



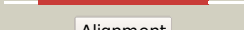

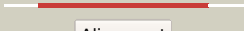









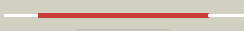








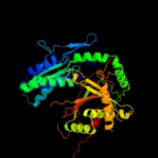
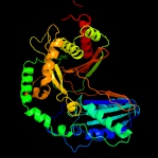






Phyre2

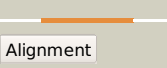
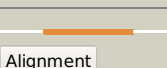
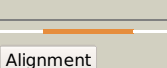
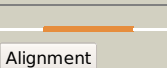
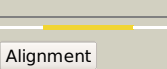
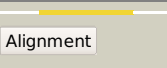
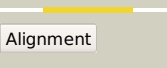
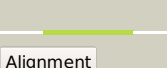
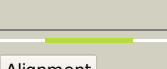
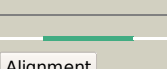
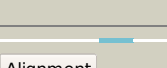
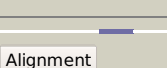


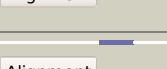
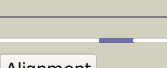
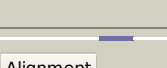
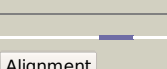
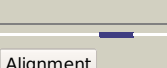
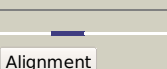
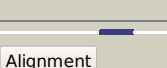
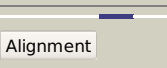
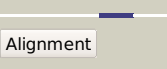
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Description	RVBD3480c (-)_3899088_3900581
Date	Fri Aug 9 18:20:15 BST 2019
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6chjB_	 Alignment		100.0	40	PDB header: transferase Chain: B; PDB Molecule: diacylglycerol o-acyltransferase; PDBTitle: wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
2	c6n8eA_	 Alignment		100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
3	c6aefB_	 Alignment		100.0	11	PDB header: transferase Chain: B; PDB Molecule: polyketide synthase associated protein papa2; PDBTitle: papa2 acyl transferase
4	c5m6pB_	 Alignment		100.0	13	PDB header: isomerase Chain: B; PDB Molecule: tyrocidine synthase 2; PDBTitle: crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e)
5	c5t81A_	 Alignment		100.0	13	PDB header: biosynthetic protein Chain: A; PDB Molecule: epob; PDBTitle: rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
6	c2vsaA_	 Alignment		100.0	12	PDB header: ligase Chain: A; PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
7	c2xhgA_	 Alignment		100.0	13	PDB header: isomerase Chain: A; PDB Molecule: tyrocidine synthetase a; PDBTitle: crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
8	c5t3eA_	 Alignment		100.0	9	PDB header: ligase Chain: A; PDB Molecule: bacillamide synthetase heterocyclization domain; PDBTitle: crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
9	c6p1jA_	 Alignment		100.0	17	PDB header: biosynthetic protein Chain: A; PDB Molecule: txo2; PDBTitle: the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo2 serine module
10	c6ad3A_	 Alignment		100.0	10	PDB header: biosynthetic protein Chain: A; PDB Molecule: lovastatin nonaketide synthase moka; PDBTitle: structural characterization of the condensation domain from monacolin2 k polyketide synthase moka
11	c5u89A_	 Alignment		100.0	16	PDB header: hydrolase/inhibitor Chain: A; PDB Molecule: amino acid adenylation domain protein; PDBTitle: crystal structure of a cross-module fragment from the dimodular nrps2 dhbf

12	c4zxiA	Alignment		100.0	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
13	c4znmB	Alignment		100.0	14	PDB header: ligase Chain: B: PDB Molecule: c-domain type ii peptide synthetase; PDBTitle: crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
14	c4zxiA	Alignment		100.0	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: enterobactin synthase component f; PDBTitle: crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation
15	c6cgoB	Alignment		100.0	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: condensation domain protein; PDBTitle: molecular basis for condensation domain-mediated chain release from2 the enacyloxin polyketide synthase
16	c5ja2A	Alignment		100.0	13	PDB header: ligase Chain: A: PDB Molecule: enterobactin synthase component f; PDBTitle: entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
17	c4jn3B	Alignment		100.0	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: cda peptide synthetase i; PDBTitle: crystal structures of the first condensation domain of the cda2 synthetase
18	c6m7IB	Alignment		100.0	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: putative non-ribosomal peptide synthetase; PDBTitle: complex of oxa with the x-domain from gpa biosynthesis
19	c2jgpA	Alignment		100.0	11	PDB header: ligase Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
20	c1l5aA	Alignment		100.0	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: amide synthase; PDBTitle: crystal structure of vibh, an nrps condensation enzyme
21	c4tx3B	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide synthetase, module 7; PDBTitle: complex of the x-domain and oxyb from teicoplanin biosynthesis
22	c6ozvA	Alignment	not modelled	100.0	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: txo1; PDBTitle: the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
23	c5dijA	Alignment	not modelled	100.0	11	PDB header: unknown function Chain: A: PDB Molecule: tqaa; PDBTitle: the crystal structure of ct
24	c1q9jA	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: polyketide synthase associated protein 5; PDBTitle: structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
25	c4hvmC	Alignment	not modelled	100.0	14	PDB header: biosynthetic protein Chain: C: PDB Molecule: tlmii; PDBTitle: crystal structure of tallysomycin biosynthesis protein tlmii
26	c3fotA	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A: PDB Molecule: 15-o-acetyltransferase; PDBTitle: structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
27	c6dd2A	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: probable hydroxycinnamoyl transferase; PDBTitle: crystal structure of selaginella moellendorffii hct
28	d1l5aa1	Alignment	not modelled	99.9	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)

29	c4g0bA	Alignment	not modelled	99.8	9	PDB header: transferase Chain: A: PDB Molecule: hydroxycinnamoyl-coa shikimate/quinate PDBTitle: structure of native hct from coffea canephora
30	c2e1uA	Alignment	not modelled	99.7	15	PDB header: transferase Chain: A: PDB Molecule: acyl transferase; PDBTitle: crystal structure of dendranthema morifolium dmat
31	d1q9ja1	Alignment	not modelled	99.7	17	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
32	d1l5aa2	Alignment	not modelled	99.7	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
33	d1q9ja2	Alignment	not modelled	99.7	17	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
34	c2bghA	Alignment	not modelled	99.6	14	PDB header: transferase Chain: A: PDB Molecule: vinorine synthase; PDBTitle: crystal structure of vinorine synthase
35	c2xr7A	Alignment	not modelled	99.5	15	PDB header: transferase Chain: A: PDB Molecule: malonyltransferase; PDBTitle: crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
36	c3b2sA	Alignment	not modelled	99.4	10	PDB header: transferase Chain: A: PDB Molecule: trichothecene 3-o-acetyltransferase; PDBTitle: crystal structure of f. graminearum tri101 complexed with coenzyme a2 and deoxynivalenol
37	c4ke4A	Alignment	not modelled	99.4	15	PDB header: transferase Chain: A: PDB Molecule: hydroxycinnamoyl-coa:shikimate hydroxycinnamoyl PDBTitle: elucidation of the structure and reaction mechanism of sorghum bicolor2 hydroxycinnamoyltransferase and its structural relationship to other3 coa-dependent transferases and synthases
38	c2zbaD	Alignment	not modelled	98.8	11	PDB header: transferase Chain: D: PDB Molecule: trichothecene 3-o-acetyltransferase; PDBTitle: crystal structure of f. sporotrichoides tri101 complexed with2 coenzyme a and t-2
39	c6eqoB	Alignment	not modelled	98.0	10	PDB header: oxidoreductase Chain: B: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester
40	c1t7qA	Alignment	not modelled	97.2	14	PDB header: transferase Chain: A: PDB Molecule: carnitine acetyltransferase; PDBTitle: crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
41	c2fy2A	Alignment	not modelled	97.2	15	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: structures of ligand bound human choline acetyltransferase provide2 insight into regulation of acetylcholine synthesis
42	c1q6xA	Alignment	not modelled	96.6	15	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: crystal structure of rat choline acetyltransferase
43	d1ndba2	Alignment	not modelled	96.3	15	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
44	c1xl8B	Alignment	not modelled	96.2	12	PDB header: transferase Chain: B: PDB Molecule: peroxisomal carnitine o-octanoyltransferase; PDBTitle: crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
45	d1nm8a2	Alignment	not modelled	96.0	16	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
46	d1q23a	Alignment	not modelled	94.1	12	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
47	d1tlua2	Alignment	not modelled	93.4	11	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
48	c5es8A	Alignment	not modelled	92.6	5	PDB header: ligase Chain: A: PDB Molecule: linear gramicidin synthetase subunit a; PDBTitle: crystal structure of the initiation module of lgra in the thiolation2 state
49	c2h4tB	Alignment	not modelled	92.5	12	PDB header: transferase Chain: B: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase ii
50	d1xl7a2	Alignment	not modelled	90.9	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
51	d3claa	Alignment	not modelled	90.6	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
52	c3b8kA	Alignment	not modelled	90.1	9	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoylysine-residue acetyltransferase; PDBTitle: structure of the truncated human dihydrolipoyl acetyltransferase (e2)
53	c2fyoA	Alignment	not modelled	88.5	12	PDB header: transferase Chain: A: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212

54	c3maeA	 Alignment	not modelled	85.7	11	PDB header: transferase Chain: A: PDB Molecule: 2-oxoisovalerate dehydrogenase e2 component, PDBTitle: crystal structure of probable dihydrolipoamide acetyltransferase from <i>listeria monocytogenes</i> 4b f2365
55	c4n72B	 Alignment	not modelled	84.2	11	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyltransacetylase) PDBTitle: catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from <i>escherichia coli</i>
56	d1dpba	 Alignment	not modelled	84.2	16	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
57	c6h60A	 Alignment	not modelled	82.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component, mitochondrial; PDBTitle: pseudo-atomic structural model of the e3bp component of the human2 pyruvate dehydrogenase multienzyme complex
58	d1b5sa	 Alignment	not modelled	79.2	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
59	c2i9dC	 Alignment	not modelled	78.9	9	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
60	c3l60A	 Alignment	not modelled	78.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: branched-chain alpha-keto acid dehydrogenase; PDBTitle: crystal structure of branched-chain alpha-keto acid dehydrogenase2 subunit e2 from <i>mycobacterium tuberculosis</i>
61	c2ii4C	 Alignment	not modelled	69.5	13	PDB header: transferase Chain: C: PDB Molecule: lipoamide acyltransferase component of branched-chain PDBTitle: crystal structure of a cubic core of the dihydrolipoamide2 acyltransferase (e2b) component in the branched-chain alpha-ketoacid3 dehydrogenase complex (bckdc), coenzyme a-bound form
62	d1scza	 Alignment	not modelled	67.2	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
63	c3rqcB	 Alignment	not modelled	46.5	11	PDB header: transferase Chain: B: PDB Molecule: probable lipoamide acyltransferase; PDBTitle: crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from <i>thermoplasma acidophilum</i>
64	c2huuA	 Alignment	not modelled	33.0	20	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of <i>aedes aegypti</i> alanine glyoxylate aminotransferase2 in complex with alanine
65	c5zsqA	 Alignment	not modelled	19.2	8	PDB header: biosynthetic protein Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: nifs from <i>hydrogenimonas thermophila</i> , soaked with l-cysteine for 4 min
66	c3ke3A	 Alignment	not modelled	18.6	27	PDB header: transferase Chain: A: PDB Molecule: putative serine-pyruvate aminotransferase; PDBTitle: crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from <i>psychrobacter arcticum</i> 273-4 at 2.20 a resolution
67	c3nuiA	 Alignment	not modelled	14.5	11	PDB header: transferase Chain: A: PDB Molecule: pyruvate transaminase; PDBTitle: crystal structure of omega-transferase from <i>vibrio fluvialis</i> js17
68	c4eb5B	 Alignment	not modelled	13.8	20	PDB header: transferase/metal binding protein Chain: B: PDB Molecule: probable cysteine desulfurase 2; PDBTitle: a. fulgidus iscs-iscu complex structure
69	c4q6rB	 Alignment	not modelled	12.7	12	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: sphingosine-1-phosphate lyase 1; PDBTitle: crystal structure of human sphingosine-1-phosphate lyase in complex2 with inhibitor 6-[(2r)-4-(4-benzyl-7-chlorophthalazin-1-yl)-2-3 methylpiperazin-1-yl]pyridine-3-carbonitrile
70	c3mafB	 Alignment	not modelled	12.0	9	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
71	c6g4dB	 Alignment	not modelled	10.1	13	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase family protein; PDBTitle: crystal structure of the omega transaminase from <i>pseudomonas jessenii</i> 2 in complex with plp
72	d2ch1a1	 Alignment	not modelled	9.6	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
73	c6dy3G	 Alignment	not modelled	9.1	15	PDB header: hydrolase Chain: G: PDB Molecule: n-acylethanolamine-hydrolyzing acid amidase alpha-subunit; PDBTitle: caenorhabditis elegans n-acylethanolamine-hydrolyzing acid amidase2 (naaa) ortholog
74	d2fm8a1	 Alignment	not modelled	8.8	15	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
75	c4isyB	 Alignment	not modelled	8.8	11	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of iscs from <i>mycobacterium tuberculosis</i>
76	c3dodA	 Alignment	not modelled	7.9	7	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 <i>bacillus subtilis</i>

77	d1ry9a_	Alignment	not modelled	7.5	15	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
78	c2h0uA_	Alignment	not modelled	7.3	8	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-flavin oxidoreductase; PDBTitle: crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
79	d1h0ca_	Alignment	not modelled	7.1	25	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
80	c5usrG_	Alignment	not modelled	7.0	12	PDB header: transferase Chain: G: PDB Molecule: cysteine desulfurase, mitochondrial; PDBTitle: crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
81	c5ti8A_	Alignment	not modelled	6.8	19	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aspartate aminotransferase from pseudomonas
82	c3eo8A_	Alignment	not modelled	6.8	6	PDB header: flavoprotein Chain: A: PDB Molecule: blub-like flavoprotein; PDBTitle: crystal structure of blub-like flavoprotein (yp_001089088.1) from2 clostridium difficile 630 at 1.74 a resolution
83	c3gfaB_	Alignment	not modelled	6.5	11	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroreductase; PDBTitle: crystal structure of a putative nitroreductase in complex with fmn2 (cd3205) from clostridium difficile 630 at 1.35 a resolution
84	d1qb2a_	Alignment	not modelled	6.4	18	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
85	c4xcoC_	Alignment	not modelled	6.4	35	PDB header: rna binding protein Chain: C: PDB Molecule: signal recognition particle 54 kda protein,signal sequence; PDBTitle: signal-sequence induced conformational changes in the signal2 recognition particle
86	c2fyfB_	Alignment	not modelled	6.3	10	PDB header: transferase Chain: B: PDB Molecule: phosphoserine aminotransferase; PDBTitle: structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
87	c3of4A_	Alignment	not modelled	6.1	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nitroreductase; PDBTitle: crystal structure of a fmn/fad- and nad(p)h-dependent nitroreductase2 (nfnb, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution
88	d1ywqa1	Alignment	not modelled	6.0	2	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
89	c5wmma_	Alignment	not modelled	5.7	0	PDB header: biosynthetic protein Chain: A: PDB Molecule: nmps; PDBTitle: crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
90	c4urpB_	Alignment	not modelled	5.7	11	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty acid repression mutant protein 2; PDBTitle: the crystal structure of nitroreductase from saccharomyces2 cerevisiae
91	c2jqeA_	Alignment	not modelled	5.6	18	PDB header: signaling protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: sotion structure of af54 m-domain
92	d1hq1a_	Alignment	not modelled	5.6	29	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
93	d2ffha2	Alignment	not modelled	5.6	24	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
94	c2rriA_	Alignment	not modelled	5.5	8	PDB header: protein transport Chain: A: PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the flik
95	c4lw2C_	Alignment	not modelled	5.4	28	PDB header: lyase Chain: C: PDB Molecule: cysteine sulfinate desulfinase; PDBTitle: structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration
96	d1qzxa2	Alignment	not modelled	5.3	18	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
97	d2q3la1	Alignment	not modelled	5.3	7	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
98	c3mc6C_	Alignment	not modelled	5.2	9	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
99	c5b87B_	Alignment	not modelled	5.1	21	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of a cysteine desulfurase from thermococcus2 onnurineus na1 in complex with alanine at 2.3 angstrom resolution