	24	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**ribonucleases p/mrp protein subunit pop6; **PDBTitle:** crystal structure of rnase p /rnase mrp proteins pop6, pop72 in a complex with the p3 domain of rnase mrp rna
83	d1m7ja1	Alignment	not modelled	10.2	16	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**D-aminoacylase
84	d2chha1	Alignment	not modelled	10.1	32	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
85	c1swiC_	Alignment	not modelled	10.1	53	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene
86	c1unxB_	Alignment	not modelled	10.0	47	**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
87	d1miwa2	Alignment	not modelled	10.0	53	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
88	c2ztaA_	Alignment	not modelled	9.9	53	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4 leucine zipper; **PDBTitle:** x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil
89	c2ztaB_	Alignment	not modelled	9.9	53	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**gcn4 leucine zipper; **PDBTitle:** x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil
90	d1r11a3	Alignment	not modelled	9.9	44	**Fold:**MutS N-terminal domain-like **Superfamily:**tRNA-intron endonuclease N-terminal domain-like **Family:**tRNA-intron endonuclease N-terminal domain-like
91	c1u9fA_	Alignment	not modelled	9.8	46	**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)
92	c1ij2A_	Alignment	not modelled	9.8	53	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
93	d1ts9a_	Alignment	not modelled	9.8	36	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**RNase P subunit p29-like
94	c1rb4C_	Alignment	not modelled	9.7	53	**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	d1dl6a_	Alignment	not modelled	9.6	38	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
96	c1swiB_	Alignment	not modelled	9.5	53	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene
97	c1rb1C_	Alignment	not modelled	9.5	53	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
98	c3k7zC_	Alignment	not modelled	9.5	53	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
99	c1p0gA_	Alignment	not modelled	9.5	39	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** structure of antimicrobial peptide, hp (2-20) and its2 analogues derived from helicobacter pylori, as determined3 by 1h nmr spectroscopy