






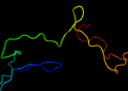



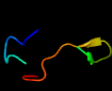

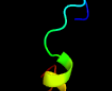

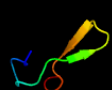

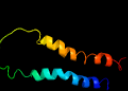



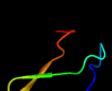

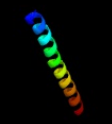
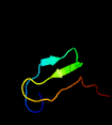
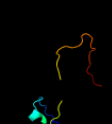
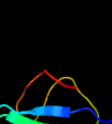
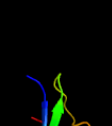
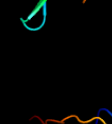




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3843c_(-)_4315746_4316774
Date	Sat Aug 10 22:05:02 BST 2019
Unique Job ID	52945d06adc34148

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kdxA_	 Alignment		54.2	17	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
2	c1fftG_	 Alignment		51.3	11	PDB header: oxidoreductase Chain: G: PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli
3	d2gmga1	 Alignment		41.3	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF0610-like
4	c4nl6C_	 Alignment		41.2	12	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
5	d1ee8a3	 Alignment		40.4	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
6	d1k3xa3	 Alignment		38.5	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
7	d2fiya1	 Alignment		36.5	39	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
8	d1tdza3	 Alignment		35.7	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
9	d1fftb2	 Alignment		30.8	6	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
10	d1l1ta3	 Alignment		30.3	42	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
11	d1r2za3	 Alignment		30.1	42	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins

12	d1k82a3	Alignment		29.9	29	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
13	c6agfB	Alignment		26.0	14	PDB header: membrane protein Chain: B: PDB Molecule: sodium channel subunit beta-1; PDBTitle: structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1
14	c2gb5B	Alignment		25.3	23	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
15	c5zb8B	Alignment		23.5	30	PDB header: dna binding protein Chain: B: PDB Molecule: pfuendoq; PDBTitle: crystal structure of the novel lesion-specific endonuclease pfuendoq2 from pyrococcus furiosus
16	c6ok1B	Alignment		23.3	36	PDB header: transport protein Chain: B: PDB Molecule: chsh2(duf35); PDBTitle: ltp2-chsh2(duf35) aldolase
17	c5mg5W	Alignment		23.1	18	PDB header: transferase Chain: W: PDB Molecule: 2,4-diacetylphloroglucinol biosynthesis protein; PDBTitle: a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (mapg)
18	c3cngC	Alignment		21.4	31	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
19	c4rkuL	Alignment		20.7	29	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: crystal structure of plant photosystem i at 3 angstrom resolution
20	d2gnra1	Alignment		20.3	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: SSO2064-like
21	c3a44D	Alignment	not modelled	20.2	22	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
22	c4y28I	Alignment	not modelled	18.3	29	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: the structure of plant photosystem i super-complex at 2.8 angstrom2 resolution.
23	d2e74d2	Alignment	not modelled	17.1	28	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
24	d1zfoa	Alignment	not modelled	16.7	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LASP-1
25	c2mvwA	Alignment	not modelled	14.3	41	PDB header: metal binding protein Chain: A: PDB Molecule: protein pml; PDBTitle: solution structure of the trim19 b-box1 (b1) of human promyelocytic2 leukemia (pml)
26	c4xk8I	Alignment	not modelled	14.2	24	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: crystal structure of plant photosystem i-lhci super-complex at 2.82 angstrom resolution
27	c4xk8i	Alignment	not modelled	14.1	24	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: crystal structure of plant photosystem i-lhci super-complex at 2.82 angstrom resolution
28	c6et9H	Alignment	not modelled	13.7	38	PDB header: transferase Chain: H: PDB Molecule: pfam duf35; PDBTitle: structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a

29	c5l8rl	Alignment	not modelled	13.6	24	PDB header: oxidoreductase Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: the structure of plant photosystem i super-complex at 2.6 angstrom2 resolution.
30	c2o01l	Alignment	not modelled	12.7	29	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
31	c6ijoL	Alignment	not modelled	12.5	18	PDB header: photosynthesis Chain: I: PDB Molecule: psai; PDBTitle: photosystem i of chlamydomonas reinhardtii
32	c5zjil	Alignment	not modelled	12.1	24	PDB header: membrane protein Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: structure of photosystem i supercomplex with light-harvesting2 complexes i and ii
33	c6igzl	Alignment	not modelled	11.9	14	PDB header: plant protein Chain: I: PDB Molecule: psai; PDBTitle: structure of psi-lhci
34	c2micA	Alignment	not modelled	11.9	29	PDB header: membrane protein Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
35	c2micB	Alignment	not modelled	11.9	29	PDB header: membrane protein Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
36	c2pziA	Alignment	not modelled	11.7	24	PDB header: transferase Chain: A: PDB Molecule: probable serine/threonine-protein kinase pkng; PDBTitle: crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
37	d1libia1	Alignment	not modelled	11.6	31	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
38	c5iy9Q	Alignment	not modelled	11.6	19	PDB header: transcription, transferase/dna/rna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the initial transcribing state (no iis)
39	c2yevB	Alignment	not modelled	11.3	11	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of caa3-type cytochrome oxidase
40	d1x6ha1	Alignment	not modelled	11.1	83	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
41	c2i5oA	Alignment	not modelled	10.8	31	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 gamma-polymerase eta
42	c3chxG	Alignment	not modelled	10.7	10	PDB header: membrane protein Chain: G: PDB Molecule: pmoc; PDBTitle: crystal structure of methylosinus trichosporium ob3b particulate2 methane monooxygenase (pmmo)
43	c1g5jB	Alignment	not modelled	10.2	41	PDB header: apoptosis Chain: B: PDB Molecule: bad protein; PDBTitle: complex of bcl-xl with peptide from bad
44	c6o3pA	Alignment	not modelled	9.6	39	PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
45	c1iflA	Alignment	not modelled	9.6	13	PDB header: virus Chain: A: PDB Molecule: inovirus; PDBTitle: molecular models and structural comparisons of native and2 mutant class i filamentous bacteriophages ff (fd, f1, m13),3 if1 and ike
46	c6jo5l	Alignment	not modelled	9.3	14	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: structure of the green algal photosystem i supercomplex with light-2 harvesting complex i
47	c1yewC	Alignment	not modelled	9.2	11	PDB header: oxidoreductase, membrane protein Chain: C: PDB Molecule: particulate methane monooxygenase subunit c2; PDBTitle: crystal structure of particulate methane monooxygenase
48	c2pptA	Alignment	not modelled	9.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2
49	c2lvuA	Alignment	not modelled	8.7	50	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 10
50	c4u3eA	Alignment	not modelled	8.5	29	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
51	c6hmsB	Alignment	not modelled	8.2	29	PDB header: replication Chain: B: PDB Molecule: dna polymerase ii large subunit,dna polymerase ii large PDBTitle: cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
52	c2ki9A	Alignment	not modelled	8.1	31	PDB header: membrane protein Chain: A: PDB Molecule: cannabinoid receptor 2; PDBTitle: human cannabinoid receptor-2 helix 6
53	c5lnku	Alignment	not modelled	8.0	38	PDB header: oxidoreductase Chain: U: PDB Molecule: PDBTitle: entire ovine respiratory complex i

54	c2bzwB_	Alignment	not modelled	8.0	41	PDB header: transcription Chain: B: PDB Molecule: bcl2-antagonist of cell death; PDBTitle: the crystal structure of bcl-xl in complex with full-length bad
55	c5oqmW_	Alignment	not modelled	7.8	32	PDB header: transcription Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
56	c6hwhB_	Alignment	not modelled	7.7	7	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
57	c3j1rE_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: E: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
58	c3j1rU_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: U: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
59	c3j1rJ_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: J: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
60	c3j1rH_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: H: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
61	c3j1rT_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: T: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
62	c3j1rO_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: O: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
63	c3j1rF_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: F: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
64	c3j1rK_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: K: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
65	c3j1rN_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: N: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
66	c3j1rA_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: A: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
67	c3j1rL_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: L: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
68	c3j1rI_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: I: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
69	c3j1rQ_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: Q: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
70	c3j1rS_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: S: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
71	c3j1rC_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: C: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
72	c3j1rP_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: P: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
73	c3j1rM_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: M: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
74	c3j1rR_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: R: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
75	c3j1rB_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: B: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
76	c3j1rD_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: D: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
77	c3j1rG_	Alignment	not modelled	7.6	36	PDB header: cell adhesion, structural protein Chain: G: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
78	c6hwhL_	Alignment	not modelled	7.5	10	PDB header: electron transport Chain: L: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
						PDB header: oxidoreductase/immune system Chain: B: PDB Molecule: cytochrome c oxidase polypeptide ii:

79	c1qleB_	Alignment	not modelled	7.5	15	PDBTitle: cryo-structure of the paracoccus denitrificans four-subunit cytochrome2 c oxidase in the completely oxidized state complexed with an antibody3 fv fragment PDB header: complex (oxidoreductase/antibody) Chain: B: PDB Molecule: cytochrome c oxidase; PDBTitle: structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
80	c1ar1B_	Alignment	not modelled	7.5	15	PDB header: viral protein/rna Chain: M: PDB Molecule: maturation protein; PDBTitle: in situ structures of the genome and genome-delivery apparatus in2 ssrna bacteriophage ms2
81	c5tc1M_	Alignment	not modelled	7.5	26	PDB header: transport protein/inhibitor Chain: A: PDB Molecule: m2 protein, bm2 protein chimera; PDBTitle: structure of the influenza am2-bm2 chimeric channel bound to2 rimantadine
82	c2ljcA_	Alignment	not modelled	7.1	28	PDB header: virus Chain: P: PDB Molecule: protein p16; PDBTitle: structural analysis of prd1
83	c1w8xP_	Alignment	not modelled	7.0	14	PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
84	c2kluA_	Alignment	not modelled	6.9	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: TxnI5-like
85	d1v9wa_	Alignment	not modelled	6.9	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
86	d1bboa1	Alignment	not modelled	6.7	33	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
87	c2d3hF_	Alignment	not modelled	6.6	30	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: crystal structure of the bacterial nss member mhst in an2 occluded inward-facing state
88	c4us3A_	Alignment	not modelled	6.6	13	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
89	c5ijlA_	Alignment	not modelled	6.5	26	PDB header: membrane protein Chain: A: PDB Molecule: merf; PDBTitle: structure of merft, a membrane protein with two trans-2 membrane helices
90	c2h3oA_	Alignment	not modelled	6.4	32	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
91	d1ma3a_	Alignment	not modelled	6.4	18	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccdist)
92	c6gymW_	Alignment	not modelled	6.2	32	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
93	c3a19F_	Alignment	not modelled	6.2	30	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
94	c3a08D_	Alignment	not modelled	6.2	30	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
95	c2d3hD_	Alignment	not modelled	6.2	30	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
96	d1ubdc2	Alignment	not modelled	6.1	50	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
97	d1m2ka_	Alignment	not modelled	6.0	24	PDB header: hydrolase inhibitor/hydrolase Chain: E: PDB Molecule: hnh endonuclease family protein; PDBTitle: fnobh+acriic2
98	c6j9lE_	Alignment	not modelled	5.9	50	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of zitp zinc finger
99	c2nb9A_	Alignment	not modelled	5.9	23	