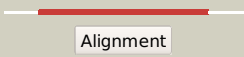
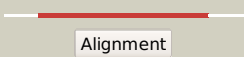
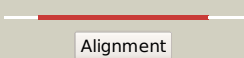
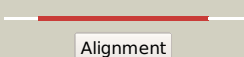
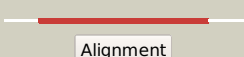
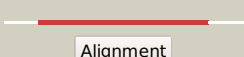
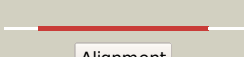
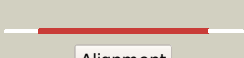
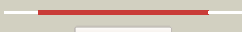
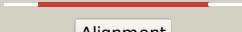
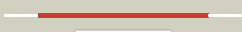
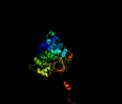
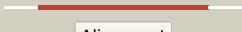
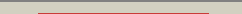
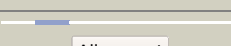
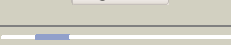
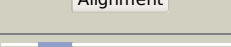
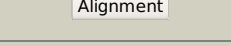
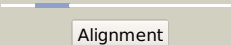
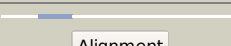
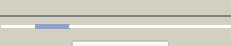
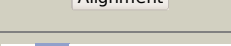
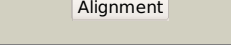
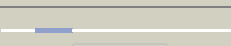
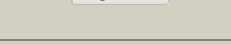
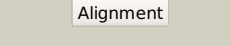
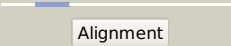
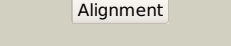


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pg4a_	 Alignment		100.0	21	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
2	d1ry2a_	 Alignment		100.0	23	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
3	c4wd1A_	 Alignment		100.0	16	PDB header: ligase Chain: A: PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
4	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
5	c3etcB_	 Alignment		100.0	23	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
6	c3e7wA_	 Alignment		100.0	17	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
7	d3cw9a1	 Alignment		100.0	21	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
8	d1mdba_	 Alignment		100.0	20	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
9	c3vngA_	 Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
10	c4eatB_	 Alignment		100.0	23	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
11	c3ni2A_	 Alignment		100.0	26	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

12	c4dg8A_	 Alignment		100.0	16	PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and pcp2 domains
13	c3r44A_	 Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
14	d1amua_	 Alignment		100.0	20	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
15	d1v25a_	 Alignment		100.0	22	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
16	c1amuB_	 Alignment		100.0	20	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
17	c3iplB_	 Alignment		100.0	21	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
18	c4fuqD_	 Alignment		100.0	25	PDB header: ligase Chain: D: PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodopseudomonas palustris
19	c3tsyA_	 Alignment		100.0	21	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
20	c4oxiA_	 Alignment		100.0	15	PDB header: ligase Chain: A: PDB Molecule: enterobactin synthetase component f-related protein; PDBTitle: crystal structure of vibrio cholerae adenylation domain alme in2 complex with glycyl-adenosine-5'-phosphate
21	c3eynB_	 Alignment	not modelled	100.0	22	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
22	c3rg2H_	 Alignment	not modelled	100.0	19	PDB header: ligase Chain: H: PDB Molecule: enterobactin synthase component e (ente), 2,3-dihydro-2,3- PDBTitle: structure of a two-domain nrps fusion protein containing the ente2 adenylation domain and entb aryl-carrier protein from enterobactin3 biosynthesis
23	c4ir7A_	 Alignment	not modelled	100.0	20	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
24	c2d1tA_	 Alignment	not modelled	100.0	24	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
25	c3nyrA_	 Alignment	not modelled	100.0	25	PDB header: ligase Chain: A: PDB Molecule: malonyl-coa ligase; PDBTitle: malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
26	c4dg9A_	 Alignment	not modelled	100.0	16	PDB header: ligase/inhibitor Chain: A: PDB Molecule: pa1221; PDBTitle: structure of holo-pa1221, an nrps protein containing adenylation and2 pcp domains bound to vinylsulfonamide inhibitor
27	c3dhvA_	 Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of dlta protein in complex with d-alanine2 adenylate
		 Alignment				PDB header: ligase

28	c3iteB_	Alignment	not modelled	100.0	17	Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
29	c2v7bB_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
30	c3gqwB_	Alignment	not modelled	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
31	d1lcia_	Alignment	not modelled	100.0	23	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
32	c3g7sA_	Alignment	not modelled	100.0	26	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
33	c3kxwA_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
34	c3l8cA_	Alignment	not modelled	100.0	17	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
35	c4gr5B_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of sign1deltaasub in complex with ampcpp
36	c3o82B_	Alignment	not modelled	100.0	19	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
37	c3o82A_	Alignment	not modelled	100.0	19	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
38	c3ivrA_	Alignment	not modelled	100.0	20	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
39	c3qyaA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
40	c4lgcA_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: bile acid-coenzyme a ligase; PDBTitle: crystal structure of a bile acid-coenzyme a ligase (baib) from2 clostridium scindens (vpi 12708) at 2.19 a resolution
41	c3t5cA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: probable chain-fatty-acid-coa ligase fadd13; PDBTitle: crystal structure of n-terminal domain of fac113 from mycobacterium2 tuberculosis in different space group c2
42	c3wv4B_	Alignment	not modelled	100.0	26	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of vinn
43	c3e53A_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: fatty-acid-coa ligase fadd28; PDBTitle: crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis
44	c2y4oA_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
45	c2y27B_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
46	c3qovD_	Alignment	not modelled	100.0	15	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
47	c4gs5A_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: acyl-coa synthetase (amp-forming)/amp-acid ligase ii-like PDBTitle: the crystal structure of acyl-coa synthetase (amp-forming)/amp-acid2 ligase ii-like protein from dyadobacter fermentans dsm 18053
48	c3laxA_	Alignment	not modelled	99.2	13	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
49	c3hguB_	Alignment	not modelled	99.0	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
50	c4eplA_	Alignment	not modelled	98.0	18	PDB header: ligase Chain: A: PDB Molecule: jasmonic acid-amido synthetase jar1; PDBTitle: crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile
51	c4b2gB_	Alignment	not modelled	97.9	13	PDB header: signaling protein Chain: B: PDB Molecule: gh3-1 auxin conjugating enzyme; PDBTitle: crystal structure of an indole-3-acetic acid amido synthase2 from vitis vinifera involved in auxin homeostasis
52	c4gwwB_	Alignment	not modelled	96.2	11	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase

52	c4ewvD	Alignment	not modelled	90.2	11	gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
53	d2ayia1	Alignment	not modelled	78.3	17	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)
54	c3u5rG	Alignment	not modelled	61.2	18	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein smc02350 from2 sinorhizobium meliloti 1021
55	d1piwa2	Alignment	not modelled	61.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
56	d1kola2	Alignment	not modelled	58.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
57	c3smaD	Alignment	not modelled	58.8	25	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
58	d1e3ja2	Alignment	not modelled	57.7	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
59	c2ywiA	Alignment	not modelled	52.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
60	c4k2bA	Alignment	not modelled	49.8	26	PDB header: transferase Chain: A: PDB Molecule: ntd biosynthesis operon protein ntda; PDBTitle: crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
61	c3e4fB	Alignment	not modelled	44.4	23	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside n3-acetyltransferase; PDBTitle: crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
62	d1pl8a2	Alignment	not modelled	43.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
63	d1rjwa2	Alignment	not modelled	43.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
64	d2nyga1	Alignment	not modelled	42.1	25	Fold: TTHA0583/YokD-like Superfamily: TTHA0583/YokD-like Family: Aminoglycoside 3-N-acetyltransferase-like
65	d1d1ta2	Alignment	not modelled	40.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
66	c3ippA	Alignment	not modelled	38.5	5	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
67	d1iz0a2	Alignment	not modelled	37.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
68	c4lmaA	Alignment	not modelled	37.7	9	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure analysis of o-acetylserine sulfhydrylase cysk1 from2 microcystis aeruginosa 7806
69	c1uarA	Alignment	not modelled	37.6	10	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
70	d1ilga2	Alignment	not modelled	37.2	18	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
71	d1llua2	Alignment	not modelled	37.1	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
72	d1e3ia2	Alignment	not modelled	36.3	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
73	d1p0fa2	Alignment	not modelled	34.4	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
74	d1ykfa2	Alignment	not modelled	32.6	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
75	d1udxa3	Alignment	not modelled	32.0	19	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
76	d1aisa1	Alignment	not modelled	31.5	24	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
77	c4d0kC	Alignment	not modelled	31.4	21	PDB header: gene regulation Chain: C: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit PDBTitle: complex of chaetomium thermophilum pan2 (wd40-cs1) with pan3 (c-term)
78	d1z7wa1	Alignment	not modelled	30.5	10	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

79	c4aecB	 Alignment	not modelled	29.5	9	PDB header: lyase Chain: B: PDB Molecule: cysteine synthase, mitochondrial; PDBTitle: crystal structure of the arabidopsis thaliana o-acetyl-2 serine-(thiol)-lyase c
80	d1uufa2	 Alignment	not modelled	28.3	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
81	c4trbA	 Alignment	not modelled	27.5	20	PDB header: transferase Chain: A: PDB Molecule: purine phosphoribosyltransferase (gpt-1); PDBTitle: sulfolobus solfataricus adenine phosphoribosyltransferase
82	c3olhA	 Alignment	not modelled	27.0	15	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
83	d1l9xa	 Alignment	not modelled	26.8	31	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
84	c1l9xA	 Alignment	not modelled	26.8	31	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
85	c3vbeA	 Alignment	not modelled	26.6	11	PDB header: transferase Chain: A: PDB Molecule: beta-cyanoalanine synthase; PDBTitle: crystal structure of beta-cyanoalanine synthase in soybean
86	d1jqba2	 Alignment	not modelled	26.4	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
87	c4l8fA	 Alignment	not modelled	26.1	24	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtX
88	d1jvba2	 Alignment	not modelled	25.2	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
89	d1wi0a	 Alignment	not modelled	24.7	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
90	c2jwlB	 Alignment	not modelled	24.5	23	PDB header: membrane protein Chain: B: PDB Molecule: protein tolR; PDBTitle: solution structure of periplasmic domain of tolR from h.2 influenzae with saxes data
91	c1yj7A	 Alignment	not modelled	24.0	26	PDB header: protein transport Chain: A: PDB Molecule: escJ; PDBTitle: crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escJ
92	d1u3wa2	 Alignment	not modelled	23.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
93	d2jhfa2	 Alignment	not modelled	23.4	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
94	d1y7la1	 Alignment	not modelled	23.1	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
95	d1cdoa2	 Alignment	not modelled	22.6	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
96	d1wkva1	 Alignment	not modelled	22.0	8	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
97	c2zbcH	 Alignment	not modelled	21.7	28	PDB header: transcription Chain: H: PDB Molecule: 83aa long hypothetical transcriptional regulator asnc; PDBTitle: crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
98	c1ydnA	 Alignment	not modelled	21.2	18	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.
99	c3ewbX	 Alignment	not modelled	21.1	14	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
100	d2fzwa2	 Alignment	not modelled	21.0	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
101	c3aaxB	 Alignment	not modelled	20.7	13	PDB header: transferase Chain: B: PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form