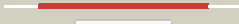


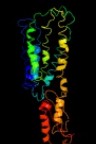
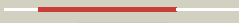






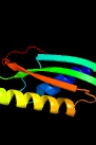










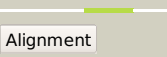
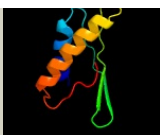
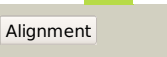

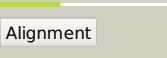

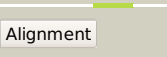

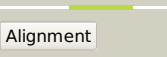
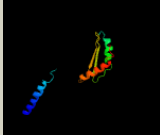
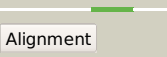

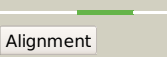

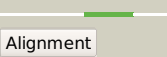

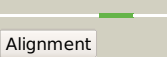

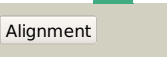
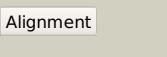
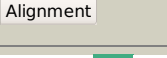
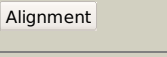
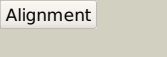
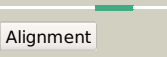
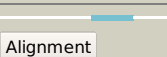
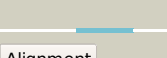


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2025c_(-)_2270758_2271756
Date	Mon Aug 5 13:25:13 BST 2019
Unique Job ID	26726650cc81fde8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j1zP_	 Alignment		100.0	23	PDB header: metal transport Chain: P: PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiip revealed by2 cryo-electron microscopy
2	c2qfiB_	 Alignment		100.0	24	PDB header: transport protein Chain: B: PDB Molecule: ferrous-iron efflux pump fief; PDBTitle: structure of the zinc transporter yiip
3	d2qfia2	 Alignment		100.0	24	Fold: Cation efflux protein transmembrane domain-like Superfamily: Cation efflux protein transmembrane domain-like Family: Cation efflux protein transmembrane domain-like
4	c5ho5D_	 Alignment		99.7	17	PDB header: metal transport Chain: D: PDB Molecule: magnetosome protein mamb; PDBTitle: mamb
5	c2zztA_	 Alignment		99.7	20	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
6	c6g6iB_	 Alignment		99.7	24	PDB header: metal transport Chain: B: PDB Molecule: magnetosome protein mamm; PDBTitle: mamm ctd w247a
7	d3bypa1	 Alignment		99.7	28	Fold: Alpha-lytic protease prodomain-like Superfamily: Cation efflux protein cytoplasmic domain-like Family: Cation efflux protein cytoplasmic domain-like
8	c3w66A_	 Alignment		99.7	23	PDB header: metal transport Chain: A: PDB Molecule: magnetosome protein mamm; PDBTitle: mamm-ctd d249a and h285a
9	c6qekB_	 Alignment		99.7	23	PDB header: transport protein Chain: B: PDB Molecule: magnetosome protein; PDBTitle: putative membrane transporter, magnetosome protein mamm ctd2 [desulfamplus magnetovallimortis bw-1]
10	d2qfia1	 Alignment		99.5	23	Fold: Alpha-lytic protease prodomain-like Superfamily: Cation efflux protein cytoplasmic domain-like Family: Cation efflux protein cytoplasmic domain-like
11	c6qfiA_	 Alignment		97.4	19	PDB header: transport protein Chain: A: PDB Molecule: magnetosome membrane protein mamb, putative co/zncd cation PDBTitle: mamb ctd magnetosome protein [desulfamplus magnetovallimortis bw-1]

12	c3cd0B_	 Alignment		68.4	10	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxy-3-methylglutaryl-coenzyme a reductase; PDBTitle: thermodynamic and structure guided design of statin hmg-coa reductase2 inhibitors
13	c1hwjB_	 Alignment		66.6	10	PDB header: oxidoreductase Chain: B: PDB Molecule: hmg-coa reductase; PDBTitle: complex of the catalytic portion of human hmg-coa reductase2 with cerivastatin
14	c4djiA_	 Alignment		65.3	9	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
15	d1ib8a2	 Alignment		62.0	10	Fold: Alpha-lytic protease prodomain-like Superfamily: YhbC-like, N-terminal domain Family: YhbC-like, N-terminal domain
16	c1oy8A_	 Alignment		60.4	13	PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
17	c4ir7A_	 Alignment		57.5	11	PDB header: transferase Chain: A: PDB Molecule: long chain fatty acid coa ligase fadd10; PDBTitle: crystal structure of mtb fadd10 in complex with dodecanoyl-amp
18	d1u8sa1	 Alignment		51.8	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
19	d1dqaa1	 Alignment		50.9	10	Fold: Ferredoxin-like Superfamily: NAD-binding domain of HMG-CoA reductase Family: NAD-binding domain of HMG-CoA reductase
20	d1iwga3	 Alignment		50.1	5	Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
21	c1u8sB_	 Alignment	not modelled	48.0	19	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
22	c3lnoA_	 Alignment	not modelled	46.4	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of domain of unknown function duf59 from2 bacillus anthracis
23	d1ghha_	 Alignment	not modelled	44.5	8	Fold: DNA damage-inducible protein DinI Superfamily: DNA damage-inducible protein DinI Family: DNA damage-inducible protein DinI
24	d1u8sa2	 Alignment	not modelled	43.3	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
25	c2jp3A_	 Alignment	not modelled	40.5	9	PDB header: transcription Chain: A: PDB Molecule: fyxd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
26	d2fca1	 Alignment	not modelled	40.3	18	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
27	c3eynB_	 Alignment	not modelled	39.0	10	PDB header: ligase Chain: B: PDB Molecule: acyl-coenzyme a synthetase acsm2a; PDBTitle: crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa
28	c5irdA_	 Alignment	not modelled	38.5	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of rv1466 from mycobacterium tuberculosis, a2 protein associated with [fe-s] complex assembly and repair - seattle3 structural genomics center for infectious disease target4 mytd.17486.a

29	c5ensA	Alignment	not modelled	37.4	6	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb,multidrug efflux pump PDBTitle: rhodamine bound structure of bacterial efflux pump.
30	d1fftb2	Alignment	not modelled	36.3	14	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
31	c1v55B	Alignment	not modelled	35.4	11	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: bovine heart cytochrome c oxidase at the fully reduced state
32	d1xhja	Alignment	not modelled	34.8	11	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
33	c6hu9n	Alignment	not modelled	31.4	11	PDB header: oxidoreductase/electron transport Chain: N: PDB Molecule: cytochrome b; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
34	c3b47A	Alignment	not modelled	31.4	14	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: periplasmic sensor domain of chemotaxis protein gsu0582
35	d2cu6a1	Alignment	not modelled	29.7	10	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
36	d1zpva1	Alignment	not modelled	28.8	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: SPO238-like
37	c1ib8A	Alignment	not modelled	28.8	10	PDB header: nucleic acid binding protein Chain: A: PDB Molecule: conserved protein sp14.3; PDBTitle: solution structure and function of a conserved protein2 sp14.3 encoded by an essential streptococcus pneumoniae3 gene
38	d1iwga1	Alignment	not modelled	28.4	10	Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
39	c2zxeG	Alignment	not modelled	27.2	28	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
40	c4a01B	Alignment	not modelled	26.5	8	PDB header: hydrolase Chain: B: PDB Molecule: proton pyrophosphatase; PDBTitle: crystal structure of the h-translocating pyrophosphatase
41	d1dlca3	Alignment	not modelled	25.1	15	Fold: Toxins' membrane translocation domains Superfamily: delta-Endotoxin (insecticide), N-terminal domain Family: delta-Endotoxin (insecticide), N-terminal domain
42	d1ji6a3	Alignment	not modelled	24.8	15	Fold: Toxins' membrane translocation domains Superfamily: delta-Endotoxin (insecticide), N-terminal domain Family: delta-Endotoxin (insecticide), N-terminal domain
43	c6humB	Alignment	not modelled	23.9	12	PDB header: proton transport Chain: B: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 2; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
44	c3uz0A	Alignment	not modelled	23.2	8	PDB header: transport protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: crystal structure of spoiiiah and spoiiq complex
45	c6nplA	Alignment	not modelled	21.8	14	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 12 (sodium/potassium/chloride) PDBTitle: cryo-em structure of nkcc1
46	c2yevB	Alignment	not modelled	21.3	15	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of caa3-type cytochrome oxidase
47	c3e7wA	Alignment	not modelled	20.8	12	PDB header: ligase Chain: A: PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 1; PDBTitle: crystal structure of dlta: implications for the reaction mechanism of2 non-ribosomal peptide synthetase (nrps) adenylation domains
48	c5udtD	Alignment	not modelled	19.9	9	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
49	c2jo1A	Alignment	not modelled	18.5	14	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
50	c1ji6A	Alignment	not modelled	18.2	13	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry3bb; PDBTitle: crystal structure of the insecticidal bacterial del endotoxin cry3bb12 bacillus thuringiensis
51	c5ifiA	Alignment	not modelled	17.6	16	PDB header: ligase Chain: A: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: crystal structure of acetyl-coa synthetase in complex with adenosine-2 5'-propylphosphate from cryptococcus neoformans h99
52	c2y27B	Alignment	not modelled	17.2	14	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
53	c2jnvA	Alignment	not modelled	16.5	16	PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 1, chloroplast; PDBTitle: solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
54	c3tufA	Alianment	not modelled	15.5	11	PDB header: signaling protein Chain: A: PDB Molecule: stage iii sporulation protein ah;

						PDBTitle: structure of the spoiiq-spoiiiah pore forming complex.
55	c2mkvA	Alignment	not modelled	15.1	11	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
56	c3qovD	Alignment	not modelled	14.9	12	PDB header: ligase Chain: D: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of a hypothetical acyl-coa ligase (bt_0428) from bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
57	c5m87A	Alignment	not modelled	14.6	17	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of eremococcus coleocola manganese transporter
58	d1x38a2	Alignment	not modelled	14.5	17	Fold: Flavodoxin-like Superfamily: Beta-D-glucan exohydrolase, C-terminal domain Family: Beta-D-glucan exohydrolase, C-terminal domain
59	c3l8cA	Alignment	not modelled	14.3	13	PDB header: ligase Chain: A: PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 1; PDBTitle: structure of probable d-alanine--poly(phosphoribitol) ligase subunit-12 from streptococcus pyogenes
60	d1knya2	Alignment	not modelled	14.2	9	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
61	d1ofua2	Alignment	not modelled	14.0	16	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
62	c5gxdA	Alignment	not modelled	13.9	15	PDB header: lyase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: structure of acryloyl-coa lyase prpe from dinoroseobacter shibae df12_12
63	c4jcuC	Alignment	not modelled	13.9	15	PDB header: isomerase Chain: C: PDB Molecule: 5-carboxymethyl-2-hydroxy muconate isomerase; PDBTitle: crystal structure of a 5-carboxymethyl-2-hydroxy muconate isomerase2 from deinococcus radiodurans r1
64	c3dhvA	Alignment	not modelled	13.6	15	PDB header: ligase Chain: A: PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of delta protein in complex with d-alanine2 adenylate
65	c4px7A	Alignment	not modelled	13.4	12	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pgpb
66	c1qlcB	Alignment	not modelled	13.1	6	PDB header: oxidoreductase/immune system Chain: B: PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: cryo-structure of the paracoccus denitrificans four-subunit cytochrome2 c oxidase in the completely oxidized state complexed with an antibody3 fv fragment
67	c1ar1B	Alignment	not modelled	13.1	6	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
68	c2qjvF	Alignment	not modelled	13.0	8	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative cytoplasmic protein; PDBTitle: crystal structure of a protein of unknown function from salmonella2 typhimurium
69	c4o6mA	Alignment	not modelled	13.0	14	PDB header: transferase Chain: A: PDB Molecule: af2299, a cdp-alcohol phosphotransferase; PDBTitle: structure of af2299, a cdp-alcohol phosphotransferase (cmp-bound)
70	d1uwda	Alignment	not modelled	12.7	16	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
71	c6raoH	Alignment	not modelled	12.5	11	PDB header: virus like particle Chain: H: PDB Molecule: afp9; PDBTitle: cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised
72	c5ql6A	Alignment	not modelled	12.3	19	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome maturation factor rimp; PDBTitle: msmeg rimp
73	c2kz0A	Alignment	not modelled	11.2	17	PDB header: transcription Chain: A: PDB Molecule: bola family protein; PDBTitle: solution structure of a bola protein (ech_0303) from ehrlichia2 chaffeensis. seattle structural genomics center for infectious3 disease target ehcha.10365.a
74	d1th5a1	Alignment	not modelled	11.0	10	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
75	c3j20C	Alignment	not modelled	11.0	8	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
76	c3eb7B	Alignment	not modelled	10.9	21	PDB header: toxin Chain: B: PDB Molecule: insecticidal delta-endotoxin cry8ea1; PDBTitle: crystal structure of insecticidal delta-endotoxin cry8ea1 from2 bacillus thuringiensis at 2.2 angstroms resolution
77	c1ex1A	Alignment	not modelled	10.8	17	PDB header: hydrolase Chain: A: PDB Molecule: protein (beta-d-glucan exohydrolase isoenzyme exo1); PDBTitle: beta-d-glucan exohydrolase from barley
78	d3dtub2	Alignment	not modelled	10.8	8	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region

						Family: Cytochrome c oxidase subunit II-like, transmembrane region
79	d1mlia_	Alignment	not modelled	10.6	19	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Muconalactone isomerase, MLI
80	c2kwaA_	Alignment	not modelled	10.6	11	PDB header: transferase inhibitor Chain: A: PDB Molecule: kinase a inhibitor; PDBTitle: 1h, 13c and 15n backbone and side chain resonance assignments of the 2 n-terminal domain of the histidine kinase inhibitor kipi from <i>Bacillus subtilis</i>
81	c3rfuC_	Alignment	not modelled	10.4	12	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
82	c3a0hi_	Alignment	not modelled	10.4	25	PDB header: electron transport Chain: I: PDB Molecule: photosystem ii reaction center protein i; PDBTitle: crystal structure of i-substituted photosystem ii complex
83	d2axti1_	Alignment	not modelled	10.4	25	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein I, Psbl Family: Psbl-like
84	c4mndA_	Alignment	not modelled	10.3	6	PDB header: transferase Chain: A: PDB Molecule: ctp I-myo-inositol-1-phosphate cytidyltransferase/cdp-l PDBTitle: crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
85	c2phcB_	Alignment	not modelled	10.1	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein ph0987; PDBTitle: crystal structure of conserved uncharacterized protein ph0987 from <i>Pyrococcus horikoshii</i>
86	c3upsA_	Alignment	not modelled	10.0	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: iojap-like protein; PDBTitle: crystal structure of iojap-like protein from <i>Zymomonas mobilis</i>
87	c5lw6A_	Alignment	not modelled	10.0	14	PDB header: adp-ribose binding protein Chain: A: PDB Molecule: ddb_g0293866; PDBTitle: crystal structure of a se-met substituted dictyostelium discoideum2 adp-ribose binding macrodomain (residues 342-563) of ddb_g0293866
88	c3zz1A_	Alignment	not modelled	9.8	31	PDB header: hydrolase Chain: A: PDB Molecule: beta-d-glucoside glucohydrolase; PDBTitle: crystal structure of a glycoside hydrolase family 3 beta-glucosidase,2 bgl1 from <i>Hypocrea jecorina</i> at 2.1a resolution.
89	d1bdfa1_	Alignment	not modelled	9.7	12	Fold: DCoH-like Superfamily: RBP11-like subunits of RNA polymerase Family: RNA polymerase alpha subunit dimerisation domain
90	c3ibwA_	Alignment	not modelled	9.7	8	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp pyrophosphokinase of <i>Chlorobium tepidum</i> . northeast structural genomics consortium target3 ctr148a
91	c1dlcA_	Alignment	not modelled	9.7	15	PDB header: toxin Chain: A: PDB Molecule: delta-endotoxin cryiia; PDBTitle: crystal structure of insecticidal delta-endotoxin from <i>Bacillus thuringiensis</i> at 2.5 angstroms resolution
92	c3abfB_	Alignment	not modelled	9.7	2	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
93	d1m56d_	Alignment	not modelled	9.6	5	Fold: Single transmembrane helix Superfamily: Bacterial aa3 type cytochrome c oxidase subunit IV Family: Bacterial aa3 type cytochrome c oxidase subunit IV
94	c3b64A_	Alignment	not modelled	9.5	10	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: macrophage migration inhibitory factor (mif) from <i>Leishmania major</i>
95	d2qjva1_	Alignment	not modelled	9.5	8	Fold: Phage tail protein-like Superfamily: Phage tail protein-like Family: STM4215-like
96	d2atza1_	Alignment	not modelled	9.4	11	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: HP0184-like
97	c3iteB_	Alignment	not modelled	9.3	9	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
98	d1i1ga2_	Alignment	not modelled	9.2	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
99	c4i3gB_	Alignment	not modelled	9.1	13	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of desr, a beta-glucosidase from <i>Streptomyces venezuelae</i> in complex with d-glucose.