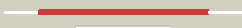









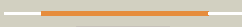



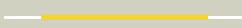

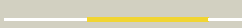




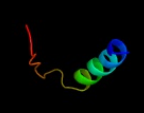
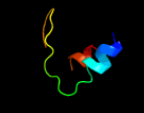
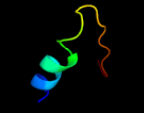
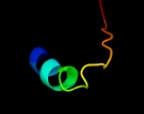
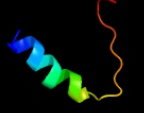
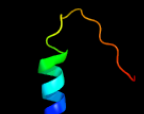

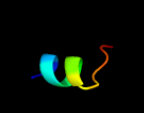
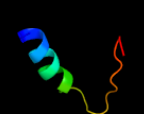
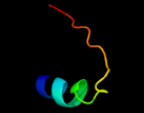


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2881c_cdsA_3190711_3191631
 Date Thu Aug 8 16:20:03 BST 2019
 Unique Job ID 3b17d187cb4edae1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4q2eA	 Alignment		100.0	22	PDB header: transferase Chain: A; PDB Molecule: phosphatidate cytidyltransferase; PDBTitle: crystal structure of an intramembrane cdp-dag synthetase central for2 phospholipid biosynthesis (s200c/s258c, active mutant)
2	c4q2gA	 Alignment		100.0	23	PDB header: transferase Chain: A; PDB Molecule: phosphatidate cytidyltransferase; PDBTitle: crystal structure of an intramembrane cdp-dag synthetase central for2 phospholipid biosynthesis (s200c/s223c, inactive mutant)
3	c5gufA	 Alignment		100.0	21	PDB header: transferase Chain: A; PDB Molecule: cdp-archaeol synthase; PDBTitle: structural insight into an intramembrane enzyme for archaeal membrane2 lipids biosynthesis
4	c3b9yA	 Alignment		96.0	16	PDB header: transport protein Chain: A; PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
5	c5aexJ	 Alignment		88.2	12	PDB header: membrane protein Chain: J; PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2
6	c5aexB	 Alignment		85.3	17	PDB header: membrane protein Chain: B; PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2
7	c2nuuF	 Alignment		83.0	14	PDB header: transport protein/signaling protein Chain: F; PDB Molecule: ammonia channel; PDBTitle: regulating the escherichia coli ammonia channel: the crystal structure2 of the amtB-glnK complex
8	c6eu6A	 Alignment		77.0	19	PDB header: membrane protein Chain: A; PDB Molecule: ammonium transporter; PDBTitle: sensor amt protein
9	c3hd6A	 Alignment		75.7	12	PDB header: membrane protein, transport protein Chain: A; PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg
10	c5aexZ	 Alignment		62.7	15	PDB header: membrane protein Chain: A; PDB Molecule: mep2; PDBTitle: crystal structure of candida albicans mep2
11	c3r2uC	 Alignment		61.7	22	PDB header: hydrolase Chain: C; PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col

12	d2p97a1	Alignment		57.4	30	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Ava3068-like
13	c2gcuD	Alignment		57.1	21	PDB header: hydrolase Chain: D: PDB Molecule: putative hydroxyacylglutathione hydrolase 3; PDBTitle: x-ray structure of gene product from arabidopsis thaliana at1g53580
14	c4ch1A	Alignment		55.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: persulfide dioxygenase ethe1, mitochondrial; PDBTitle: human ethylmalonic encephalopathy protein 1 (hethe1)
15	c2xf4A	Alignment		54.3	27	PDB header: hydrolase Chain: A: PDB Molecule: hydroxyacylglutathione hydrolase; PDBTitle: crystal structure of salmonella enterica serovar2 typhimurium ycb1
16	c5ve5C	Alignment		54.1	12	PDB header: oxidoreductase, transferase Chain: C: PDB Molecule: bpprf; PDBTitle: crystal structure of persulfide dioxygenase rhodanese fusion protein2 with rhodanese domain inactivating mutation (c314s) from burkholderia3 phytofirmans in complex with glutathione
17	c4yskA	Alignment		53.2	32	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of apo-form sdoa from pseudomonas putida
18	c2mc5A	Alignment		51.8	62	PDB header: protein binding Chain: A: PDB Molecule: 451; PDBTitle: a bacteriophage transcription regulator inhibits bacterial2 transcription initiation by -factor displacement
19	c3tp9B	Alignment		50.8	24	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase and rhodanese domain protein; PDBTitle: crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
20	c4ysbB	Alignment		50.6	25	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of ethe1 from myxococcus xanthus
21	c4efzB	Alignment	not modelled	50.0	25	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of a hypothetical metallo-beta-lactamase from2 burkholderia pseudomallei
22	c2kogA	Alignment	not modelled	47.4	30	PDB header: membrane protein Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: lipid-bound synaptobrevin solution nmr structure
23	d1mqoa	Alignment	not modelled	45.8	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
24	d1qh5a	Alignment	not modelled	43.1	11	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
25	c4ad9E	Alignment	not modelled	41.9	32	PDB header: hydrolase Chain: E: PDB Molecule: beta-lactamase-like protein 2; PDBTitle: crystal structure of human lactb2.
26	c4awyB	Alignment	not modelled	41.9	12	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase aim-1; PDBTitle: crystal structure of the mobile metallo-beta-lactamase aim-1 from2 pseudomonas aeruginosa: insights into antibiotic binding and the role3 of gln157
27	d1xm8a	Alignment	not modelled	40.6	13	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
28	c5sxpG	Alignment	not modelled	40.4	20	PDB header: signaling protein/ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix

29	d1u7ga_	Alignment	not modelled	37.4	18	Fold: Ammonium transporter Superfamily: Ammonium transporter Family: Ammonium transporter
30	d2aioa1	Alignment	not modelled	34.8	21	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
31	d1znba_	Alignment	not modelled	34.8	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
32	d1bh9b_	Alignment	not modelled	29.0	27	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
33	c5i0pB_	Alignment	not modelled	28.8	23	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of a beta-lactamase domain protein from burkholderia2 ambifaria
34	c6h0cA_	Alignment	not modelled	28.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: flv1 flavodiiron core from synechocystis sp. pcc6803
35	c3hnnD_	Alignment	not modelled	28.5	21	PDB header: oxidoreductase Chain: D: PDB Molecule: putative diflavin flavoprotein a 5; PDBTitle: crystal structure of putative diflavin flavoprotein a 5 (fragment 1-2 254) from nostoc sp. pcc 7120, northeast structural genomics3 consortium target nsr435a
36	d2qeda1	Alignment	not modelled	28.2	10	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
37	c3c1iA_	Alignment	not modelled	27.5	16	PDB header: transport protein Chain: A: PDB Molecule: ammonia channel; PDBTitle: substrate binding, deprotonation and selectivity at the periplasmic2 entrance of the e. coli ammonia channel ambt
38	c2p18A_	Alignment	not modelled	26.3	13	PDB header: hydrolase Chain: A: PDB Molecule: glyoxalase ii; PDBTitle: crystal structure of the leishmania infantum glyoxalase ii
39	c2z04A_	Alignment	not modelled	25.4	26	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of metallo-beta-lactamase family protein ttha14292 from thermus thermophilus hb8
40	c1vmeB_	Alignment	not modelled	23.8	17	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
41	c5ja9D_	Alignment	not modelled	23.1	42	PDB header: toxin Chain: D: PDB Molecule: toxin hgb-2; PDBTitle: crystal structure of the hgb2 toxin in complex with nb6
42	c2zwrA_	Alignment	not modelled	22.0	42	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase superfamily protein; PDBTitle: crystal structure of ttha1623 from thermus thermophilus hb8
43	c4v0hC_	Alignment	not modelled	21.4	41	PDB header: hydrolase Chain: C: PDB Molecule: metallo-beta-lactamase domain-containing protein 1 1; PDBTitle: human metallo beta lactamase domain containing protein 1 (hmblac1)
44	d1m2xa_	Alignment	not modelled	21.2	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
45	d1ycga2	Alignment	not modelled	20.8	15	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
46	c4wd6B_	Alignment	not modelled	20.2	21	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of dim-1 metallo-beta-lactamase
47	c6n36A_	Alignment	not modelled	20.1	20	PDB header: ligase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from chitinophaga pinensis
48	c3dh4A_	Alignment	not modelled	20.0	11	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
49	c3l6nA_	Alignment	not modelled	19.8	14	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of metallo-beta-lactamase ind-7
50	c5al6A_	Alignment	not modelled	19.4	25	PDB header: structural protein Chain: A: PDB Molecule: anastral spindle 2; PDBTitle: central coiled-coil domain (cccd) of drosophila melanogaster ana2. a2 natural, parallel, tetrameric coiled-coil bundle.
51	c2jpjA_	Alignment	not modelled	19.1	40	PDB header: antimicrobial protein Chain: A: PDB Molecule: bacteriocin lactococcin-g subunit alpha; PDBTitle: lactococcin g-a in dpc
52	c2jplA_	Alignment	not modelled	19.1	40	PDB header: antimicrobial protein Chain: A: PDB Molecule: bacteriocin lactococcin-g subunit alpha; PDBTitle: lactococcin g-a in tfe
53	c2q9uB_	Alignment	not modelled	18.6	10	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
54	c6oitG_	Alignment	not modelled	18.5	25	PDB header: plant protein Chain: G: PDB Molecule: protein chromatin remodeling 35; PDBTitle: cryoem structure of arabidopsis ddr' complex (drd1 peptide-dms3-rdm1)

55	c6aufB_	Alignment	not modelled	18.0	13	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase-like protein; PDBTitle: crystal structure of metalo beta lactamases mim-1 from novosphingobium2 pentaromatorans
56	c3lvzA_	Alignment	not modelled	17.3	17	PDB header: hydrolase Chain: A: PDB Molecule: blr6230 protein; PDBTitle: new refinement of the crystal structure of bjp-1, a subclass b32 metallo-beta-lactamase of bradyrhizobium japonicum
57	c2yz3B_	Alignment	not modelled	17.1	17	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystallographic investigation of inhibition mode of the2 vim-2 metallo-beta-lactamase from pseudomonas aeruginosa3 with mercaptocarboxylate inhibitor
58	c5k0wA_	Alignment	not modelled	17.0	7	PDB header: hydrolase Chain: A: PDB Molecule: class b carbapenemase gob-18; PDBTitle: crystal structure of the metallo-beta-lactamase gob-18 from2 elizabethkingia meningoseptica
59	c6grqB_	Alignment	not modelled	17.0	18	PDB header: signaling protein Chain: B: PDB Molecule: oxygen-binding diiron protein; PDBTitle: apo conformation of chemotaxis sensor odp
60	d1nxca_	Alignment	not modelled	16.9	13	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1;2-mannosidase, catalytic domain
61	d1dl2a_	Alignment	not modelled	16.8	14	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1;2-mannosidase, catalytic domain
62	c2kdcC_	Alignment	not modelled	16.3	19	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
63	c5aebA_	Alignment	not modelled	16.1	4	PDB header: hydrolase Chain: A: PDB Molecule: lra-12; PDBTitle: crystal structure of the class b3 di-zinc metallo-beta-lactamase lra-2 12 from an alaskan soil metagenome.
64	c2e55D_	Alignment	not modelled	16.0	43	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of aq2163 protein from aquifex aeolicus
65	c3bboU_	Alignment	not modelled	15.6	22	PDB header: ribosome Chain: U: PDB Molecule: ribosomal protein l22; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
66	d2gmna1	Alignment	not modelled	15.6	26	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
67	d2ey4a2	Alignment	not modelled	15.3	35	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
68	c6ixhQ_	Alignment	not modelled	15.3	17	PDB header: membrane protein Chain: Q: PDB Molecule: type vi secretion system tssm; PDBTitle: type vi secretion system membrane core complex
69	c4binA_	Alignment	not modelled	15.1	100	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase amic; PDBTitle: crystal structure of the e. coli n-acetylmuramoyl-l-alanine amidase2 amic
70	d2nn6h2	Alignment	not modelled	14.9	33	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
71	c1s1iN_	Alignment	not modelled	14.7	33	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
72	d2gycq1	Alignment	not modelled	14.1	29	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
73	d1ko3a_	Alignment	not modelled	14.1	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
74	c3pisA_	Alignment	not modelled	13.5	63	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: kazal-type serine protease inhibitor spi-1; PDBTitle: crystal structure of carcinoscorpis rotundicauda serine protease2 inhibitor domain 1
75	c3dmpD_	Alignment	not modelled	13.4	38	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase from2 burkholderia pseudomallei
76	c6dn4A_	Alignment	not modelled	13.4	18	PDB header: metal binding protein Chain: A: PDB Molecule: beta-lactamase; PDBTitle: cronobacter sakazakii (enterobacter sakazakii) metallo-beta-lactamase2 harldq motif
77	c5j72B_	Alignment	not modelled	12.9	100	PDB header: hydrolase Chain: B: PDB Molecule: putative n-acetylmuramoyl-l-alanine amidase,autolysin cwp6; PDBTitle: cwp6 from clostridium difficile
78	c3sd9B_	Alignment	not modelled	12.8	15	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of serratia fonticola sfh-i: source of the2 nucleophile in the catalytic mechanism of mono-zinc metallo-beta-3 lactamases
79	c3u5eP_	Alignment	not modelled	12.8	33	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a
						Fold: Nucleotide-diphospho-sugar transferases

80	d1jv1a_	Alignment	not modelled	12.4	42	Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
81	d1i5ea_	Alignment	not modelled	12.4	43	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
82	c1ychD_	Alignment	not modelled	12.3	14	PDB header: oxidoreductase Chain: D: PDB Molecule: nitric oxide reductase; PDBTitle: x-ray crystal structures of moorella thermoacetica fra. novel diiron2 site structure and mechanistic insights into a scavenging nitric3 oxide reductase
83	d2icya2	Alignment	not modelled	12.3	50	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
84	c3jywN_	Alignment	not modelled	11.9	33	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l17(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
85	d1k8wa5	Alignment	not modelled	11.9	35	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
86	c3zf7R_	Alignment	not modelled	11.8	22	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein l17, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
87	c1k8wA_	Alignment	not modelled	11.2	38	PDB header: lyase/rna Chain: A: PDB Molecule: trna pseudouridine synthase b; PDBTitle: crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
88	c5e38D_	Alignment	not modelled	11.2	33	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structural basis of mapping the spontaneous mutations with 5-2 flourouracil in uracil phosphoribosyltransferase from mycobacterium3 tuberculosis
89	c3oc9A_	Alignment	not modelled	11.2	50	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
90	c1e5dA_	Alignment	not modelled	11.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin\oxygen oxidoreductase; PDBTitle: rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas
91	c2fhxB_	Alignment	not modelled	10.9	28	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: spm-1; PDBTitle: pseudomonas aeruginosa spm-1 metallo-beta-lactamase
92	d1sgva2	Alignment	not modelled	10.8	30	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
93	c3zf7Y_	Alignment	not modelled	10.8	44	PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein l24, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
94	c3pesA_	Alignment	not modelled	10.8	67	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein gp49; PDBTitle: crystal structure of uncharacterized protein from pseudomonas phage2 yua
95	c6cqsA_	Alignment	not modelled	10.8	31	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: sediminispirochaeta smaragdinae sps-1 metallo-beta-lactamase
96	c2zvrA_	Alignment	not modelled	10.8	33	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related protein from2 thermotoga maritima
97	c6nu9A_	Alignment	not modelled	10.7	33	PDB header: viral protein Chain: A: PDB Molecule: zinc-binding non-structural protein; PDBTitle: crystal structure of a zinc-binding non-structural protein from the2 hepatitis e virus
98	c3vqzA_	Alignment	not modelled	10.7	7	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of metallo-beta-lactamase, smb-1, in a complex with2 mercaptoacetic acid
99	c3fvvA_	Alignment	not modelled	10.6	31	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl-peptidase 3; PDBTitle: crystal structure of human dipeptidyl peptidase iii