

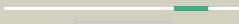
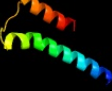



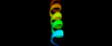

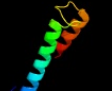

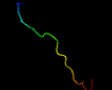














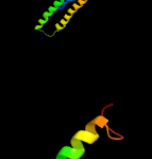
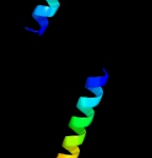

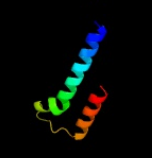
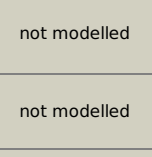


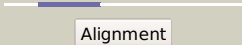
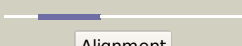




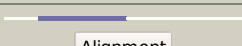
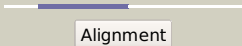

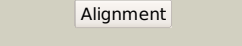
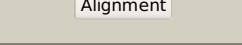
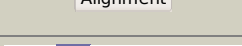
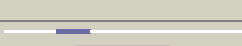
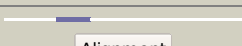



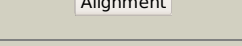





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2723_(-)_3034919_3036112
Date	Wed Aug 7 12:50:37 BST 2019
Unique Job ID	0c4a4686d3cde8bc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5fmnB_	 Alignment		47.3	17	PDB header: dna binding protein Chain: B: PDB Molecule: inrs; PDBTitle: the nickel-responsive transcriptional regulator inrs
2	c5lbnD_	 Alignment		41.1	23	PDB header: transcription Chain: D: PDB Molecule: transcriptional repressor frmr; PDBTitle: the asymmetric tetrameric structure of the formaldehyde sensing2 transcriptional repressor frmr from escherichia coli
3	c4m1pA_	 Alignment		40.1	17	PDB header: transcription repressor Chain: A: PDB Molecule: copper-sensitive operon repressor (csor); PDBTitle: crystal structure of the copper-sensing repressor csor with cu(i) from2 geobacillus thermodenitrificans ng80-2
4	c6e8wC_	 Alignment		39.1	19	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein gp160; PDBTitle: mper-tm domain of hiv-1 envelope glycoprotein (env)
5	c5lcyD_	 Alignment		37.3	17	PDB header: transcription Chain: D: PDB Molecule: frmr; PDBTitle: formaldehyde-responsive regulator frmr e64h variant from salmonella2 enterica serovar typhimurium
6	c2f49C_	 Alignment		32.5	47	PDB header: transferase Chain: C: PDB Molecule: ste5 peptide; PDBTitle: crystal structure of fus3 in complex with a ste5 peptide
7	c5yc0Q_	 Alignment		25.4	21	PDB header: viral protein/inhibitor Chain: Q: PDB Molecule: lp-46; PDBTitle: crystal structure of lp-46/n44
8	c5yc0W_	 Alignment		25.4	21	PDB header: viral protein/inhibitor Chain: W: PDB Molecule: lp-46; PDBTitle: crystal structure of lp-46/n44
9	c5yc0I_	 Alignment		25.4	21	PDB header: viral protein/inhibitor Chain: I: PDB Molecule: lp-46; PDBTitle: crystal structure of lp-46/n44
10	c5yc0P_	 Alignment		24.3	21	PDB header: viral protein/inhibitor Chain: P: PDB Molecule: lp-46; PDBTitle: crystal structure of lp-46/n44
11	c5yc0G_	 Alignment		24.3	21	PDB header: viral protein/inhibitor Chain: G: PDB Molecule: lp-46; PDBTitle: crystal structure of lp-46/n44

12	c2sivD_	Alignment		21.3	21	PDB header: envelope glycoprotein Chain: D: PDB Molecule: siv gp41 glycoprotein; PDBTitle: siv gp41 core structure
13	c5yqrA_	Alignment		19.7	26	PDB header: transport protein Chain: A: PDB Molecule: endolysin/membrane-anchored lipid-binding protein lam6 PDBTitle: crystal structure of the ph-like domain of lam6
14	c6btmD_	Alignment		19.6	15	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
15	c5jr0A_	Alignment		17.7	23	PDB header: metal binding protein Chain: A: PDB Molecule: sodium channel protein type 4 subunit alpha; PDBTitle: domain 4 segment 6 of voltage-gated sodium channel nav1.4
16	c2bg9B_	Alignment		17.6	16	PDB header: ion channel/receptor Chain: B: PDB Molecule: acetylcholine receptor protein, beta chain; PDBTitle: refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
17	c1yewI_	Alignment		17.4	9	PDB header: oxidoreductase, membrane protein Chain: I: PDB Molecule: particulate methane monooxygenase, b subunit; PDBTitle: crystal structure of particulate methane monooxygenase
18	c3rgbA_	Alignment		17.4	9	PDB header: oxidoreductase Chain: A: PDB Molecule: methane monooxygenase subunit b2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
19	c6dmoA_	Alignment		17.4	11	PDB header: protein binding Chain: A: PDB Molecule: protein patched homolog 1; PDBTitle: cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l
20	c4adzA_	Alignment		16.7	20	PDB header: transcription Chain: A: PDB Molecule: csor; PDBTitle: crystal structure of the apo form of a copper-sensitive operon2 regulator (csor) protein from streptomyces lividans
21	c3h00A_	Alignment	not modelled	16.0	25	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein gp160; PDBTitle: structure of the c-terminal domain of a putative hiv-1 gp41 fusion2 intermediate
22	c5yc0H_	Alignment	not modelled	14.8	17	PDB header: viral protein/inhibitor Chain: H: PDB Molecule: lp-46; PDBTitle: crystal structure of lp-46/n44
23	c2vl0A_	Alignment	not modelled	14.3	13	PDB header: membrane protein Chain: A: PDB Molecule: elic pentameric ligand gated ion channel from PDBTitle: x-ray structure of a pentameric ligand gated ion channel2 from erwinia chrysanthemi (elic)
24	c4qidB_	Alignment	not modelled	14.1	10	PDB header: membrane protein Chain: B: PDB Molecule: bacteriorhodopsin-i; PDBTitle: crystal structure of haloquadratum walsbyi bacteriorhodopsin
25	c5wdaL_	Alignment	not modelled	13.9	19	PDB header: protein transport Chain: L: PDB Molecule: general secretion pathway protein g; PDBTitle: structure of the pulg pseudopilus
26	c3u3iA_	Alignment	not modelled	13.4	23	PDB header: rna binding protein Chain: A: PDB Molecule: nucleocapsid protein; PDBTitle: a rna binding protein from crimean-congo hemorrhagic fever virus
27	c6ckoC_	Alignment	not modelled	13.2	22	PDB header: dna binding protein/transferase Chain: C: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-79 specific; PDBTitle: crystal structure of an af10 fragment
28	c6ckoD_	Alignment	not modelled	13.2	22	PDB header: dna binding protein/transferase Chain: D: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-79 specific; PDBTitle: crystal structure of an af10 fragment

29	c6nr2A_		Alignment	not modelled	12.8	22	PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
30	c6nr2C_		Alignment	not modelled	12.8	22	PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
31	c6nr2B_		Alignment	not modelled	12.8	22	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
32	c6nr2D_		Alignment	not modelled	12.8	22	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
33	c3k07A_		Alignment	not modelled	12.5	14	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
34	c4aq5B_		Alignment	not modelled	12.4	16	PDB header: membrane protein Chain: B: PDB Molecule: acetylcholine receptor beta subunit; PDBTitle: gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
35	c3wt9A_		Alignment	not modelled	11.9	15	PDB header: proton transport Chain: A: PDB Molecule: rhodopsin i; PDBTitle: crystal structure of the cell-free synthesized membrane protein,2 acetabularia rhodopsin i, at 1.48 angstrom
36	d1h2sa_		Alignment	not modelled	11.8	17	Fold: Family A G protein-coupled receptor-like Superfamily: Family A G protein-coupled receptor-like Family: Bacteriorhodopsin-like
37	c4pj0L_		Alignment	not modelled	11.6	22	PDB header: oxidoreductase, electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
38	c4pj0I_		Alignment	not modelled	11.6	22	PDB header: oxidoreductase, electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
39	c4ub6I_		Alignment	not modelled	11.4	22	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
40	c5e7cl_		Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: macromolecular diffractive imaging using imperfect crystals - bragg2 data
41	c4ixql_		Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt fs x-ray diffraction of photosystem ii, dark state
42	c4fbyd_		Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: D: PDB Molecule: photosystem ii d2 protein; PDBTitle: fs x-ray diffraction of photosystem ii
43	c3bz2L_		Alignment	not modelled	11.4	22	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 2 of 2). this2 file contains second monomer of psii dimer
44	c4ub8I_		Alignment	not modelled	11.4	22	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
45	c1s5lL_		Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
46	c4fbyL_		Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: fs x-ray diffraction of photosystem ii
47	c4tnil_		Alignment	not modelled	11.4	22	PDB header: electron transport,photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution
48	c4il6I_		Alignment	not modelled	11.4	22	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: structure of sr-substituted photosystem ii
49	c2axtl_		Alignment	not modelled	11.4	22	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
50	c4rvyl_		Alignment	not modelled	11.4	22	PDB header: oxidoreductase Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: serial time resolved crystallography of photosystem ii using a2 femtosecond x-ray laser. the s state after two flashes (s3)
51	c4rvyl_		Alignment	not modelled	11.4	22	PDB header: oxidoreductase Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: serial time resolved crystallography of photosystem ii using a2 femtosecond x-ray laser. the s state after two flashes (s3)
52	c4tnhl_		Alignment	not modelled	11.4	22	PDB header: electron transport,photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
53	c3prql_		Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer

54	c5e7cL_	Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: macromolecular diffractive imaging using imperfect crystals - bragg2 data
55	c3kziL_	Alignment	not modelled	11.4	22	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of monomeric form of cyanobacterial photosystem ii
56	c3arcL_	Alignment	not modelled	11.4	22	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
57	c3bz1L_	Alignment	not modelled	11.4	22	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 1 of 2). this2 file contains first monomer of psii dimer
58	c4ixrL_	Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt fs x-ray diffraction of photosystem ii, first illuminated state
59	c2axtL_	Alignment	not modelled	11.4	22	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
60	d2axt1	Alignment	not modelled	11.4	22	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein L, PsbL Family: PsbL-like
61	c4tnkL_	Alignment	not modelled	11.4	22	PDB header: electron transport,photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution
62	c4ixqL_	Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt fs x-ray diffraction of photosystem ii, dark state
63	c4tnil_	Alignment	not modelled	11.4	22	PDB header: electron transport,photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution
64	c4il6L_	Alignment	not modelled	11.4	22	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: structure of sr-substituted photosystem ii
65	c3prrL_	Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
66	c4ub8L_	Alignment	not modelled	11.4	22	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
67	c3wu2L_	Alignment	not modelled	11.4	22	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure analysis of photosystem ii complex
68	c4ub6L_	Alignment	not modelled	11.4	22	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
69	c4tnjL_	Alignment	not modelled	11.4	22	PDB header: electron transport,photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
70	c4ixrL_	Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt fs x-ray diffraction of photosystem ii, first illuminated state
71	c1s5ll_	Alignment	not modelled	11.4	22	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
72	c3wu2L_	Alignment	not modelled	11.4	22	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure analysis of photosystem ii complex
73	c4tnhl_	Alignment	not modelled	11.4	22	PDB header: electron transport,photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
74	c4tnkL_	Alignment	not modelled	11.4	22	PDB header: electron transport,photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution
75	c4tnjl_	Alignment	not modelled	11.4	22	PDB header: electron transport,photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
76	c3a0hL_	Alignment	not modelled	10.9	22	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
77	c3a0hl_	Alignment	not modelled	10.9	22	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
78	c3a0bl_	Alignment	not modelled	10.9	22	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of br-substituted photosystem ii complex
79	c2hh7A_	Alignment	not modelled	10.4	9	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein csor; PDBTitle: crystal structure of cu(i) bound csor from mycobacterium tuberculosis. PDB header: photoreceptor

80	c1bhbA_	Alignment	not modelled	10.2	34	Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: three-dimensional structure of (1-71) bacterioopsin2 solubilized in methanol-chloroform and sds micelles3 determined by 15n-1h heteronuclear nmr spectroscopy
81	c6nr3A_	Alignment	not modelled	10.0	22	PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium
82	c6nr3D_	Alignment	not modelled	10.0	22	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium
83	c6nr3B_	Alignment	not modelled	10.0	22	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium
84	c6nr3C_	Alignment	not modelled	10.0	22	PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium
85	c6mq2D_	Alignment	not modelled	9.9	23	PDB header: de novo protein Chain: D: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
86	d1ix1a_	Alignment	not modelled	9.9	13	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
87	d1xeoa1	Alignment	not modelled	9.7	16	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
88	c2lowA_	Alignment	not modelled	9.4	6	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip
89	c6d73B_	Alignment	not modelled	9.3	17	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel, subfamily m; PDBTitle: cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+
90	c3a0bL_	Alignment	not modelled	9.3	22	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein l; PDBTitle: crystal structure of br-substituted photosystem ii complex
91	c6owsB_	Alignment	not modelled	9.2	19	PDB header: membrane protein Chain: B: PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
92	d1r89a1	Alignment	not modelled	9.1	35	Fold: PAP/OAS1 substrate-binding domain Superfamily: PAP/OAS1 substrate-binding domain Family: Archaeal tRNA CCA-adding enzyme substrate-binding domain
93	c6drkD_	Alignment	not modelled	9.0	15	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel, subfamily m, PDBTitle: structure of trpm2 ion channel receptor by single particle electron2 cryo-microscopy, apo state
94	c2m4eA_	Alignment	not modelled	9.0	25	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution nmr structure of vv2_0175 from vibrio vulnificus, nesg target2 vnr1 and csqid target idp91333
95	c3vieF_	Alignment	not modelled	8.8	33	PDB header: viral protein/antiviral protein Chain: F: PDB Molecule: sifuvirtide; PDBTitle: hiv-gp41 fusion inhibitor sifuvirtide
96	c3h87D_	Alignment	not modelled	8.7	38	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
97	c4wxlB_	Alignment	not modelled	8.6	14	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of a peptide deformylase from haemophilus influenzae2 complex with actinonin
98	c3jcul_	Alignment	not modelled	8.5	15	PDB header: membrane protein Chain: L: PDB Molecule: protein photosystem ii reaction center protein l; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
99	c1aikC_	Alignment	not modelled	8.2	27	PDB header: viral protein Chain: C: PDB Molecule: hiv-1 gp41 glycoprotein; PDBTitle: hiv gp41 core structure