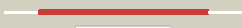
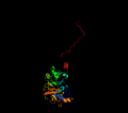
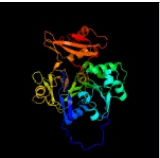
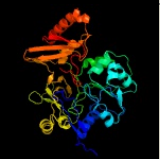
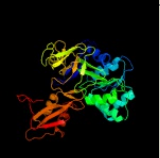
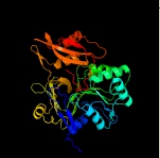
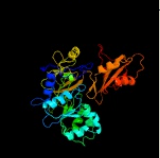
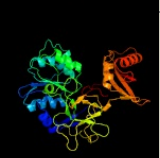
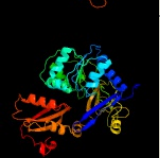
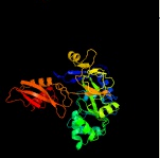


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qovD_	 Alignment		100.0	23	PDB header: ligase Chain: D: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
2	c2y27B_	 Alignment		100.0	24	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
3	c2y4oA_	 Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
4	d1pg4a_	 Alignment		100.0	16	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
5	c3hguB_	 Alignment		100.0	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
6	c2vsgA_	 Alignment		100.0	14	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
7	c4wd1A_	 Alignment		100.0	14	PDB header: ligase Chain: A: PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
8	d1ry2a_	 Alignment		100.0	16	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
9	c3tsyA_	 Alignment		100.0	14	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
10	c3etcB_	 Alignment		100.0	13	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
11	c3e7wA_	 Alignment		100.0	14	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

12	d1mdba_	Alignment		100.0	15	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
13	c3gqwB_	Alignment		100.0	15	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
14	d3cw9a1	Alignment		100.0	17	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
15	c3vngA_	Alignment		100.0	14	PDB header: ligase Chain: A: PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
16	c3ni2A_	Alignment		100.0	13	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
17	c3eynB_	Alignment		100.0	13	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
18	c3rg2H_	Alignment		100.0	13	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
19	c3kxwA_	Alignment		100.0	12	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
20	c3nyrA_	Alignment		100.0	16	PDB header: ligase Chain: A: PDB Molecule: malonyl-coa ligase; PDBTitle: malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
21	c4eatB_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
22	c3iplB_	Alignment	not modelled	100.0	15	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
23	c3iteB_	Alignment	not modelled	100.0	13	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide synthetase
24	c4dg8A_	Alignment	not modelled	100.0	12	PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and2 pcp domains
25	c4gs5A_	Alignment	not modelled	100.0	18	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
26	c4dg9A_	Alignment	not modelled	100.0	13	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	c4ir7A_	Alignment	not modelled	100.0	13	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
28	c2v7bB_	Alignment	not modelled	100.0	13	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structures of a benzoate coa ligase from2

					burkholderia xenovorans lb400
29	c2d1tA_	Alignment	not modelled	99.9	12 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
30	c4oxiA_	Alignment	not modelled	99.9	13 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 glycyi-adenosine-5'-phosphate
31	d1v25a_	Alignment	not modelled	99.9	16 Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
32	c4fuqD_	Alignment	not modelled	99.9	12 PDB header: ligase Chain: D: PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodopseudomonas palustris
33	c3r44A_	Alignment	not modelled	99.9	12 PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
34	c3g7sA_	Alignment	not modelled	99.9	13 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
35	c1amuB_	Alignment	not modelled	99.9	13 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
36	d1amua_	Alignment	not modelled	99.9	13 Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
37	c3dhvA_	Alignment	not modelled	99.9	13 PDB header: ligase Chain: A: PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of dlta protein in complex with d-alanine2 adenylate
38	c4gr5B_	Alignment	not modelled	99.9	17 PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
39	c3l8cA_	Alignment	not modelled	99.9	14 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
40	d1lcia_	Alignment	not modelled	99.9	10 Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
41	c4eplA_	Alignment	not modelled	99.9	14 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
42	c4lqcA_	Alignment	not modelled	99.9	10 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
43	c4b2gB_	Alignment	not modelled	99.8	16 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
44	c3o82B_	Alignment	not modelled	99.8	16 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
45	c3qyaA_	Alignment	not modelled	99.7	10 PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
46	c3o82A_	Alignment	not modelled	99.7	16 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
47	c3e53A_	Alignment	not modelled	99.7	14 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
48	c3ivrA_	Alignment	not modelled	99.6	13 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
49	c3wv4B_	Alignment	not modelled	99.6	13 PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of vinn
50	c4ewvB_	Alignment	not modelled	99.5	15 PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
51	c3t5cA_	Alignment	not modelled	99.3	13 PDB header: ligase Chain: A: PDB Molecule: probable chain-fatty-acid-coa ligase fadd13; PDBTitle: crystal structure of n-terminal domain of facl13 from mycobacterium2 tuberculosis in different space group c2
52	c3laxA_	Alignment	not modelled	99.3	19 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
					PDB header: transferase

53	c3ezxA	Alignment	not modelled	85.2	12	Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
54	c4jgiB	Alignment	not modelled	83.1	13	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
55	c2i2xD	Alignment	not modelled	81.2	13	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
56	c1y80A	Alignment	not modelled	76.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
57	c3whpA	Alignment	not modelled	72.0	16	PDB header: gene regulation Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
58	d3bula2	Alignment	not modelled	67.8	11	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
59	c1bmtB	Alignment	not modelled	65.7	11	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
60	c1k98A	Alignment	not modelled	54.9	12	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
61	c1xrsB	Alignment	not modelled	53.9	18	PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
62	c3k0IA	Alignment	not modelled	44.3	12	PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
63	d1ccwa	Alignment	not modelled	39.0	8	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
64	c3ebrA	Alignment	not modelled	37.6	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized rmlc-like cupin; PDBTitle: crystal structure of an rmlc-like cupin protein (reut a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
65	d2fbia1	Alignment	not modelled	36.3	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
66	d1xrsb1	Alignment	not modelled	31.7	20	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
67	c2yxBA	Alignment	not modelled	29.3	12	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
68	d1e4ft2	Alignment	not modelled	25.8	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
69	c2iruA	Alignment	not modelled	25.4	17	PDB header: transferase Chain: A: PDB Molecule: putative dna ligase-like protein rv0938/mt0965; PDBTitle: crystal structure of the polymerase domain from mycobacterium2 tuberculosis ligase d
70	c3bjaA	Alignment	not modelled	23.5	8	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
71	c3tadB	Alignment	not modelled	21.6	36	PDB header: protein binding Chain: B: PDB Molecule: liprin-alpha-2; PDBTitle: crystal structure of the liprin-alpha/liprin-beta complex
72	c2wh7A	Alignment	not modelled	21.1	31	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase-phage associated; PDBTitle: the partial structure of a group a streptpcoccal phage-2 encoded tail fibre hyaluronate lyase hylp2
73	c3e6mD	Alignment	not modelled	20.3	12	PDB header: transcription regulator Chain: D: PDB Molecule: marr family transcriptional regulator; PDBTitle: the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
74	d1whua	Alignment	not modelled	19.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 Family: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3
75	c2q60C	Alignment	not modelled	17.6	15	PDB header: transcription Chain: C: PDB Molecule: retinoid x receptor; PDBTitle: crystal structure of the ligand binding domain of polyandrocarpa2 misakiensis rxr in tetramer in absence of ligand
76	c4hh3C	Alignment	not modelled	16.4	12	PDB header: flavoprotein/transcription Chain: C: PDB Molecule: appa protein; PDBTitle: structure of the appa-ppsr2 core complex from rb. sphaeroides
77	c1stzB	Alignment	not modelled	16.2	13	PDB header: transcription Chain: B: PDB Molecule: heat-inducible transcription repressor hrca homolog; PDBTitle: crystal structure of a hypothetical protein at 2.2 a resolution
						PDB header: ligase

78	c3oqhB_	Alignment	not modelled	15.9	21	Chain: B: PDB Molecule: putative uncharacterized protein yvmc; PDBTitle: crystal structure of b. licheniformis cdps yvmc-blic
79	c2oceA_	Alignment	not modelled	15.7	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
80	d2a61a1	Alignment	not modelled	13.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
81	d7reqa2	Alignment	not modelled	13.3	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
82	c2faoB_	Alignment	not modelled	13.3	28	PDB header: hydrolase/transferase Chain: B: PDB Molecule: probable atp-dependent dna ligase; PDBTitle: crystal structure of pseudomonas aeruginosa ligd polymerase2 domain
83	d1rcwa_	Alignment	not modelled	13.2	18	Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: PqQC-like
84	d1coka_	Alignment	not modelled	12.9	27	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
85	c4ryaA_	Alignment	not modelled	12.9	8	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate binding protein (sorbitol); PDBTitle: crystal structure of abc transporter solute binding protein avi_35672 from agrobacterium vitis s4, target efi-510645, with bound d-mannitol
86	d3bzka3	Alignment	not modelled	12.9	11	Fold: Tex N-terminal region-like Superfamily: Tex N-terminal region-like Family: Tex N-terminal region-like
87	c2kncB_	Alignment	not modelled	12.8	30	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaib-beta3 transmembrane-cytoplasmic2 heterocomplex
88	d1nzpa_	Alignment	not modelled	12.7	15	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
89	c2ltdA_	Alignment	not modelled	12.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ydbc; PDBTitle: solution nmr structure of apo ydbc from lactococcus lactis, northeast2 structural genomics consortium (nesg) target kr150
90	d1uwda_	Alignment	not modelled	12.6	19	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
91	d2fmpa1	Alignment	not modelled	12.6	19	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
92	d1q6za2	Alignment	not modelled	12.3	7	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
93	c3g3zA_	Alignment	not modelled	12.2	7	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
94	c3lvmB_	Alignment	not modelled	12.2	13	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
95	d1wu4a1	Alignment	not modelled	11.7	25	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
96	c3d6kB_	Alignment	not modelled	11.6	13	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
97	c2l3aA_	Alignment	not modelled	11.6	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of homodimer protein sp_0782 (7-79) from2 streptococcus pneumoniae northeast structural genomics consortium3 target spr104 .
98	c2pjka_	Alignment	not modelled	11.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 178aa long hypothetical molybdenum cofactor PDBTitle: structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
99	d1wdds_	Alignment	not modelled	11.3	25	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit