



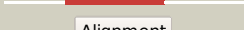

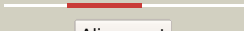
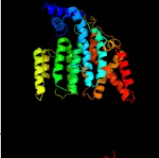
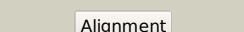

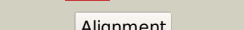

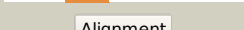

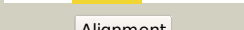


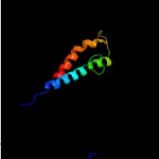

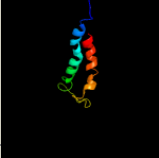

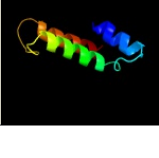
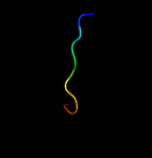
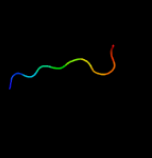
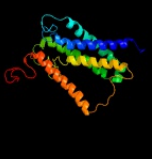
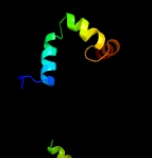

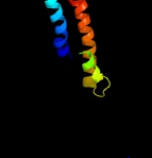
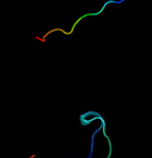
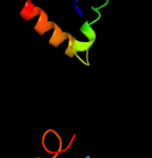



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3793_(embC)_4240041_4243325
Date	Fri Aug 9 18:20:50 BST 2019
Unique Job ID	c0665ccb099601df

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ptyA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: arabinosyltransferase c; PDBTitle: crystal structure of the c-terminal extracellular domain of2 mycobacterium tuberculosis embc
2	c3bywB_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: putative arabinofuranosyltransferase; PDBTitle: crystal structure of the c-terminal extracellular domain of2 arabinofuranosyltransferase from corynebacterium diphtheriae
3	c5f15A_	 Alignment		99.2	13	PDB header: transferase Chain: A: PDB Molecule: 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; PDBTitle: crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate
4	c3rceA_	 Alignment		98.6	14	PDB header: transferase/peptide Chain: A: PDB Molecule: oligosaccharide transferase to n-glycosylate proteins; PDBTitle: bacterial oligosaccharyltransferase pglb
5	c3wajA_	 Alignment		97.5	13	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
6	c6p2rB_	 Alignment		93.4	14	PDB header: transferase Chain: B: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 2; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
7	c6p25A_	 Alignment		89.0	12	PDB header: transferase Chain: A: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 1; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
8	c6eznF_	 Alignment		76.1	10	PDB header: membrane protein Chain: F: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
9	c6btmD_	 Alignment		74.3	19	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
10	c6f0kD_	 Alignment		53.6	17	PDB header: membrane protein Chain: D: PDB Molecule: actd; PDBTitle: alternative complex iii
11	c2lopA_	 Alignment		46.2	5	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane protein 14a; PDBTitle: backbone structure of human membrane protein tmem14a

12	c4rrfD_	Alignment		38.7	55	PDB header: ligase Chain: D: PDB Molecule: threonine--trna ligase; PDBTitle: editing domain of threonyl-trna synthetase from methanococcus2 jannaschii with l-ser3aa
13	c2hl2A_	Alignment		37.0	55	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
14	c6iedA_	Alignment		35.5	13	PDB header: membrane protein Chain: A: PDB Molecule: heme a synthase; PDBTitle: crystal structure of heme a synthase from bacillus subtilis
15	c5zr1F_	Alignment		34.4	24	PDB header: dna binding protein/dna Chain: F: PDB Molecule: origin recognition complex subunit 6; PDBTitle: saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
16	c3jd8A_	Alignment		33.5	25	PDB header: membrane protein Chain: A: PDB Molecule: niemann-pick c1 protein; PDBTitle: cryo-em structure of the full-length human npc1 at 4.4 angstrom
17	c5khnB_	Alignment		32.7	20	PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
18	c4rrcA_	Alignment		31.9	55	PDB header: ligase Chain: A: PDB Molecule: probable threonine--trna ligase 2; PDBTitle: n-terminal editing domain of threonyl-trna synthetase from aeropyrum2 pernix with l-thr3aa (snapshot 3)
19	c4rlrA_	Alignment		31.8	29	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c, 1 heme-binding site; PDBTitle: structure of monoheme cytochrome pcch from geobacter sulfurreducens
20	c5x5iC_	Alignment		29.6	17	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator rcda; PDBTitle: the x-ray crystal structure of a tetr family transcription regulator2 rcda involved in the regulation of biofilm formation in escherichia3 coli
21	c2m20B_	Alignment	not modelled	29.5	26	PDB header: signaling protein Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
22	c2mc7A_	Alignment	not modelled	27.6	44	PDB header: membrane protein Chain: A: PDB Molecule: regulatory peptide; PDBTitle: structure of salmonella mgtr
23	d1gmnb1	Alignment	not modelled	23.1	40	Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Hairpin loop containing domain
24	c6dmoA_	Alignment	not modelled	23.0	13	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
25	c6ajjA_	Alignment	not modelled	22.8	14	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
26	c2losA_	Alignment	not modelled	21.3	10	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane protein 14c; PDBTitle: backbone structure of human membrane protein tmem14c
27	d3cx5c1	Alignment	not modelled	19.7	25	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
						Fold: Ferredoxin-like

28	d1rwua_	Alignment	not modelled	19.7	33	Superfamily: YbeD/HP0495-like Family: YbeD-like
29	c1rwuA_	Alignment	not modelled	19.7	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0250 protein ybed; PDBTitle: solution structure of conserved protein ybed from e. coli
30	d1rc2a_	Alignment	not modelled	19.1	18	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
31	c5v2dA_	Alignment	not modelled	18.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dioxygenase; PDBTitle: crystal structure of pseudomonas brassicacearum lignostilbene2 dioxygenase
32	c1emzA_	Alignment	not modelled	18.0	67	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
33	c5ovyA_	Alignment	not modelled	17.7	24	PDB header: dna binding protein Chain: A: PDB Molecule: putative transcriptional regulator, tetr family; PDBTitle: crystal structure of mab_4384 tetr
34	c4nhyC_	Alignment	not modelled	17.0	22	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: C: PDB Molecule: 2-oxoglutarate and iron-dependent oxygenase domain- PDBTitle: crystal structure of human ogfod1, 2-oxoglutarate and iron-dependent2 oxygenase domain containing 1, in complex with pyridine-2,4-3 dicarboxylic acid (2,4-pdca)
35	c6cfwE_	Alignment	not modelled	16.8	12	PDB header: membrane protein Chain: E: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
36	d1ppc1_	Alignment	not modelled	16.6	13	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
37	c5j54A_	Alignment	not modelled	16.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: carotenoid oxygenase; PDBTitle: the structure and mechanism of nov1, a resveratrol-cleaving2 dioxygenase
38	c2n2aA_	Alignment	not modelled	16.3	17	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: spatial structure of her2/erbB2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
39	c3zqiB_	Alignment	not modelled	15.8	14	PDB header: transcription Chain: B: PDB Molecule: tetracycline repressor protein class b from transposon PDBTitle: structure of tetracycline repressor in complex with inducer peptide-2 tip2
40	c5u90A_	Alignment	not modelled	15.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: carotenoid oxygenase 1; PDBTitle: crystal structure of co-cao1 in complex with resveratrol
41	c1hymB_	Alignment	not modelled	14.9	32	PDB header: hydrolase (serine proteinase) Chain: B: PDB Molecule: hydrolyzed cucurbita maxima trypsin inhibitor v; PDBTitle: hydrolyzed trypsin inhibitor (cmti-v, minimized average nmr structure)
42	c6ithA_	Alignment	not modelled	14.9	35	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
43	c2h31A_	Alignment	not modelled	14.1	15	PDB header: ligase, lyase Chain: A: PDB Molecule: multifunctional protein ade2; PDBTitle: crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
44	c2y0nE_	Alignment	not modelled	13.9	50	PDB header: transcription Chain: E: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and msl3
45	c1t0jA_	Alignment	not modelled	13.4	4	PDB header: signaling protein Chain: A: PDB Molecule: voltage-gated calcium channel subunit beta2a; PDBTitle: crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
46	c2y0nG_	Alignment	not modelled	13.4	63	PDB header: transcription Chain: G: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and msl3
47	c2y0nH_	Alignment	not modelled	13.4	63	PDB header: transcription Chain: H: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and msl3
48	c3fsnA_	Alignment	not modelled	12.4	36	PDB header: isomerase Chain: A: PDB Molecule: retinal pigment epithelium-specific 65 kda protein; PDBTitle: crystal structure of rpe65 at 2.14 angstrom resolution
49	d1fpoa1_	Alignment	not modelled	12.3	33	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
50	d1bdsa_	Alignment	not modelled	12.2	45	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
51	c1bdsA_	Alignment	not modelled	12.2	45	PDB header: anti-hypertensive, anti-viral protein Chain: A: PDB Molecule: bds-i; PDBTitle: determination of the three-dimensional solution structure of the2 antihypertensive and antiviral protein bds-i from the sea anemone3 anemone sulcata. a study using nuclear magnetic resonance and hybrid4 distance geometry-dynamical simulated

						annealing
52	c1w8jD_	Alignment	not modelled	12.2	21	PDB header: motor protein Chain: D: PDB Molecule: myosin va; PDBTitle: crystal structure of myosin v motor domain -2 nucleotide-free
53	d1iyb3	Alignment	not modelled	11.8	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
54	c1ldaA_	Alignment	not modelled	11.5	18	PDB header: transport protein Chain: A: PDB Molecule: glycerol uptake facilitator protein; PDBTitle: crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
55	d1fx8a_	Alignment	not modelled	11.5	18	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
56	c4rfuB_	Alignment	not modelled	11.5	22	PDB header: viral protein Chain: B: PDB Molecule: coat protein; PDBTitle: crystal structure of truncated p-domain from grouper nervous necrosis2 virus capsid protein at 1.2a
57	c2pptA_	Alignment	not modelled	11.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2
58	c5wcoC_	Alignment	not modelled	11.3	57	PDB header: viral protein Chain: C: PDB Molecule: ns2; PDBTitle: matrix protein (m1) of infectious salmon anaemia virus
59	d1y0ja1	Alignment	not modelled	11.3	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
60	d2do3a1	Alignment	not modelled	11.2	17	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
61	d2ie1a1	Alignment	not modelled	11.0	27	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
62	c4s21B_	Alignment	not modelled	11.0	36	PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome (light-regulated signal transduction PDBTitle: crystal structure of the photosensory core module of2 bacteriophytochrome rpa3015 from r. palustris
63	c5i0hA_	Alignment	not modelled	10.8	17	PDB header: motor protein Chain: A: PDB Molecule: unconventional myosin-x; PDBTitle: crystal structure of myosin x motor domain in pre-powerstroke state
64	c2kcyA_	Alignment	not modelled	10.8	19	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s8e; PDBTitle: solution structure of ribosomal protein s8e from2 methanothermobacter thermautotrophicus,3 northeaststructural genomics consortium (nseg) target tr71d
65	c4z9cA_	Alignment	not modelled	10.7	26	PDB header: transferase Chain: A: PDB Molecule: pertussis toxin-like subunit arta; PDBTitle: ecpltab oxidized
66	c6ir8A_	Alignment	not modelled	10.7	19	PDB header: transcription/dna Chain: A: PDB Molecule: oswrky45; PDBTitle: rice wrky/dna complex
67	c5v7pA_	Alignment	not modelled	10.7	7	PDB header: transferase Chain: A: PDB Molecule: protein-s-isoprenylcysteine o-methyltransferase; PDBTitle: atomic structure of the eukaryotic intramembrane ras methyltransferase2 icmt (isoprenylcysteine carboxyl methyltransferase), in complex with3 a monobody
68	c4ruvA_	Alignment	not modelled	10.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 2 from staphylococcus aureus nctc8325
69	c5dynA_	Alignment	not modelled	10.5	33	PDB header: hydrolase Chain: A: PDB Molecule: putative peptidase; PDBTitle: b. fragilis cysteine protease
70	c4zg4E_	Alignment	not modelled	10.3	10	PDB header: motor protein Chain: E: PDB Molecule: myosin-vc; PDBTitle: myosin vc pre-powerstroke
71	c6f0kA_	Alignment	not modelled	10.3	22	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
72	d2joqa1	Alignment	not modelled	10.2	22	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: HP0495-like
73	c1iyjB_	Alignment	not modelled	10.2	21	PDB header: gene regulation/antitumor protein Chain: B: PDB Molecule: breast cancer susceptibility; PDBTitle: structure of a brca2-dss1 complex
74	d1oedc_	Alignment	not modelled	10.2	29	Fold: Neurotransmitter-gated ion-channel transmembrane pore Superfamily: Neurotransmitter-gated ion-channel transmembrane pore Family: Neurotransmitter-gated ion-channel transmembrane pore
75	c2biwC_	Alignment	not modelled	10.2	26	PDB header: oxidoreductase Chain: C: PDB Molecule: apocarotenoid-cleaving oxygenase; PDBTitle: crystal structure of apocarotenoid cleavage oxygenase from2 synechocystis, native enzyme
76	c6d6vE_	Alignment	not modelled	10.2	42	PDB header: replication Chain: E: PDB Molecule: telomerase holoenzyme teb2 subunit; PDBTitle: cryoem structure of tetrahymena telomerase with telomeric dna at 4.82 angstrom resolution
77	c3d7rB_	Alignment	not modelled	10.2	8	PDB header: hydrolase Chain: B: PDB Molecule: esterase;

77	c0u71B_	Alignment	not modelled	10.2	0	PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
78	c2lx0A_	Alignment	not modelled	10.1	31	PDB header: membrane protein Chain: A: PDB Molecule: membrane fusion protein p14; PDBTitle: arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
79	d1osna_	Alignment	not modelled	10.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
80	c4xesA_	Alignment	not modelled	10.0	9	PDB header: signaling protein, hydrolase Chain: A: PDB Molecule: neurotensin receptor type 1, endolysin chimera; PDBTitle: structure of active-like neurotensin receptor
81	c2k58B_	Alignment	not modelled	9.7	29	PDB header: transport protein Chain: B: PDB Molecule: neuronal acetylcholine receptor subunit beta-2; PDBTitle: nmr structures of the first transmembrane domain of the2 neuronal acetylcholine receptor beta 2 subunit
82	c5j7dG_	Alignment	not modelled	9.7	16	PDB header: de novo protein Chain: G: PDB Molecule: designed thioredoxin df106; PDBTitle: computationally designed thioredoxin df106
83	c2mn8A_	Alignment	not modelled	9.6	47	PDB header: antimicrobial protein Chain: A: PDB Molecule: maculatin g15; PDBTitle: nmr structure of a peptoid analogue of maculatin g15 containing cis-2 nleu at position 13
84	c2mn9A_	Alignment	not modelled	9.6	47	PDB header: antimicrobial protein Chain: A: PDB Molecule: maculatin g15; PDBTitle: peptoid analogue of maculatin g15 - peptoid trans-nleu at position 13
85	c2b2hA_	Alignment	not modelled	9.6	14	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter; PDBTitle: ammonium transporter amt-1 from a. fulgidus (as)
86	c3llqB_	Alignment	not modelled	9.5	19	PDB header: membrane protein Chain: B: PDB Molecule: aquaporin z 2; PDBTitle: aquaporin structure from plant pathogen agrobacterium tumerfaciens
87	c3npeA_	Alignment	not modelled	9.5	32	PDB header: oxidoreductase Chain: A: PDB Molecule: 9-cis-epoxycarotenoid dioxygenase 1, chloroplastic; PDBTitle: structure of vp14 in complex with oxygen
88	c6ojrA_	Alignment	not modelled	9.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: lignostilbene-alpha,beta-dioxygenase isozyme i; PDBTitle: crystal structure of sphingomonas paucimobilis tmy1009 apo-lsda
89	c5n8nR_	Alignment	not modelled	9.5	48	PDB header: structural protein Chain: R: PDB Molecule: evpb family type vi secretion protein; PDBTitle: contracted sheath of a pseudomonas aeruginosa type six secretion2 system consisting of tssb1 and tssc1
90	c2pxqA_	Alignment	not modelled	9.4	30	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein; PDBTitle: nmr solution structure of omla
91	d1bccc2	Alignment	not modelled	9.4	15	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
92	c6ohuC_	Alignment	not modelled	9.3	15	PDB header: membrane protein, isomerase/inhibitor Chain: C: PDB Molecule: 3-beta-hydroxysteroid-delta(8),delta(7)-isomerase; PDBTitle: structure of ebp and tamoxifen
93	c2a2jA_	Alignment	not modelled	9.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
94	c2mmjA_	Alignment	not modelled	9.2	47	PDB header: antimicrobial protein Chain: A: PDB Molecule: maculatin g15; PDBTitle: structure of a peptoid analogue of maculatin g15 in dpc micelles
95	c4wkkA_	Alignment	not modelled	9.2	36	PDB header: signaling protein Chain: A: PDB Molecule: bacteriophytochrome protein; PDBTitle: the photosensory module (pas-gaf-phy) of the bacterial phytochrome2 agp1 (atbphp1) in the pr form, chromophore modelled with an exocyclic3 double bond at pyrrole ring a.
96	d1gpqa_	Alignment	not modelled	9.2	22	Fold: Inhibitor of vertebrate lysozyme, lvy Superfamily: Inhibitor of vertebrate lysozyme, lvy Family: Inhibitor of vertebrate lysozyme, lvy
97	c2lonA_	Alignment	not modelled	9.2	15	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1b; PDBTitle: backbone structure of human membrane protein higd1b
98	c4huqS_	Alignment	not modelled	9.1	13	PDB header: hydrolase Chain: S: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a transporter
99	c5udtD_	Alignment	not modelled	9.0	17	PDB header: transferase Chain: D: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp