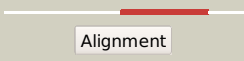



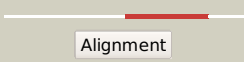

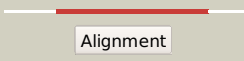
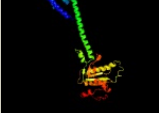
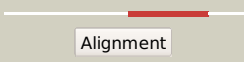

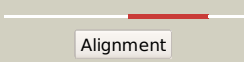

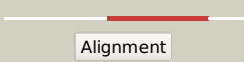

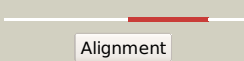

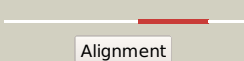

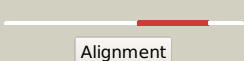

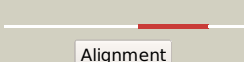




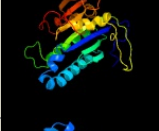


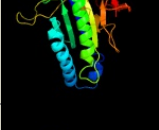

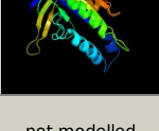




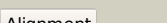
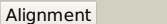

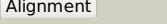
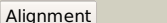
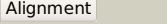

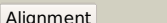
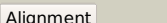
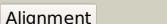
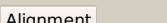
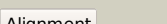
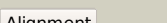

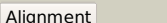
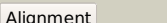

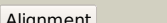
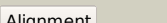
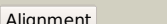
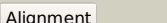

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1320c_(-)_1482520_1484223
Date	Wed Jul 31 22:05:41 BST 2019
Unique Job ID	9af9ece8cb4b0331

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fhtB_	 Alignment		100.0	28	PDB header: lyase Chain: B; PDB Molecule: bacteriophytochrome,adenylate cyclase; PDBTitle: crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
2	c4yusA_	 Alignment		100.0	25	PDB header: lyase Chain: A; PDB Molecule: family 3 adenylate cyclase; PDBTitle: crystal structure of photoactivated adenyl cyclase of a2 cyanobacteriaosillatoria acuminata in hexagonal form
3	c5nbyA_	 Alignment		100.0	23	PDB header: lyase Chain: A; PDB Molecule: beta subunit of photoactivated adenyl cyclase; PDBTitle: structure of a bacterial light-regulated adenyl cyclase
4	c6r4oA_	 Alignment		100.0	21	PDB header: membrane protein Chain: A; PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a truncated adenyl cyclase bound to mant-gtp, forskolin2 and an activated stimulatory galphas protein
5	c4cliA_	 Alignment		100.0	27	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase type 10; PDBTitle: crystal structure of human soluble adenyl cyclase in complex with2 bicarbonate
6	c6r4pA_	 Alignment		100.0	20	PDB header: membrane protein Chain: A; PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a soluble domain of adenyl cyclase bound to an2 activated stimulatory g protein
7	c1y10C_	 Alignment		100.0	22	PDB header: lyase Chain: C; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: mycobacterial adenyl cyclase rv1264, holoenzyme, inhibited state
8	c5o5kC_	 Alignment		100.0	25	PDB header: membrane protein Chain: C; PDB Molecule: adenylate cyclase; PDBTitle: x-ray structure of a bacterial adenyl cyclase soluble domain
9	c1wc6B_	 Alignment		100.0	33	PDB header: lyase Chain: B; PDB Molecule: adenylate cyclase; PDBTitle: soluble adenyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
10	c2w01C_	 Alignment		100.0	29	PDB header: lyase Chain: C; PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the guanylyl cyclase cya2
11	d1wc1a_	 Alignment		100.0	34	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain

12	c1cjkA	Alignment		100.0	20	PDB header: lyase/lyase/signaling protein Chain: A: PDB Molecule: adenylate cyclase, type v; PDBTitle: complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
13	c3r5gB	Alignment		100.0	26	PDB header: lyase Chain: B: PDB Molecule: cyab; PDBTitle: crystal structure of the adenylyl cyclase cyab from p. aeruginosa
14	d1azsa	Alignment		100.0	20	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
15	d1fx2a	Alignment		100.0	14	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
16	c3uvjC	Alignment		100.0	20	PDB header: lyase Chain: C: PDB Molecule: guanylate cyclase soluble subunit alpha-3; PDBTitle: crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
17	d1fx4a	Alignment		100.0	15	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
18	c3et6A	Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
19	c3mr7B	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: adenylate/guanylate cyclase/hydrolase, alpha/beta fold PDBTitle: crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
20	c2wz1B	Alignment		100.0	21	PDB header: lyase Chain: B: PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: structure of the catalytic domain of human soluble guanylate cyclase 12 beta 3.
21	d1azsb	Alignment	not modelled	100.0	19	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
22	c1ybuA	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: lipj; PDBTitle: mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
23	c1yk9A	Alignment	not modelled	100.0	24	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
24	c4wp3E	Alignment	not modelled	100.0	25	PDB header: lyase Chain: E: PDB Molecule: ma1120; PDBTitle: crystal structure of adenylyl cyclase from mycobacterium avium ma11202 wild type
25	c6aoaA	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: bacterio-rhodopsin/guanylyl cyclase 1 fusion protein; PDBTitle: monomeric crystal structure of the e497/c566d double mutant of the2 guanylyl cyclase domain of the rhogc fusion protein from the aquatic3 fungus blastocladiella emersonii
26	c5jefA	Alignment	not modelled	99.4	20	PDB header: transferase Chain: A: PDB Molecule: nitrate/nitrite sensor protein narq; PDBTitle: fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
27	c4gn0D	Alignment	not modelled	99.3	13	PDB header: signaling protein Chain: D: PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
28	c3lnrA	Alignment	not modelled	99.0	14	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2

29	c3zx6A_	 Alignment	not modelled	98.8	15	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
30	d2asxa1	 Alignment	not modelled	98.7	16	Fold: HAMP domain-like Superfamily: HAMP domain-like Family: HAMP domain
31	c3zrwB_	 Alignment	not modelled	98.4	17	PDB header: signaling protein Chain: B: PDB Molecule: af1503 protein, osmolarity sensor protein envz; PDBTitle: the structure of the dimeric hamp-dhp fusion a291v mutant
32	c4i5sA_	 Alignment	not modelled	98.3	21	PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase
33	c4ctiA_	 Alignment	not modelled	97.9	16	PDB header: signaling protein Chain: A: PDB Molecule: osmolarity sensor protein envz, af1503; PDBTitle: escherichia coli envz histidine kinase catalytic part fused to2 archaeoglobus fulgidus af1503 hamp domain
34	c4biuB_	 Alignment	not modelled	97.9	23	PDB header: transferase Chain: B: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (orthorhombic form 1)
35	c2qv6D_	 Alignment	not modelled	97.3	19	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase iii; PDBTitle: gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
36	c2rm8A_	 Alignment	not modelled	97.2	29	PDB header: signaling protein Chain: A: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis
37	c3i5cA_	 Alignment	not modelled	95.0	13	PDB header: signaling protein Chain: A: PDB Molecule: fusion of general control protein gcn4 and wspr response PDBTitle: crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa
38	c1w25B_	 Alignment	not modelled	94.8	14	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
39	c4wxoA_	 Alignment	not modelled	94.3	10	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: sadc (300-487) from pseudomonas aeruginosa pao1
40	c3ungC_	 Alignment	not modelled	93.7	24	PDB header: unknown function Chain: C: PDB Molecule: cmr2dhd; PDBTitle: structure of the cmr2 subunit of the crispr rna silencing complex
41	c3i5aA_	 Alignment	not modelled	92.3	16	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wspr from pseudomonas syringae
42	c6d9mA_	 Alignment	not modelled	92.0	19	PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef
43	c3mtkA_	 Alignment	not modelled	91.8	11	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase/phosphodiesterase; PDBTitle: x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
44	c3breA_	 Alignment	not modelled	91.4	15	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
45	c4zmuD_	 Alignment	not modelled	91.4	14	PDB header: lyase Chain: D: PDB Molecule: diguanylate cyclase; PDBTitle: dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
46	c3ignA_	 Alignment	not modelled	90.1	12	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of the ggdef domain from marinobacter aquaeolei2 diguanylate cyclase complexed with c-di-gmp - northeast structural3 genomics consortium target mqr89a
47	c3hvwA_	 Alignment	not modelled	89.2	13	PDB header: lyase Chain: A: PDB Molecule: diguanylate-cyclase (dgc); PDBTitle: crystal structure of the ggdef domain of the pa2567 protein from2 pseudomonas aeruginosa, northeast structural genomics consortium3 target par365c
48	c3i5bA_	 Alignment	not modelled	89.1	14	PDB header: signaling protein Chain: A: PDB Molecule: wspr response regulator; PDBTitle: crystal structure of the isolated ggdef domain of wspr from2 pseudomonas aeruginosa
49	c3ezuA_	 Alignment	not modelled	88.4	18	PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
50	d1w25a3	 Alignment	not modelled	87.8	14	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: GGDEF domain
51	c5llxB_	 Alignment	not modelled	87.0	10	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase (ggdef) domain-containing protein; PDBTitle: bacteriophytochrome activated diguanylyl cyclase from idiomarina2 species a28l with gtp bound
52	c4h54B_	 Alignment	not modelled	84.9	14	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase ydeh; PDBTitle: crystal structure of the diguanylate cyclase dgcz

53	c4w8yA	Alignment	not modelled	83.7	17	PDB header: rna binding protein Chain: A: PDB Molecule: crispr system cmr subunit cmr2; PDBTitle: structure of full length cmr2 from pyrococcus furiosus (manganese2 bound form)
54	c3hvaA	Alignment	not modelled	80.7	16	PDB header: transferase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx ggdef domain from pseudomonas aeruginosa
55	c4ymeA	Alignment	not modelled	80.3	17	PDB header: lyase Chain: A: PDB Molecule: sensory box/ggdef family protein; PDBTitle: crystal structure of a sensory box/ggdef family protein (cc_0091) from2 caulobacter crescentus cb15 at 1.40 a resolution (psi community3 target, shapiro)
56	c5euhA	Alignment	not modelled	78.5	15	PDB header: membrane protein Chain: A: PDB Molecule: putative ggdef domain membrane protein; PDBTitle: crystal structure of the c-di-gmp-bound ggdef domain of p. fluorescens2 gcbc
57	c3pjwA	Alignment	not modelled	75.5	14	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescens lapd ggdef-eal dual domain, i23
58	c4iobA	Alignment	not modelled	73.4	17	PDB header: lyase Chain: A: PDB Molecule: diguanylate cyclase tpbb; PDBTitle: crystal structure of the ggdef domain of pa1120 (yfin or tpbb) from2 pseudomonas aeruginosa at 2.7 ang.
59	c4zvhB	Alignment	not modelled	72.4	19	PDB header: signaling protein Chain: B: PDB Molecule: diguanylate cyclase dosc; PDBTitle: crystal structure of ggdef domain of the e. coli dosc - form iv
60	c4urgB	Alignment	not modelled	72.1	21	PDB header: lyase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of ggdef domain from t.maritima (active-like dimer)
61	c3icIA	Alignment	not modelled	70.4	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: eal/ggdef domain protein; PDBTitle: x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium target mcr174c
62	c6eibC	Alignment	not modelled	70.1	11	PDB header: transferase Chain: C: PDB Molecule: sensory box/ggdef family protein; PDBTitle: structure of the active ggeef domain of a diguanylate cyclase from2 vibrio cholerae.
63	c5m3cB	Alignment	not modelled	67.9	18	PDB header: hydrolase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: structure of the hybrid domain (ggdef-eal) of pa0575 from pseudomonas2 aeruginosa pao1 at 2.8 ang. with gtp and ca2+ bound to the active3 site of the ggdef domain
64	c3hlsE	Alignment	not modelled	67.5	19	PDB header: signaling protein Chain: E: PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: crystal structure of the signaling helix coiled-coil domain2 of the beta-1 subunit of the soluble guanylyl cyclase
65	c5xgdA	Alignment	not modelled	65.7	15	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein pa0861; PDBTitle: crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp
66	c3tvkA	Alignment	not modelled	55.6	16	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase dgcz; PDBTitle: diguanylate cyclase domain of dgcz
67	c4dmzB	Alignment	not modelled	55.2	7	PDB header: nucleotide-binding protein Chain: B: PDB Molecule: putative uncharacterized protein peld; PDBTitle: peld 156-455 from pseudomonas aeruginosa pa14, apo form
68	c3qyyB	Alignment	not modelled	39.8	17	PDB header: signaling protein/inhibitor Chain: B: PDB Molecule: response regulator; PDBTitle: a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp
69	c4zmmB	Alignment	not modelled	38.6	13	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: ggdef domain of dcsbis complexed with c-di-gmp
70	c4biyD	Alignment	not modelled	36.2	19	PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2)
71	c5buzC	Alignment	not modelled	31.0	19	PDB header: transport protein Chain: C: PDB Molecule: snap receptor-like protein; PDBTitle: crystal structure of a complex between the snare vam3 and the hops2 vps33-vps16 subcomplex from chaetomium thermophilum
72	c2x5eA	Alignment	not modelled	29.4	15	PDB header: unknown function Chain: A: PDB Molecule: upf0271 protein pa4511; PDBTitle: crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
73	d2dfaa1	Alignment	not modelled	27.9	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
74	d1v6ta	Alignment	not modelled	26.9	7	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
75	c4euvA	Alignment	not modelled	26.0	11	PDB header: signaling protein Chain: A: PDB Molecule: peld; PDBTitle: crystal structure of peld 158-ct from pseudomonas aeruginosa pao1, in2 complex with c-di-gmp, form 1
76	c6ifnA	Alignment	not modelled	22.8	19	PDB header: rna binding protein Chain: A: PDB Molecule: type iii-a crispr-associated protein csm1; PDBTitle: crystal structure of type iii-a crispr csm complex
77	c2cwoD	Alignment	not modelled	20.1	24	PDB header: rna binding protein Chain: D: PDB Molecule: rna silencing suppressor; PDBTitle: crystal structure of rna silencing suppressor p21 from beet yellows2 virus PDB header: transcription

78	c5n9jB_	Alignment	not modelled	19.0	14	Chain: B: PDB Molecule: mediator of rna polymerase ii transcription subunit 10; PDBTitle: core mediator of transcriptional regulation
79	c4rnhA_	Alignment	not modelled	15.3	24	PDB header: transferase, hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
80	c3dcaC_	Alignment	not modelled	14.3	11	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: rpa0582; PDBTitle: crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
81	c2xgvA_	Alignment	not modelled	12.8	22	PDB header: viral protein Chain: A: PDB Molecule: psiv capsid n-terminal domain; PDBTitle: structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik)
82	c4ymkA_	Alignment	not modelled	12.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa desaturase 1; PDBTitle: crystal structure of stearyl-coenzyme a desaturase 1
83	c5mm2C_	Alignment	not modelled	12.5	29	PDB header: virus Chain: C: PDB Molecule: capsid protein vp4a; PDBTitle: nora virus structure
84	c2n5lA_	Alignment	not modelled	12.2	24	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: regnase-1 c-terminal domain
85	d1veha_	Alignment	not modelled	12.2	28	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
86	d1m9dc_	Alignment	not modelled	11.7	17	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
87	d1q8ka2	Alignment	not modelled	11.7	16	Fold: Ferredoxin-like Superfamily: eIF-2-alpha, C-terminal domain Family: eIF-2-alpha, C-terminal domain
88	d2eiaa2	Alignment	not modelled	11.3	17	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
89	d1m9fd_	Alignment	not modelled	11.3	17	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
90	c4axkB_	Alignment	not modelled	11.0	32	PDB header: isomerase Chain: B: PDB Molecule: 1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) PDBTitle: crystal structure of subhisa from the thermophile corynebacterium2 efficiens
91	c3vvfA_	Alignment	not modelled	10.6	19	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, binding protein; PDBTitle: crystal structure of ttc0807 complexed with arginine
92	d2pxrc1	Alignment	not modelled	10.6	17	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
93	c3nvbA_	Alignment	not modelled	10.4	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
94	c2wlvA_	Alignment	not modelled	10.3	17	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal capsid domain of hiv-2
95	c2o01L_	Alignment	not modelled	10.1	25	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem i reaction center subunit xi, chloroplast; PDBTitle: the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
96	c4zv2A_	Alignment	not modelled	10.1	17	PDB header: solute-binding protein Chain: A: PDB Molecule: ancqr; PDBTitle: an ancestral arginine-binding protein bound to glutamine
97	c2f7tA_	Alignment	not modelled	9.7	3	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
98	c4r29D_	Alignment	not modelled	8.5	42	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of bacterial cysteine methyltransferase effector2 nlee
99	d1jb0L_	Alignment	not modelled	8.4	15	Fold: Photosystem I reaction center subunit XI, PsaL Superfamily: Photosystem I reaction center subunit XI, PsaL Family: Photosystem I reaction center subunit XI, PsaL