Phyre2

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Description	RVBD2939_(papA5)_3274959_3276227
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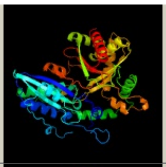
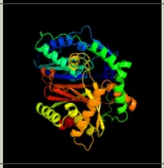
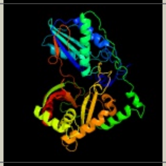
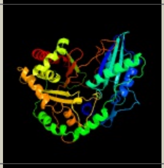
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1q9jA_	Alignment		100.0	98	**PDB header:**ligase **Chain:** A: **PDB Molecule:**polyketide synthase associated protein 5; **PDBTitle:** structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
2	c6n8eA_	Alignment		100.0	12	**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	c2vsqA_	Alignment		100.0	10	**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
4	c6p1jA_	Alignment		100.0	16	**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
5	c4zxiA_	Alignment		100.0	11	**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
6	c5ja2A_	Alignment		100.0	14	**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
7	c4zxjA_	Alignment		100.0	15	**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
8	c5u89A_	Alignment		100.0	12	**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
9	c6cgoB_	Alignment		100.0	12	**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
10	c5t81A_	Alignment		100.0	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**epob; **PDBTitle:** rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
11	c4znmB_	Alignment		100.0	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**c-domain type ii peptide synthetase; **PDBTitle:** crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)

12	c6aefB_	Alignment		100.0	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyketide synthase associated protein papa2; **PDBTitle:** papa2 acyl transferase
13	c2jgpA_	Alignment		100.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrocidine synthetase 3; **PDBTitle:** structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
14	c5t3eA_	Alignment		100.0	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**bacillamide synthetase heterocyclization domain; **PDBTitle:** crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
15	c4tx3B_	Alignment		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
16	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)
17	c4jn3B_	Alignment		100.0	13	**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	c2xhgA_	Alignment		100.0	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tyrocidine synthetase a; **PDBTitle:** crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
19	c6m7lB_	Alignment		100.0	12	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**putative non-ribosomal peptide synthetase; **PDBTitle:** complex of oxya with the x-domain from gpa biosynthesis
20	c6ozvA_	Alignment		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
21	c6ad3A_	Alignment	not modelled	100.0	11	**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
22	c1l5aA_	Alignment	not modelled	100.0	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**amide synthase; **PDBTitle:** crystal structure of vibh, an nrps condensation enzyme
23	c5dijA_	Alignment	not modelled	100.0	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**tqaa; **PDBTitle:** the crystal structure of ct
24	c4hvmC_	Alignment	not modelled	100.0	11	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**tlmii; **PDBTitle:** crystal structure of tallysomycin biosynthesis protein tlmii
25	c3fotA_	Alignment	not modelled	100.0	12	**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
26	d1q9ja2	Alignment	not modelled	100.0	97	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
27	c6chjB_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**diacylglycerol o-acyltransferase; **PDBTitle:** wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
28	d1q9ja1	Alignment	not modelled	100.0	100	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)

29	c6dd2A_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable hydroxycinnamoyl transferase; **PDBTitle:** crystal structure of selaginella moellendorffii hct
30	d1l5aa1	Alignment	not modelled	99.9	12	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
31	c4g0bA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydroxycinnamoyl-coa shikimate/quinate **PDBTitle:** structure of native hct from coffea canephora
32	d1l5aa2	Alignment	not modelled	99.9	9	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
33	c2bghA_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vinorine synthase; **PDBTitle:** crystal structure of vinorine synthase
34	c2e1uA_	Alignment	not modelled	99.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl transferase; **PDBTitle:** crystal structure of dendranthema morifolium dmat
35	c2xr7A_	Alignment	not modelled	99.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyltransferase; **PDBTitle:** crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
36	c4ke4A_	Alignment	not modelled	99.5	17	**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
37	c3b2sA_	Alignment	not modelled	99.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trichothecene 3-o-acetyltransferase; **PDBTitle:** crystal structure of f. graminearum tri101 complexed with coenzyme a2 and deoxynivalenol
38	c2zbaD_	Alignment	not modelled	99.3	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trichothecene 3-o-acetyltransferase; **PDBTitle:** crystal structure of f. sporotrichioides tri101 complexed with2 coenzyme a and t-2
39	c6eqoB_	Alignment	not modelled	99.0	12	**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	c5es8A_	Alignment	not modelled	97.4	9	**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
41	c2i9dC_	Alignment	not modelled	91.6	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** chloramphenicol acetyltransferase
42	c3rqcB_	Alignment	not modelled	91.1	19	**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 thermoplasma acidophilum
43	d1q23a_	Alignment	not modelled	84.3	25	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
44	d3claa_	Alignment	not modelled	81.6	31	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
45	c3maeA_	Alignment	not modelled	76.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-oxoisovalerate dehydrogenase e2 component, **PDBTitle:** crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
46	c6h60A_	Alignment	not modelled	72.5	8	**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
47	d1scza_	Alignment	not modelled	69.4	21	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
48	c4n72B_	Alignment	not modelled	62.4	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate dehydrogenase (dihydrolipoyltransacetylase **PDBTitle:** catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
49	d1p94a_	Alignment	not modelled	55.2	10	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
50	c3b8kA_	Alignment	not modelled	47.3	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase; **PDBTitle:** structure of the truncated human dihydrolipoyl acetyltransferase (e2)
51	c2ii4C_	Alignment	not modelled	44.4	14	**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
52	d1b5sa_	Alignment	not modelled	42.9	24	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
						Fold: Hypothetical protein YjiA, C-terminal domain

53	d1nija2	Alignment	not modelled	42.8	21	**Superfamily:**Hypothetical protein YjiA, C-terminal domain **Family:**Hypothetical protein YjiA, C-terminal domain
54	d1dpba_	Alignment	not modelled	39.0	19	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
55	d2cpga_	Alignment	not modelled	39.0	26	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
56	c1ea4K_	Alignment	not modelled	39.0	26	**PDB header:**gene regulation/dna **Chain:** K: **PDB Molecule:**transcriptional repressor copg; **PDBTitle:** transcriptional repressor copg/22bp dsdna complex
57	c2k5jB_	Alignment	not modelled	27.0	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
58	c6g1nB_	Alignment	not modelled	24.7	10	**PDB header:**antitoxin **Chain:** B: **PDB Molecule:**antitoxin hicb; **PDBTitle:** crystal structure of the burkholderia pseudomallei antitoxin hicb
59	c1xl8B_	Alignment	not modelled	23.7	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**peroxisomal carnitine o-octanoyltransferase; **PDBTitle:** crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
60	c2vsnB_	Alignment	not modelled	23.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**xcogt; **PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
61	c3l60A_	Alignment	not modelled	23.6	20	**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 mycobacterium tuberculosis
62	c6iyaD_	Alignment	not modelled	21.4	10	**PDB header:**antitoxin **Chain:** D: **PDB Molecule:**transcriptional regulator copg family; **PDBTitle:** structure of the dna binding domain of antitoxin copaso
63	c2k9iB_	Alignment	not modelled	20.2	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**uncharacterized protein orf56; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from sulfolobus2 islandicus
64	c2fy2A_	Alignment	not modelled	19.8	25	**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
65	c3fwcO_	Alignment	not modelled	19.5	31	**PDB header:**cell cycle, transcription **Chain:** O: **PDB Molecule:**protein sus1; **PDBTitle:** sac3:sus1:cdc31 complex
66	d2ay0a1	Alignment	not modelled	18.9	10	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**PutA pre-N-terminal region-like
67	c2k29A_	Alignment	not modelled	16.4	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
68	c1nijA_	Alignment	not modelled	15.8	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yjia; **PDBTitle:** yjia protein
69	c3kk4B_	Alignment	not modelled	15.7	6	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bp1543; **PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i
70	c2jvwA_	Alignment	not modelled	15.3	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein q5e7h1 from vibrio2 fischeri. northeast structural genomics target vfr117
71	d1mnta_	Alignment	not modelled	14.9	8	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
72	c4fxeB_	Alignment	not modelled	14.8	5	**PDB header:**toxin/toxin inhibitor **Chain:** B: **PDB Molecule:**antitoxin relb; **PDBTitle:** crystal structure of the intact e. coli relbe toxin-antitoxin complex
73	c6gtsC_	Alignment	not modelled	14.0	8	**PDB header:**transcription **Chain:** C: **PDB Molecule:**duf1778 domain-containing protein; **PDBTitle:** structure of the atat-atar complex bound dna
74	c2h4tB_	Alignment	not modelled	13.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carnitine o-palmitoyltransferase ii, mitochondrial; **PDBTitle:** crystal structure of rat carnitine palmitoyltransferase ii
75	c2rbfB_	Alignment	not modelled	13.8	10	**PDB header:**oxidoreductase/dna **Chain:** B: **PDB Molecule:**bifunctional protein puta; **PDBTitle:** structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
76	c2kelB_	Alignment	not modelled	13.6	15	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**uncharacterized protein 56b; **PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
77	c2fyoA_	Alignment	not modelled	13.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carnitine o-palmitoyltransferase ii, mitochondrial; **PDBTitle:** crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212
						PDB header:transport protein/dna binding protein

78	c4dhxC_	Alignment	not modelled	12.9	38	**Chain:** C: **PDB Molecule:**enhancer of yellow 2 transcription factor homolog; **PDBTitle:** eny2:ganp complex
79	d1t1ua2	Alignment	not modelled	12.3	17	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
80	c4q2uM_	Alignment	not modelled	11.3	8	**PDB header:**toxin/toxin repressor **Chain:** M: **PDB Molecule:**antitoxin dinj; **PDBTitle:** crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
81	d1nm8a2	Alignment	not modelled	11.3	21	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
82	c5cw9A_	Alignment	not modelled	11.0	25	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed ferredoxin-ferredoxin domain insertion **PDBTitle:** crystal structure of de novo designed ferredoxin-ferredoxin domain2 insertion protein
83	c1t7qA_	Alignment	not modelled	10.3	17	**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
84	d1ndba2	Alignment	not modelled	10.1	21	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
85	c6ajnF_	Alignment	not modelled	10.1	10	**PDB header:**toxin **Chain:** F: **PDB Molecule:**duf1778 domain-containing protein; **PDBTitle:** crystal structure of atatr bound with accoa
86	c6noyB_	Alignment	not modelled	9.4	15	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**maintenance of carboxysome positioning b protein, mcsb; **PDBTitle:** structure of cyanothece mcdb
87	c5wmmA_	Alignment	not modelled	8.6	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**nrps; **PDBTitle:** crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
88	c3luyA_	Alignment	not modelled	8.4	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
89	d1wh7a_	Alignment	not modelled	7.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
90	c6h6pA_	Alignment	not modelled	7.0	13	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**ubiquinone biosynthesis protein ubij; **PDBTitle:** ubij-scp2 ubiquinone synthesis protein
91	c3cjeA_	Alignment	not modelled	6.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**osmc-like protein; **PDBTitle:** crystal structure of an osmc-like hydroperoxide resistance protein2 (jann_2040) from jannaschia sp. ccs1 at 1.70 a resolution
92	d2gmwa2	Alignment	not modelled	6.5	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
93	d2dy1a4	Alignment	not modelled	6.1	21	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
94	d1xl7a2	Alignment	not modelled	6.1	15	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
95	c1vs3B_	Alignment	not modelled	6.0	30	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trna pseudouridine synthase a; **PDBTitle:** crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
96	c2mdvB_	Alignment	not modelled	6.0	29	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**designed protein; **PDBTitle:** nmr structure of beta alpha alpha 38
97	d1y9ba1	Alignment	not modelled	5.8	16	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**VCA0319-like
98	c3eerA_	Alignment	not modelled	5.8	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**organic hydroperoxide resistance protein, putative; **PDBTitle:** high resolution structure of putative organic hydroperoxide resistance2 protein from vibrio cholerae o1 biovar eltor str. n16961
99	d1myla_	Alignment	not modelled	5.5	11	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors