






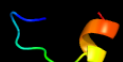









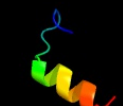

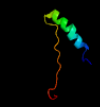

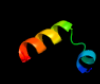


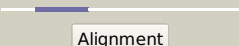
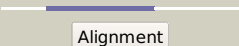

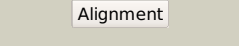
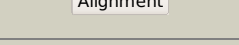
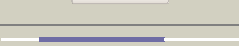

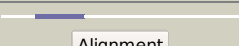
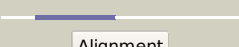
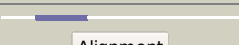


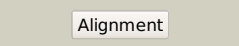
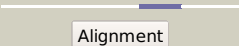


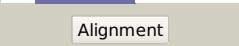


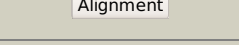
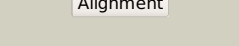
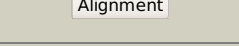
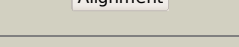


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2663 (-) _2981863_2982096
Date	Wed Aug 7 12:50:31 BST 2019
Unique Job ID	27bb8b8841c82996

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3u97A_	 Alignment		96.1	11	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease toxin brnt; PDBTitle: 1.1 angstrom-resolution crystal structure of the brucella abortus2 ribonuclease toxin, brnt
2	c3su8X_	 Alignment		76.3	40	PDB header: apoptosis/signaling protein Chain: X: PDB Molecule: plexin-b1; PDBTitle: crystal structure of a truncated intracellular domain of plexin-b1 in2 complex with rac1
3	c4m8nB_	 Alignment		75.5	33	PDB header: signaling protein Chain: B: PDB Molecule: plexinc1 intracellular region; PDBTitle: crystal structure of plexinc1/rap1b complex
4	c3hm6X_	 Alignment		74.9	40	PDB header: signaling protein Chain: X: PDB Molecule: plexin-b1; PDBTitle: crystal structure of the cytoplasmic domain of human plexin b1
5	c5e6pA_	 Alignment		74.3	40	PDB header: signaling protein Chain: A: PDB Molecule: plexin-b2; PDBTitle: plexinb2 cytoplasmic region/pdz-rhogef pdz domain complex
6	c5v6rB_	 Alignment		73.8	47	PDB header: protein binding Chain: B: PDB Molecule: plexin-d1; PDBTitle: structure of plexin d1 intracellular domain
7	c3ig3A_	 Alignment		72.5	27	PDB header: signaling protein, membrane protein Chain: A: PDB Molecule: plxna3 protein; PDBTitle: crystal structure of mouse plexin a3 intracellular domain
8	c3beyC_	 Alignment		39.3	25	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: conserved protein o27018; PDBTitle: crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
9	c1p8cD_	 Alignment		33.8	22	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of tm1620 (apc4843) from thermotoga2 maritima
10	c6bqzA_	 Alignment		30.2	24	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of tyrosine-trna synthetase from acinetobacter2 baumannii with bound l-tyrosine
11	c5djpB_	 Alignment		28.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxide reductase ahpd; PDBTitle: crystal structure of lpg0406 in reduced form from legionella2 pneumophila

12	c3jxeB_	Alignment		26.9	36	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
13	d2ouwa1	Alignment		24.2	21	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
14	c3gwrA_	Alignment		24.1	8	PDB header: protein binding Chain: A: PDB Molecule: putative calcium/calmodulin-dependent protein kinase type PDBTitle: crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution
15	c2qeuA_	Alignment		22.9	14	PDB header: lyase Chain: A: PDB Molecule: putative carboxymuconolactone decarboxylase; PDBTitle: crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
16	d1knca_	Alignment		22.3	24	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
17	d1vkea_	Alignment		21.6	17	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
18	c2p7pB_	Alignment		21.5	19	PDB header: metal binding protein, hydrolase Chain: B: PDB Molecule: glyoxalase family protein; PDBTitle: crystal structure of genomically encoded fosfomycin resistance2 protein, fosx, from listeria monocytogenes complexed with mn(ii) and3 sulfate ion
19	d1vkeb_	Alignment		18.6	20	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
20	c2pidB_	Alignment		17.9	26	PDB header: ligase Chain: B: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of human mitochondrial tyrosyl-trna synthetase in2 complex with an adenylate analog
21	d2cwqa1	Alignment	not modelled	17.5	22	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
22	c2oviA_	Alignment	not modelled	16.9	5	PDB header: ligand binding protein, metal transport Chain: A: PDB Molecule: hypothetical protein chux; PDBTitle: structure of the heme binding protein chux
23	c5cb9A_	Alignment	not modelled	16.3	9	PDB header: lyase Chain: A: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: crystal structure of c-as lyase with mercaptoethonal
24	c1r6uB_	Alignment	not modelled	16.2	11	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
25	c2cycB_	Alignment	not modelled	16.2	18	PDB header: ligase Chain: B: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
26	c6bjuD_	Alignment	not modelled	15.4	21	PDB header: unknown function Chain: D: PDB Molecule: atzh; PDBTitle: the structure of atzh: a little known member of the atrazine breakdown2 pathway
27	d2rcda1	Alignment	not modelled	14.7	29	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
28	d2pjsa1	Alignment	not modelled	14.6	30	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Antibiotic resistance proteins

29	c5exvD	 Alignment	not modelled	14.5	20	PDB header: heme-binding protein Chain: D: PDB Molecule: hemin-degrading hems.chux domain protein; PDBTitle: crystal structure of heme binding protein hutx from vibrio cholerae
30	d1r6ta2	 Alignment	not modelled	14.3	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
31	c2ph0A	 Alignment	not modelled	14.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q6d2t7_erwct protein from erwinia carotovora.2 nesg target ewr41.
32	c1r6tA	 Alignment	not modelled	13.9	11	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of human tryptophanyl-trna synthetase
33	c3r6aB	 Alignment	not modelled	13.8	10	PDB header: isomerase, lyase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein (hypothetical protein2 mm_3218) from methanosarcina mazei.
34	d1vcca	 Alignment	not modelled	13.7	25	Fold: DNA topoisomerase I domain Superfamily: DNA topoisomerase I domain Family: Vaccinia DNA topoisomerase I, 9 kDa N-terminal fragment
35	c3m2oB	 Alignment	not modelled	13.7	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: glyoxalase/bleomycin resistance protein; PDBTitle: crystal structure of a putative glyoxalase/bleomycin resistance2 protein from rhodopseudomonas palustris cga009
36	c4pavA	 Alignment	not modelled	13.6	18	PDB header: unknown function Chain: A: PDB Molecule: glyoxalase family protein; PDBTitle: structure of hypothetical protein sa1046 from s. aureus.
37	c5tmxA	 Alignment	not modelled	12.8	22	PDB header: transcription regulator Chain: A: PDB Molecule: protein sini; PDBTitle: solution structure of sini, antagonist to the master biofilm-regulator2 sinr in bacillus subtilis
38	c2k53A	 Alignment	not modelled	12.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a3dk08 protein; PDBTitle: nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
39	d1lq1a	 Alignment	not modelled	12.6	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: Spo0A
40	d3b7ca1	 Alignment	not modelled	12.1	26	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
41	c5z08A	 Alignment	not modelled	12.0	24	PDB header: cell cycle Chain: A: PDB Molecule: cenp-i; PDBTitle: the crystal structure of kinetochore subunits cenp-h//k triple2 complex
42	d1jifa	 Alignment	not modelled	12.0	15	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Antibiotic resistance proteins
43	c3rriB	 Alignment	not modelled	11.9	33	PDB header: metal binding protein Chain: B: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase from alicyclobacillus acidocaldarius
44	c3ct8A	 Alignment	not modelled	11.6	33	PDB header: lyase Chain: A: PDB Molecule: putative glyoxalase; PDBTitle: crystal structure of a putative glyoxalase (np_243026.1) from bacillus2 halodurans at 2.10 a resolution
45	d1fc3a	 Alignment	not modelled	11.5	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: Spo0A
46	c2ma3A	 Alignment	not modelled	11.2	6	PDB header: replication Chain: A: PDB Molecule: dna replication initiator (cdc21/cdc54); PDBTitle: nmr solution structure of the c-terminus of the minichromosome2 maintenance protein mcm from methanothermobacter thermotrophicus
47	c5ig4A	 Alignment	not modelled	11.1	6	PDB header: transferase Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of n. vectensis camkii-a hub
48	c3kolA	 Alignment	not modelled	11.0	19	PDB header: metal binding protein Chain: A: PDB Molecule: glyoxalase/bleomycin resistance PDBTitle: crystal structure of a glyoxalase/dioxygenase from nostoc2 punctiforme
49	d2hqva1	 Alignment	not modelled	10.8	21	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: ChuX-like
50	c2k5eA	 Alignment	not modelled	10.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of a putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
51	c5ihxB	 Alignment	not modelled	10.4	19	PDB header: ligase Chain: B: PDB Molecule: tyrosine--trna ligase, mitochondrial; PDBTitle: crystal structure of a c-terminally truncated aspergillus nidulans2 mitochondrial tyrosyl-trna synthetase
52	c6iptB	 Alignment	not modelled	10.4	38	PDB header: transferase Chain: B: PDB Molecule: all3014 protein; PDBTitle: crystal structure of a fosfomycin and bleomycin resistant protein from2 anabaena/nostoc cyanobacterium at 1.70 a resolution
53	c3hZR_D	 Alignment	not modelled	10.3	6	PDB header: ligase Chain: D: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase homolog from entamoeba

						histolytica
54	c3i05B_	Alignment	not modelled	10.1	16	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from trypanosoma brucei
55	c3w0ID_	Alignment	not modelled	10.1	18	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: glucokinase regulatory protein; PDBTitle: the crystal structure of xenopus glucokinase and glucokinase2 regulatory protein complex
56	c6byqA_	Alignment	not modelled	10.0	28	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of tyrosine-trna ligase from helicobacter pylori g27
57	d2af7a1_	Alignment	not modelled	9.8	15	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
58	c3g12A_	Alignment	not modelled	9.6	13	PDB header: lyase Chain: A: PDB Molecule: putative lactoylglutathione lyase; PDBTitle: crystal structure of a putative lactoylglutathione lyase from2 bdellovibrio bacteriovorus
59	c2rkjM_	Alignment	not modelled	9.3	25	PDB header: ligase/rna Chain: M: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: cocrystal structure of a tyrosyl-trna synthetase splicing factor with2 a group i intron rna
60	c1yn5B_	Alignment	not modelled	9.1	13	PDB header: unknown function Chain: B: PDB Molecule: eaph2; PDBTitle: crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens
61	d3pvia_	Alignment	not modelled	8.9	88	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease PvuII
62	c6a4zA_	Alignment	not modelled	8.9	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: chap protein; PDBTitle: oxidase chap
63	c2ip1A_	Alignment	not modelled	8.8	20	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
64	c4oudB_	Alignment	not modelled	8.8	31	PDB header: ligase Chain: B: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine
65	c2ts1A_	Alignment	not modelled	8.8	28	PDB header: ligase (synthetase) Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of tyrosyl-trna synthetase refined at 2.3 angstroms2 resolution. interaction of the enzyme with the tyrosyl adenylate3 intermediate
66	d2ts1a_	Alignment	not modelled	8.8	28	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
67	d1xrka_	Alignment	not modelled	8.7	25	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Antibiotic resistance proteins
68	d2gxba1_	Alignment	not modelled	8.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
69	c2n5jA_	Alignment	not modelled	8.5	19	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: regnase-1 n-terminal domain
70	d1qbjc_	Alignment	not modelled	8.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
71	c3zf7V_	Alignment	not modelled	8.2	24	PDB header: ribosome Chain: V: PDB Molecule: 60s ribosomal protein l22, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
72	d1h3fa1_	Alignment	not modelled	8.2	26	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
73	d2oy9a1_	Alignment	not modelled	8.1	32	Fold: BH2638-like Superfamily: BH2638-like Family: BH2638-like
74	c1h3eA_	Alignment	not modelled	8.1	29	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from thermus thermophilus complexed with wild-2 type trnatyr(gua) and with atp and tyrosinol
75	d1qiqpa_	Alignment	not modelled	8.0	30	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Glyoxalase I (lactoylglutathione lyase)
76	c4ovmE_	Alignment	not modelled	8.0	17	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus
77	c1h3oA_	Alignment	not modelled	8.0	31	PDB header: transcription/tbp-associated factors Chain: A: PDB Molecule: transcription initiation factor tfiid 135 kda subunit; PDBTitle: crystal structure of the human taf4-taf12 (tafii135-tafii20) complex
78	d1h3oa_	Alignment	not modelled	8.0	31	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
						PDB header: oxidoreductase

79	c4rt5A	Alignment	not modelled	7.9	36	Chain: A: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: the crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase protein from planctomyces limnophilus dsm 3776
80	c2m45A	Alignment	not modelled	7.9	8	PDB header: hydrolase Chain: A: PDB Molecule: minichromosome maintenance protein mcm; PDBTitle: nmr solution structure of the c-terminus of the minichromosome2 maintenance protein mcm from sulfolobus solfataricus
81	c2kjaA	Alignment	not modelled	7.6	18	PDB header: unknown function Chain: A: PDB Molecule: atc0852; PDBTitle: solution nmr structure of protein atc0852 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att2.
82	c6a52A	Alignment	not modelled	7.6	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: dioxidase chap-h1; PDBTitle: oxidase chap-h1
83	c1yn3A	Alignment	not modelled	7.5	25	PDB header: toxin, protein binding Chain: A: PDB Molecule: truncated cell surface protein map-w; PDBTitle: crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens
84	c4bbaA	Alignment	not modelled	7.5	15	PDB header: protein-binding protein Chain: A: PDB Molecule: glucokinase regulatory protein; PDBTitle: crystal structure of glucokinase regulatory protein complexed to2 phosphate
85	d1qgpa	Alignment	not modelled	7.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
86	c1yn4A	Alignment	not modelled	7.4	13	PDB header: unknown function Chain: A: PDB Molecule: seaph1; PDBTitle: crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens
87	c5ijxA	Alignment	not modelled	7.4	25	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase, mitochondrial; PDBTitle: crystal structure of a c-terminally truncated coccidioides posadasii2 mitochondrial tyrosyl-trna synthetase
88	c3a05A	Alignment	not modelled	7.4	22	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
89	c6otjA	Alignment	not modelled	7.3	31	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of tyrosyl-trna synthetase from neisseria2 gonorrhoeae with bound l-tyr
90	d1hkxa	Alignment	not modelled	7.3	17	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
91	d1id3b	Alignment	not modelled	7.2	9	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
92	d2j0pa1	Alignment	not modelled	7.0	24	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/ChuS-like
93	c3r4qB	Alignment	not modelled	7.0	30	PDB header: lyase Chain: B: PDB Molecule: lactoylglutathione lyase; PDBTitle: crystal structure of lactoylglutathione lyase from agrobacterium2 tumefaciens
94	c3ff5B	Alignment	not modelled	6.9	24	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
95	c4z04A	Alignment	not modelled	6.8	40	PDB header: lyase Chain: A: PDB Molecule: glyoxalase/bleomycin resistance /dioxygenase superfamily PDBTitle: crystal structure of a probable lactoylglutathione lyase from brucella2 melitensis in complex with glutathione
96	d1ecsa	Alignment	not modelled	6.7	50	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Antibiotic resistance proteins
97	d1jx4a1	Alignment	not modelled	6.7	24	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
98	c3h51A	Alignment	not modelled	6.7	22	PDB header: protein binding Chain: A: PDB Molecule: putative calcium/calmodulin dependent protein kinase ii PDBTitle: crystal structure of putative calcium/calmodulin dependent protein2 kinase ii association domain (np_636218.1) from xanthomonas3 campestris at 1.70 a resolution
99	c2qh0A	Alignment	not modelled	6.6	30	PDB header: lyase Chain: A: PDB Molecule: lactoylglutathione lyase; PDBTitle: crystal structure of a glyoxalase from clostridium acetobutylicum