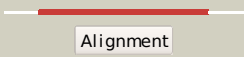

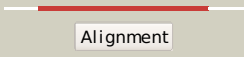

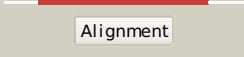

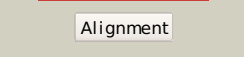

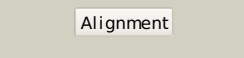

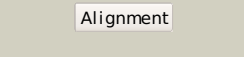

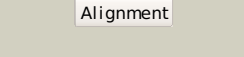

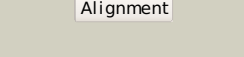



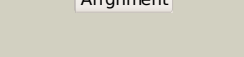

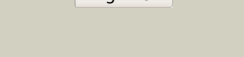


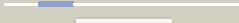


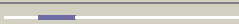

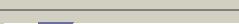

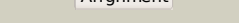

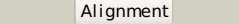
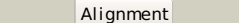
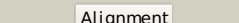



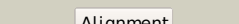

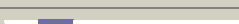


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlpg4a_	 Alignment		100.0	18	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
2	c2vsqA_	 Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a2 nonribosomal peptide synthetase termination module
3	c3e7wA_	 Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 1; PDBTitle: crystal structure of dlta: implications for the reaction2 mechanism of non-ribosomal peptide synthetase (nrps)3 adenylation domains
4	dlry2a_	 Alignment		100.0	21	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
5	dlmdba_	 Alignment		100.0	21	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
6	d3cw9a1	 Alignment		100.0	25	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
7	dlamua_	 Alignment		100.0	18	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
8	clamuB_	 Alignment		100.0	17	PDB header: peptide synthetase Chain: B: PDB Molecule: gramicidin synthetase 1; PDBTitle: phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
9	c3gqwB_	 Alignment		100.0	18	PDB header: ligase Chain: B: PDB Molecule: fatty acid amp ligase; PDBTitle: crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
10	c3ni2A_	 Alignment		100.0	23	PDB header: ligase Chain: A: PDB Molecule: 4-coumarate:coa ligase; PDBTitle: crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
11	c3eynB_	 Alignment		100.0	21	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

12	c3etcB_	Alignment		100.0	21	PDB header: ligase Chain: B: PDB Molecule: amp-binding protein; PDBTitle: 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
13	c3dhvA_	Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of dlta protein in complex with d-alanine2 adenylate
14	c3kxwA_	Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
15	c2d1tA_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferin 4-monooxygenase; PDBTitle: crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue
16	c3iteB_	Alignment		100.0	15	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-2 ribosomal peptide synthetase
17	c2v7bB_	Alignment		100.0	21	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
18	c3iplB_	Alignment		100.0	22	PDB header: ligase Chain: B: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
19	c3l8cA_	Alignment		100.0	15	PDB header: ligase Chain: A: PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 1; PDBTitle: structure of probable d-alanine--poly(phosphoribitol) ligase2 subunit-1 from streptococcus pyogenes
20	c3nyrA_	Alignment		100.0	23	PDB header: ligase Chain: A: PDB Molecule: malonyl-coa ligase; PDBTitle: malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
21	c3tsyA_	Alignment	not modelled	100.0	22	PDB header: ligase, transferase Chain: A: PDB Molecule: fusion protein 4-coumarate--coa ligase 1, resveratrol PDBTitle: 4-coumaroyl-coa ligase::stilbene synthase fusion protein
22	d1lcia_	Alignment	not modelled	100.0	18	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
23	d1v25a_	Alignment	not modelled	100.0	25	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
24	c3g7sA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: long-chain-fatty-acid--coa ligase (fadd-1); PDBTitle: crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
25	c3o82B_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B: PDB Molecule: peptide arylation enzyme; PDBTitle: structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
26	c3ivrA_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: putative long-chain-fatty-acid coa ligase; PDBTitle: crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodopseudomonas palustris cga009
27	c3o82A_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: peptide arylation enzyme; PDBTitle: structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
28	c3o53A_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: fatty-acid-coa ligase fadd28;

28	c2y3A	Alignment	not modelled	100.0	15	PDBTitle: crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis PDB header: ligase
29	c2y4oA	Alignment	not modelled	100.0	16	Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
30	c2y27B	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
31	c3qovD	Alignment	not modelled	100.0	14	PDB header: ligase Chain: D: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
32	c3laxA	Alignment	not modelled	99.4	12	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
33	c3hguB	Alignment	not modelled	99.2	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
34	d2aya1	Alignment	not modelled	62.4	14	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)
35	d1pl8a2	Alignment	not modelled	59.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
36	d1piwa2	Alignment	not modelled	57.3	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
37	d1e3ja2	Alignment	not modelled	52.9	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
38	c3ippA	Alignment	not modelled	52.2	8	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
39	c1uarA	Alignment	not modelled	51.5	10	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
40	c3e4fB	Alignment	not modelled	50.4	13	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside n3-acetyltransferase; PDBTitle: crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
41	c3smaD	Alignment	not modelled	49.3	34	PDB header: transferase Chain: D: PDB Molecule: frbf; PDBTitle: a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
42	c3bcxA	Alignment	not modelled	47.5	14	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- PDBTitle: e1 dehydrase
43	d2nyga1	Alignment	not modelled	45.4	13	Fold: TTHA0583/YokD-like Superfamily: TTHA0583/YokD-like Family: Aminoglycoside 3-N-acetyltransferase-like
44	c2jwlB	Alignment	not modelled	44.3	14	PDB header: membrane protein Chain: B: PDB Molecule: protein tolR; PDBTitle: solution structure of periplasmic domain of tolR from h.2 influenzae with saxs data
45	c3olhA	Alignment	not modelled	43.6	15	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
46	d1d1ta2	Alignment	not modelled	42.8	7	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
47	d1e3ia2	Alignment	not modelled	41.1	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
48	d1rjwa2	Alignment	not modelled	38.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
49	d1kola2	Alignment	not modelled	38.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
50	d1z7wa1	Alignment	not modelled	35.5	11	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
51	d1pkla3	Alignment	not modelled	34.8	13	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
52	c3eegB	Alignment	not modelled	34.6	15	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
53	d1p0fa2	Alignment	not modelled	34.6	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
						Fold: Ferredoxin-like

54	dli1ga2	Alignment	not modelled	33.9	16	Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
55	d1m5wa_	Alignment	not modelled	33.7	16	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
56	c1vs3B_	Alignment	not modelled	33.6	15	PDB header: isomerase Chain: B: PDB Molecule: trna pseudouridine synthase a; PDBTitle: crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
57	c3aaxB_	Alignment	not modelled	32.6	21	PDB header: transferase Chain: B: PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
58	c3ewbX_	Alignment	not modelled	32.0	13	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
59	d1udxa3	Alignment	not modelled	29.7	17	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
60	d1liua3	Alignment	not modelled	26.3	19	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
61	d1a3xa3	Alignment	not modelled	25.8	17	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
62	d2fzwa2	Alignment	not modelled	25.6	7	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
63	d1liua2	Alignment	not modelled	25.3	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
64	d2jhfa2	Alignment	not modelled	25.1	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
65	d2af4c1	Alignment	not modelled	25.0	25	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
66	d1cdoa2	Alignment	not modelled	24.9	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
67	c2zy3A_	Alignment	not modelled	24.9	14	PDB header: lyase Chain: A: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
68	d1uufa2	Alignment	not modelled	24.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
69	d1ykfa2	Alignment	not modelled	24.5	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
70	d1aisa1	Alignment	not modelled	24.5	19	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
71	d1u3wa2	Alignment	not modelled	24.3	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
72	d2g50a3	Alignment	not modelled	24.0	13	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
73	d1okga1	Alignment	not modelled	22.0	17	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multi domain sulfurtransferase (rhodanese)
74	d1wkva1	Alignment	not modelled	21.3	14	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
75	d1jqba2	Alignment	not modelled	21.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
76	d1ja1a1	Alignment	not modelled	20.8	15	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: NADPH-cytochrome p450 reductase FAD-binding domain-like
77	d1uara2	Alignment	not modelled	20.7	10	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multi domain sulfurtransferase (rhodanese)
78	d1iz0a2	Alignment	not modelled	20.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
79	c1oftC_	Alignment	not modelled	20.3	17	PDB header: bacterial cell division inhibitor Chain: C: PDB Molecule: hypothetical protein pa3008; PDBTitle: crystal structure of sula from pseudomonas aeruginosa
80	c1ydnA_	Alignment	not modelled	20.2	14	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.

81	c1e0cA	 Alignment	not modelled	20.1	14	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
82	d1f8fa2	 Alignment	not modelled	20.0	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
83	c2pfuA	 Alignment	not modelled	19.6	13	PDB header: transport protein Chain: A: PDB Molecule: biopolymer transport exbd protein; PDBTitle: nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
84	d1k92a1	 Alignment	not modelled	19.2	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
85	c3pc3A	 Alignment	not modelled	19.0	14	PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
86	c1b74A	 Alignment	not modelled	18.9	16	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus
87	d1f20a1	 Alignment	not modelled	18.6	14	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: NADPH-cytochrome p450 reductase FAD-binding domain-like
88	c1okgA	 Alignment	not modelled	18.5	17	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
89	c1l9xA	 Alignment	not modelled	18.4	34	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
90	d1l9xa	 Alignment	not modelled	18.4	34	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
91	d1ofux	 Alignment	not modelled	18.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Bacterial cell division inhibitor SulA
92	c3a2kB	 Alignment	not modelled	17.8	12	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysidine synthase; PDBTitle: crystal structure of tils complexed with trna
93	c3bleA	 Alignment	not modelled	17.7	19	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in2 complexed with malonate
94	c3g8qA	 Alignment	not modelled	17.5	22	PDB header: rna binding protein Chain: A: PDB Molecule: predicted rna-binding protein, contains thump PDBTitle: a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
95	c2jkzB	 Alignment	not modelled	17.3	4	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5' 3 - monophosphate) (orthorhombic crystal form)
96	d1nula	 Alignment	not modelled	17.2	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
97	d1uaaa2	 Alignment	not modelled	17.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
98	c3ju7B	 Alignment	not modelled	16.7	15	PDB header: transferase Chain: B: PDB Molecule: putative plp-dependent aminotransferase; PDBTitle: crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
99	c2iruA	 Alignment	not modelled	16.4	18	PDB header: transferase Chain: A: PDB Molecule: putative dna ligase-like protein rv0938/mt0965; PDBTitle: crystal structure of the polymerase domain from mycobacterium tuberculosis ligase d