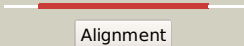

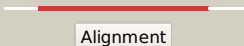

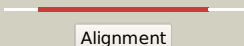




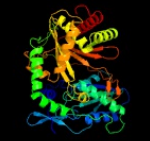


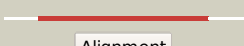









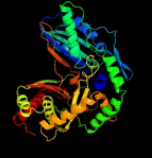
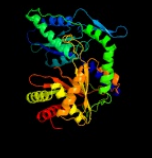




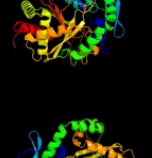
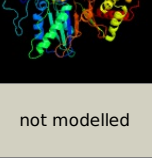


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1182_(papA3)_1320041_1321459
Date	Wed Jul 31 22:05:27 BST 2019
Unique Job ID	e913c46500c2ff70

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6aefB_</a>	 Alignment		100.0	53	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase associated protein papa2; <b>PDBTitle:</b> papa2 acyl transferase
2	<a href="#">c6n8eA_</a>	 Alignment		100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-obif1; <b>PDBTitle:</b> crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
3	<a href="#">c2vsqA_</a>	 Alignment		100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase subunit 3; <b>PDBTitle:</b> structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
4	<a href="#">c4zxiA_</a>	 Alignment		100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
5	<a href="#">c6p1jA_</a>	 Alignment		100.0	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> txo2; <b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo2 serine module
6	<a href="#">c5u89A_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid adenylation domain protein; <b>PDBTitle:</b> crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
7	<a href="#">c5t81A_</a>	 Alignment		100.0	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> epob; <b>PDBTitle:</b> rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
8	<a href="#">c4tx3B_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide synthetase, module 7; <b>PDBTitle:</b> complex of the x-domain and oxyb from teicoplanin biosynthesis
9	<a href="#">c2jgpA_</a>	 Alignment		100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
10	<a href="#">c6m7lB_</a>	 Alignment		100.0	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative non-ribosomal peptide synthetase; <b>PDBTitle:</b> complex of oxa with the x-domain from gpa biosynthesis
11	<a href="#">c6cgoB_</a>	 Alignment		100.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> condensation domain protein; <b>PDBTitle:</b> molecular basis for condensation domain-mediated chain release from2 the enacyloxin polyketide synthase

12	<a href="#">c4zxA</a>	Alignment		100.0	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation
13	<a href="#">c6ozvA</a>	Alignment		100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> txo1; <b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
14	<a href="#">c2xhgA</a>	Alignment		100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase a; <b>PDBTitle:</b> crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
15	<a href="#">c5m6pB</a>	Alignment		100.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrocidine synthase 2; <b>PDBTitle:</b> crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e)
16	<a href="#">c5t3eA</a>	Alignment		100.0	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> bacillamide synthetase heterocyclization domain; <b>PDBTitle:</b> crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
17	<a href="#">c6ad3A</a>	Alignment		100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> lovastatin nonaketide synthase moka; <b>PDBTitle:</b> structural characterization of the condensation domain from monacolin2 k polyketide synthase moka
18	<a href="#">c5ja2A</a>	Alignment		100.0	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
19	<a href="#">c4znmB</a>	Alignment		100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> c-domain type ii peptide synthetase; <b>PDBTitle:</b> crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
20	<a href="#">c4jn3B</a>	Alignment		100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> cda peptide synthetase i; <b>PDBTitle:</b> crystal structures of the first condensation domain of the cda2 synthetase
21	<a href="#">c1l5aA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> amide synthase; <b>PDBTitle:</b> crystal structure of vibh, an nrps condensation enzyme
22	<a href="#">c5dijA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tqaa; <b>PDBTitle:</b> the crystal structure of ct
23	<a href="#">c4hvmC</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> tlmii; <b>PDBTitle:</b> crystal structure of tallisomycin biosynthesis protein tlmii
24	<a href="#">c3fotA</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 15-o-acetyltransferase; <b>PDBTitle:</b> structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
25	<a href="#">c1q9jA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase associated protein 5; <b>PDBTitle:</b> structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
26	<a href="#">c6chjB</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diacylglycerol o-acyltransferase; <b>PDBTitle:</b> wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
27	<a href="#">d1l5aa2</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
28	<a href="#">d1l5aa1</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)

29	<a href="#">c6dd2A</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable hydroxycinnamoyl transferase; <b>PDBTitle:</b> crystal structure of selaginella moellendorffii hct
30	<a href="#">d1q9ja1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
31	<a href="#">c4g0bA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxycinnamoyl-coa shikimate/quinate <b>PDBTitle:</b> structure of native hct from coffea canephora
32	<a href="#">d1q9ja2</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
33	<a href="#">c2e1uA</a>	Alignment	not modelled	99.8	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl transferase; <b>PDBTitle:</b> crystal structure of dendranthema morifolium dmat
34	<a href="#">c2bghA</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vinorine synthase; <b>PDBTitle:</b> crystal structure of vinorine synthase
35	<a href="#">c6eqoB</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a synthetase; <b>PDBTitle:</b> tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nasp+ and phosphomethylphosphonic acid adenylate ester
36	<a href="#">c2xr7A</a>	Alignment	not modelled	99.7	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyltransferase; <b>PDBTitle:</b> crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
37	<a href="#">c5es8A</a>	Alignment	not modelled	99.5	9	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> linear gramicidin synthetase subunit a; <b>PDBTitle:</b> crystal structure of the initiation module of lgra in the thiolation2 state
38	<a href="#">c4ke4A</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxycinnamoyl-coa:shikimate hydroxycinnamoyl <b>PDBTitle:</b> elucidation of the structure and reaction mechanism of sorghum bicolor2 hydroxycinnamoyltransferase and its structural relationship to other3 coa-dependent transferases and synthases
39	<a href="#">c3b2sA</a>	Alignment	not modelled	99.3	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trichothecene 3-o-acetyltransferase; <b>PDBTitle:</b> crystal structure of f. graminearum tri101 complexed with coenzyme a2 and deoxynivalenol
40	<a href="#">c2zbaD</a>	Alignment	not modelled	99.1	8	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> trichothecene 3-o-acetyltransferase; <b>PDBTitle:</b> crystal structure of f. sporotrichioides tri101 complexed with2 coenzyme a and t-2
41	<a href="#">c2i9dC</a>	Alignment	not modelled	90.5	7	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> chloramphenicol acetyltransferase
42	<a href="#">d1q23a</a>	Alignment	not modelled	88.2	9	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
43	<a href="#">d3claa</a>	Alignment	not modelled	65.9	8	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
44	<a href="#">c3b8kA</a>	Alignment	not modelled	63.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase; <b>PDBTitle:</b> structure of the truncated human dihydrolipoyl acetyltransferase (e2)
45	<a href="#">d1nija2</a>	Alignment	not modelled	59.5	16	<b>Fold:</b> Hypothetical protein YjiA, C-terminal domain <b>Superfamily:</b> Hypothetical protein YjiA, C-terminal domain <b>Family:</b> Hypothetical protein YjiA, C-terminal domain
46	<a href="#">c3l60A</a>	Alignment	not modelled	51.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> branched-chain alpha-keto acid dehydrogenase; <b>PDBTitle:</b> crystal structure of branched-chain alpha-keto acid dehydrogenase2 subunit e2 from mycobacterium tuberculosis
47	<a href="#">c5wmma</a>	Alignment	not modelled	37.2	9	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> nrps; <b>PDBTitle:</b> crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
48	<a href="#">d1dpba</a>	Alignment	not modelled	29.7	12	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
49	<a href="#">d1b5sa</a>	Alignment	not modelled	29.1	14	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
50	<a href="#">c3maeA</a>	Alignment	not modelled	26.0	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-oxoisovalerate dehydrogenase e2 component, <b>PDBTitle:</b> crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
51	<a href="#">c1vs3B</a>	Alignment	not modelled	23.5	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> trna pseudouridine synthase a; <b>PDBTitle:</b> crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
52	<a href="#">c4n72B</a>	Alignment	not modelled	19.0	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate dehydrogenase (dihydrolipoyltransacetylase <b>PDBTitle:</b> catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
53	<a href="#">c6h60A</a>	Alignment	not modelled	13.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component, mitochondrial;

						<b>PDBTitle:</b> pseudo-atomic structural model of the e3bp component of the human2 pyruvate dehydrogenase multienzyme complex
54	<a href="#">d1dj0a_</a>	Alignment	not modelled	13.5	13	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase I TruA
55	<a href="#">c5ti8A_</a>	Alignment	not modelled	11.8	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of an aspartate aminotransferase from pseudomonas
56	<a href="#">c2p0yA_</a>	Alignment	not modelled	11.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein lp_0780; <b>PDBTitle:</b> crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
57	<a href="#">c1njjA_</a>	Alignment	not modelled	10.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yjia; <b>PDBTitle:</b> yjia protein
58	<a href="#">d2ay0a1</a>	Alignment	not modelled	10.8	12	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> PutA pre-N-terminal region-like
59	<a href="#">d1nm8a2</a>	Alignment	not modelled	8.9	7	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
60	<a href="#">c5hypB_</a>	Alignment	not modelled	8.9	22	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> m28 protein; <b>PDBTitle:</b> structure of human c4b-binding protein alpha cain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m283 protein
61	<a href="#">c2k5jB_</a>	Alignment	not modelled	8.8	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
62	<a href="#">d1tlua2</a>	Alignment	not modelled	8.3	11	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
63	<a href="#">d1scza_</a>	Alignment	not modelled	8.2	10	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
64	<a href="#">c2ii4C_</a>	Alignment	not modelled	7.9	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> lipamide acyltransferase component of branched-chain <b>PDBTitle:</b> 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
65	<a href="#">d2bm0a4</a>	Alignment	not modelled	7.7	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
66	<a href="#">c6iyaD_</a>	Alignment	not modelled	7.5	12	<b>PDB header:</b> antitoxin <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator copg family; <b>PDBTitle:</b> structure of the dna binding domain of antitoxin copaso
67	<a href="#">d2dy1a4</a>	Alignment	not modelled	7.4	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
68	<a href="#">d1ndba2</a>	Alignment	not modelled	7.0	7	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
69	<a href="#">c2fyoA_</a>	Alignment	not modelled	6.5	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitine o-palmitoyltransferase ii, mitochondrial; <b>PDBTitle:</b> crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212
70	<a href="#">c3dodA_</a>	Alignment	not modelled	6.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate aminotransferase; <b>PDBTitle:</b> crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
71	<a href="#">c6io1B_</a>	Alignment	not modelled	6.3	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase, class iii; <b>PDBTitle:</b> crystal structure of a novel thermostable (s)-enantioselective omega-2 transaminase from thermomicrobium roseum
72	<a href="#">c1o7dC_</a>	Alignment	not modelled	6.2	33	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> lysosomal alpha-mannosidase; <b>PDBTitle:</b> the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
73	<a href="#">c2rbfB_</a>	Alignment	not modelled	5.6	12	<b>PDB header:</b> oxidoreductase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
74	<a href="#">c3rqcB_</a>	Alignment	not modelled	5.5	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable lipamide acyltransferase; <b>PDBTitle:</b> crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum
75	<a href="#">c3nuiA_</a>	Alignment	not modelled	5.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate transaminase; <b>PDBTitle:</b> crystal structure of omega-transferase from vibrio fluvialis js17
76	<a href="#">c2h4tB_</a>	Alignment	not modelled	5.4	7	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carnitine o-palmitoyltransferase ii, mitochondrial; <b>PDBTitle:</b> crystal structure of rat carnitine palmitoyltransferase ii
77	<a href="#">c4fxeB_</a>	Alignment	not modelled	5.2	10	<b>PDB header:</b> toxin/toxin inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin relb; <b>PDBTitle:</b> crystal structure of the intact e. coli relbe toxin-antitoxin complex

78 [c3kk4B](#)

Alignment

not modelled

5.1

10

**PDB header:** structural genomics, unknown function  
**Chain:** B: **PDB Molecule:** uncharacterized protein bp1543;  
**PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis  
toham a