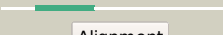
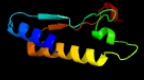





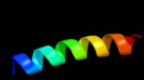


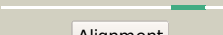

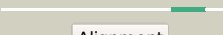


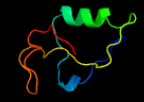


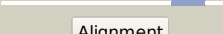





Phyre2

Email	huribertj@winthrop.edu
Description	ASR85454.1_hypothetical_protein_SEA_CAIN_55_[Mycobacterium_phage_Cain]
Date	Mon Jun 7 16:50:02 BST 2021
Unique Job ID	f9dd3da541140801

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xczA_	 Alignment		48.5	28	PDB header: hydrolase Chain: A: PDB Molecule: glucanase; PDBTitle: structure of the cellobiohydrolase cel6a from phanerochaete2 chrysosporium in complex with cellobiose at 2.1 angstrom
2	c1kddC_	 Alignment		44.4	33	PDB header: de novo protein Chain: C: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
3	c1kddF_	 Alignment		44.0	33	PDB header: de novo protein Chain: F: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
4	c1kddA_	 Alignment		44.0	33	PDB header: de novo protein Chain: A: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
5	c1kd9C_	 Alignment		42.1	33	PDB header: de novo protein Chain: C: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
6	c1kd9F_	 Alignment		42.1	33	PDB header: de novo protein Chain: F: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
7	c1kd9A_	 Alignment		42.1	33	PDB header: de novo protein Chain: A: PDB Molecule: gcn4 acid base heterodimer acid-d12la16i; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16i
8	d1tzpa_	 Alignment		32.5	21	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: MepA-like
9	c6nbhP_	 Alignment		29.6	33	PDB header: signaling protein Chain: P: PDB Molecule: long-acting parathyroid hormone analog; PDBTitle: cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein
10	c2wb7B_	 Alignment		28.0	24	PDB header: unknown function Chain: B: PDB Molecule: pt26-6p; PDBTitle: pt26-6p
11	c2n8oA_	 Alignment		21.7	33	PDB header: antimicrobial protein Chain: A: PDB Molecule: bacteriocin aureocin a53; PDBTitle: nmr solution structure of aureocin a53

12	c3f29A_	Alignment		21.7	19	PDB header: oxidoreductase Chain: A; PDB Molecule: eight-heme nitrite reductase; PDBTitle: structure of the thioalkalivibrio nitratireducens cytochrome c nitrite2 reductase in complex with sulfite
13	c1kd8F_	Alignment		20.7	29	PDB header: de novo protein Chain: F; PDB Molecule: gcn4 acid base heterodimer acid-d12ia16v; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
14	c1kd8A_	Alignment		20.7	29	PDB header: de novo protein Chain: A; PDB Molecule: gcn4 acid base heterodimer acid-d12ia16v; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
15	c1kd8C_	Alignment		20.7	29	PDB header: de novo protein Chain: C; PDB Molecule: gcn4 acid base heterodimer acid-d12ia16v; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12ia16l
16	c2yqpA_	Alignment		19.8	47	PDB header: gene regulation, hydrolase Chain: A; PDB Molecule: probable atp-dependent rna helicase ddx59; PDBTitle: solution structure of the zf-hit domain in dead (asp-glu-2 ala-asp) box polypeptide 59
17	c3h3gB_	Alignment		19.7	42	PDB header: membrane protein Chain: B; PDB Molecule: parathyroid hormone-related protein; PDBTitle: crystal structure of the extracellular domain of the human parathyroid2 hormone receptor (pth1r) in complex with parathyroid hormone-related3 protein (pthrp)
18	c3orsD_	Alignment		19.3	23	PDB header: isomerase,biosynthetic protein Chain: D; PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
19	c2ywxA_	Alignment		18.1	30	PDB header: lyase Chain: A; PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
20	d2ewca1	Alignment		15.3	11	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
21	c3wdkA_	Alignment	not modelled	15.1	65	PDB header: ligase Chain: A; PDB Molecule: 4-phosphopantoate--beta-alanine ligase; PDBTitle: crystal structure of 4-phosphopantoate-beta-alanine ligase complexed2 with reaction intermediate
22	c3vohA_	Alignment	not modelled	15.1	26	PDB header: hydrolase Chain: A; PDB Molecule: cellobiohydrolase; PDBTitle: ccel6a catalytic domain complexed with cellobiose
23	c3lp6D_	Alignment	not modelled	15.0	27	PDB header: lyase Chain: D; PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
24	d1o4va_	Alignment	not modelled	14.7	27	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
25	c4kueA_	Alignment	not modelled	14.6	23	PDB header: oxidoreductase Chain: A; PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 clostridium butyricum
26	c3trhl_	Alignment	not modelled	14.5	25	PDB header: lyase Chain: I; PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
27	d3gata_	Alignment	not modelled	13.3	35	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
28	c4kw2A_	Alignment	not modelled	13.2	16	PDB header: isomerase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein

					(bdi_1873)2 from parabacteroides distasonis atcc 8503 at 2.32 a resolution
29	c6qb7A_	Alignment	not modelled	13.0	27 PDB header: signaling protein Chain: A: PDB Molecule: btb/poz domain-containing protein kctd16; PDBTitle: structure of the h1 domain of human kctd16
30	c2kaeA_	Alignment	not modelled	13.0	17 PDB header: transcription/dna Chain: A: PDB Molecule: gata-type transcription factor; PDBTitle: data-driven model of med1:dna complex
31	d1qjwa_	Alignment	not modelled	12.9	26 Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
32	c3couA_	Alignment	not modelled	12.7	41 PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 16; PDBTitle: crystal structure of human nudix motif 16 (nudt16)
33	c2l5gB_	Alignment	not modelled	12.7	33 PDB header: transcription regulator Chain: B: PDB Molecule: putative uncharacterized protein ncor2; PDBTitle: co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
34	c3he5D_	Alignment	not modelled	12.1	38 PDB header: de novo protein Chain: D: PDB Molecule: synzip2; PDBTitle: heterospecific coiled-coil pair synzip2:synzip1
35	c3ffdP_	Alignment	not modelled	12.0	36 PDB header: immune system/hormone Chain: P: PDB Molecule: parathyroid hormone-related protein; PDBTitle: structure of parathyroid hormone-related protein complexed to a2 neutralizing monoclonal antibody
36	c3l3fX_	Alignment	not modelled	11.7	37 PDB header: protein binding Chain: X: PDB Molecule: protein doa1; PDBTitle: crystal structure of a pfu-pul domain pair of saccharomyces cerevisiae2 doa1/ufd3
37	d2fzva1	Alignment	not modelled	11.7	23 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
38	c6o55B_	Alignment	not modelled	11.5	21 PDB header: isomerase Chain: B: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 (pure) from legionella pneumophila
39	d1nc5a_	Alignment	not modelled	11.2	15 Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Hypothetical protein YteR
40	c6n7rl_	Alignment	not modelled	11.1	26 PDB header: rna binding protein Chain: I: PDB Molecule: protein luc7; PDBTitle: saccharomyces cerevisiae spliceosomal e complex (act1)
41	d1gnfa_	Alignment	not modelled	10.8	50 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
42	d1y0ja1	Alignment	not modelled	10.7	50 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
43	c4b4kK_	Alignment	not modelled	10.6	26 PDB header: isomerase Chain: K: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of bacillus anthracis pure
44	c6s9kB_	Alignment	not modelled	10.5	60 PDB header: signaling protein Chain: B: PDB Molecule: caspase-2; PDBTitle: structure of 14-3-3 gamma in complex with caspase-2 peptide containing2 14-3-3 binding motif ser139 and nls
45	c1emzA_	Alignment	not modelled	10.5	78 PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein e1; PDBTitle: solution structure of fragment (350-370) of the2 transmembrane domain of hepatitis c envelope glycoprotein3 e1
46	d2vuti1	Alignment	not modelled	10.5	50 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
47	c4mybA_	Alignment	not modelled	10.5	40 PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of francisella tularensis 2-c-methyl-d-erythritol 4-2 phosphate cytidyltransferase (ispd)
48	d1dota2	Alignment	not modelled	10.2	31 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
49	d5gata_	Alignment	not modelled	10.0	50 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
50	c3p6lA_	Alignment	not modelled	9.8	10 PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
51	d1xmpa_	Alignment	not modelled	9.8	26 Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
52	c7ns4b_	Alignment	not modelled	9.5	13 PDB header: ligase Chain: B: PDB Molecule: PDBTitle: catalytic module of yeast chelator-gid sr4 e3 ubiquitin ligase
53	c3ctvA_	Alignment	not modelled	9.4	20 PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of central domain of 3-hydroxyacyl-coa dehydrogenase2 from archaeoglobus fulgidus PDB header: blood clotting

54	c6r0xE_	Alignment	not modelled	9.3	35	Chain: E: PDB Molecule: megakaryocyte and platelet inhibitory receptor g6b; PDBTitle: the extracellular domain of g6b-b in complex with fab fragment and2 dp12 heparin oligosaccharide.
55	c3cf4A_	Alignment	not modelled	9.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: acetyl-coa decarboxylase/synthase alpha subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex
56	c1r1gB_	Alignment	not modelled	9.1	67	PDB header: toxin Chain: B: PDB Molecule: neurotoxin bmk37; PDBTitle: crystal structure of the scorpion toxin bmbkttx1
57	d1mtyd_	Alignment	not modelled	8.8	24	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
58	d1i52a_	Alignment	not modelled	8.6	58	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
59	c6bv7A_	Alignment	not modelled	8.6	18	PDB header: membrane protein Chain: A: PDB Molecule: sodium/calcium exchanger 1; PDBTitle: nmr structure of sodium/calcium exchanger 1 (ncx1) two-helix bundle2 (thb) domain
60	c4grdA_	Alignment	not modelled	8.6	25	PDB header: lyase, isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
61	c2v4xA_	Alignment	not modelled	8.4	25	PDB header: viral protein Chain: A: PDB Molecule: capsid protein p27; PDBTitle: crystal structure of jaagsiekte sheep retrovirus capsid n-2 terminal domain
62	c6sifG_	Alignment	not modelled	8.3	8	PDB header: structural protein Chain: G: PDB Molecule: epidermicin locus structural protein; PDBTitle: epidermicin antimicrobial protein from staphylococcus epidermidis
63	c2k89A_	Alignment	not modelled	8.3	55	PDB header: protein binding Chain: A: PDB Molecule: phospholipase a-2-activating protein; PDBTitle: solution structure of a novel ubiquitin-binding domain from2 human plaa (pfuc, gly76-pro77 cis isomer)
64	c1r1gA_	Alignment	not modelled	8.2	67	PDB header: toxin Chain: A: PDB Molecule: neurotoxin bmk37; PDBTitle: crystal structure of the scorpion toxin bmbkttx1
65	d1r1ga_	Alignment	not modelled	8.2	67	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
66	d2hq4a1	Alignment	not modelled	8.1	38	Fold: PH1570-like Superfamily: PH1570-like Family: PH1570-like
67	d1u11a_	Alignment	not modelled	7.9	23	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
68	c6m8sM_	Alignment	not modelled	7.9	32	PDB header: signaling protein Chain: M: PDB Molecule: btb/poz domain-containing protein kctd12; PDBTitle: crystal structure of the kctd12 h1 domain in complex with gbeta1gamma22 subunits
69	d2enda_	Alignment	not modelled	7.7	8	Fold: T4 endonuclease V Superfamily: T4 endonuclease V Family: T4 endonuclease V
70	c6mjeF_	Alignment	not modelled	7.6	33	PDB header: cell cycle Chain: F: PDB Molecule: dsn1p; PDBTitle: structure of candida glabrata csm1: s. cerevisiae dsn1 complex
71	c6mjeB_	Alignment	not modelled	7.6	33	PDB header: cell cycle Chain: B: PDB Molecule: dsn1p; PDBTitle: structure of candida glabrata csm1: s. cerevisiae dsn1 complex
72	c6mjeH_	Alignment	not modelled	7.6	33	PDB header: cell cycle Chain: H: PDB Molecule: dsn1p; PDBTitle: structure of candida glabrata csm1: s. cerevisiae dsn1 complex
73	c6mjeD_	Alignment	not modelled	7.6	33	PDB header: cell cycle Chain: D: PDB Molecule: dsn1p; PDBTitle: structure of candida glabrata csm1: s. cerevisiae dsn1 complex
74	d1qcza_	Alignment	not modelled	7.6	25	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
75	c4ky3A_	Alignment	not modelled	7.5	33	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or327; PDBTitle: three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327
76	c1kddD_	Alignment	not modelled	7.5	25	PDB header: de novo protein Chain: D: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
77	c3pstA_	Alignment	not modelled	7.3	32	PDB header: nuclear protein Chain: A: PDB Molecule: protein doa1; PDBTitle: crystal structure of pul and pfu(mutate) domain
78	c2n8pA_	Alignment	not modelled	7.2	17	PDB header: antimicrobial protein Chain: A: PDB Molecule: lactacin q; PDBTitle: solution structure of lactacin q

79	c3n41A_	Alignment	not modelled	7.2	40	PDB header: viral protein Chain: A: PDB Molecule: e3 envelope glycoprotein; PDBTitle: crystal structure of the mature envelope glycoprotein complex2 (spontaneous cleavage) of chikungunya virus.
80	c4r0rA_	Alignment	not modelled	7.2	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: eboizn21; PDBTitle: ebolavirus gp prehairpin intermediate mimic
81	c3rggD_	Alignment	not modelled	7.2	12	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
82	c3iufA_	Alignment	not modelled	7.2	50	PDB header: protein binding Chain: A: PDB Molecule: zinc finger protein ubi-d4; PDBTitle: crystal structure of the c2h2-type zinc finger domain of human ubi-d4
83	c2fw9A_	Alignment	not modelled	7.2	23	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
84	c2i5oA_	Alignment	not modelled	7.2	41	PDB header: transferase Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: solution structure of the ubiquitin-binding zinc finger2 (ubz) domain of the human dna y-polymerase eta
85	d2uube2	Alignment	not modelled	7.2	33	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
86	d1mhyd_	Alignment	not modelled	7.0	21	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
87	c4zbzA_	Alignment	not modelled	7.0	17	PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: family 4 uracil-dna glycosylase from sulfolobus tokodaii (free form,2 x-ray wavelength=1.5418)
88	c1p6gE_	Alignment	not modelled	7.0	50	PDB header: ribosome Chain: E: PDB Molecule: 30s ribosomal protein s5; PDBTitle: real space refined coordinates of the 30s subunit fitted into the low2 resolution cryo-em map of the ef-g.gtp state of e. coli 70s ribosome
89	d1pkpa2	Alignment	not modelled	6.8	50	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
90	c5ym0A_	Alignment	not modelled	6.8	32	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the crystal structure of dhad
91	c1kd8E_	Alignment	not modelled	6.7	25	PDB header: de novo protein Chain: E: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16v base-d12la16l
92	c1kddE_	Alignment	not modelled	6.7	25	PDB header: de novo protein Chain: E: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
93	c1kd9D_	Alignment	not modelled	6.7	25	PDB header: de novo protein Chain: D: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
94	c1kd9E_	Alignment	not modelled	6.7	25	PDB header: de novo protein Chain: E: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
95	d1r7aa1	Alignment	not modelled	6.7	75	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
96	c4b4fB_	Alignment	not modelled	6.6	30	PDB header: hydrolase Chain: B: PDB Molecule: beta-1,4-exocellulase; PDBTitle: thermobifida fusca cel6b(e3) co-crystallized with cellobiose
97	c1kd8B_	Alignment	not modelled	6.6	25	PDB header: de novo protein Chain: B: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16v base-d12la16l
98	c1kd8D_	Alignment	not modelled	6.6	25	PDB header: de novo protein Chain: D: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16v base-d12la16l
99	c1kddB_	Alignment	not modelled	6.6	25	PDB header: de novo protein Chain: B: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l