Phyre^2

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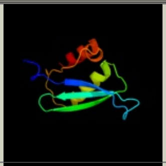
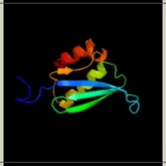
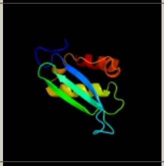
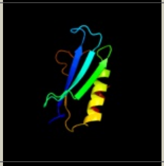
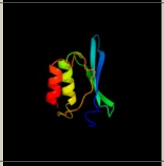
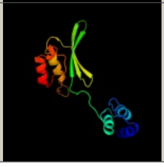
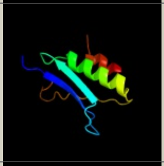
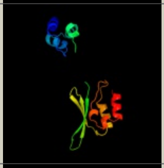
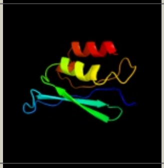
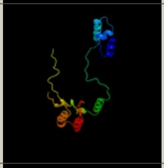
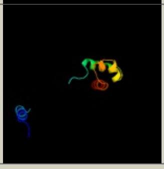
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1c0mA_	Alignment		99.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (integrase); **PDBTitle:** crystal structure of rsv two-domain integrase
2	d1asua_	Alignment		99.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
3	d1cxqa_	Alignment		99.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
4	d1c0ma2	Alignment		99.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
5	d1bcoa2	Alignment		99.3	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**mu transposase, core domain
6	d1exqa_	Alignment		99.0	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
7	c3nf9A_	Alignment		99.0	11	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
8	d1c6va_	Alignment		99.0	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
9	c1ex4A_	Alignment		98.9	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** hiv-1 integrase catalytic core and c-terminal domain
10	c3f9kV_	Alignment		98.9	10	**PDB header:**viral protein, recombination **Chain:** V: **PDB Molecule:**integrase; **PDBTitle:** two domain fragment of hiv-2 integrase in complex with ledgf ibd
11	c1k6yB_	Alignment		98.9	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a two-domain fragment of hiv-1 integrase

12	c3kksB_	Alignment		98.7	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of catalytic core domain of biv integrase in crystal2 form ii
13	c1bcoA_	Alignment		98.7	14	**PDB header:**transposase **Chain:** A: **PDB Molecule:**bacteriophage mu transposase; **PDBTitle:** bacteriophage mu transposase core domain
14	c3hpgC_	Alignment		98.6	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**integrase; **PDBTitle:** visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
15	c3dlrA_	Alignment		98.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the catalytic core domain from pfv2 integrase
16	d1hyva_	Alignment		98.5	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
17	c3l2tB_	Alignment		98.3	13	**PDB header:**recombination/dna **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
18	c3hosA_	Alignment		97.4	11	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
19	c3v4gA_	Alignment		95.4	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
20	c1u78A_	Alignment		94.6	11	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
21	d1aoya_	Alignment	not modelled	93.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
22	c1b4aA_	Alignment	not modelled	93.2	16	**PDB header:**repressor **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** structure of the arginine repressor from bacillus stearothermophilus
23	c3ereD_	Alignment	not modelled	92.1	17	**PDB header:**dna binding protein/dna **Chain:** D: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
24	c6paxA_	Alignment	not modelled	92.0	12	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
25	d1pdnc_	Alignment	not modelled	87.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
26	d1b4aa1	Alignment	not modelled	86.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
27	d2p5ka1	Alignment	not modelled	86.2	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
28	d1f9na1	Alignment	not modelled	85.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
29	c3mwmA	Alignment	not modelled	84.3	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein;

29	c3mwmA_	Alignment	not modelled	84.5	19	**PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
30	c2o03A_	Alignment	not modelled	83.4	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
31	c2o8kA_	Alignment	not modelled	83.0	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
32	c2fe3B_	Alignment	not modelled	80.8	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**peroxide operon regulator; **PDBTitle:** the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
33	c2xigA_	Alignment	not modelled	79.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
34	d1mzba_	Alignment	not modelled	79.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FUR-like
35	c2w57A_	Alignment	not modelled	72.8	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
36	c2r0qF_	Alignment	not modelled	72.8	13	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
37	c3f2kB_	Alignment	not modelled	68.3	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histone-lysine n-methyltransferase setmar; **PDBTitle:** structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
38	c2fu4B_	Alignment	not modelled	66.8	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
39	d1nkua_	Alignment	not modelled	64.4	23	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase I (Tag)
40	d1stza1	Alignment	not modelled	63.7	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
41	c2jg6A_	Alignment	not modelled	62.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
42	c3eyyA_	Alignment	not modelled	56.4	19	**PDB header:**transport **Chain:** A: **PDB Molecule:**putative iron uptake regulatory protein; **PDBTitle:** structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
43	c2xzmO_	Alignment	not modelled	55.3	13	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**rps13e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
44	c2f7tA_	Alignment	not modelled	46.5	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mos1 transposase; **PDBTitle:** crystal structure of the catalytic domain of mos1 mariner2 transposase
45	d1u17a1	Alignment	not modelled	43.6	8	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
46	c1hlvA_	Alignment	not modelled	42.4	20	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**major centromere autoantigen b; **PDBTitle:** crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
47	d1x8qa_	Alignment	not modelled	39.6	6	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
48	d2fi9a1	Alignment	not modelled	35.2	5	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
49	d2fvta1	Alignment	not modelled	33.8	6	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
50	d1nhpa3	Alignment	not modelled	22.6	16	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
51	c2i8bB_	Alignment	not modelled	22.3	12	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**minor nucleoprotein vp30; **PDBTitle:** crystal structure of the c-terminal domain of ebola virus vp30
52	c3r1fO_	Alignment	not modelled	20.8	11	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
53	d1dxla3	Alignment	not modelled	20.0	10	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal)

						domain
54	d1ebda3	Alignment	not modelled	19.2	17	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
55	c2rpiA_	Alignment	not modelled	18.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** the nmr structure of the submillisecond folding2 intermediate of the thermus thermophilus ribonuclease h
56	d3grsa3	Alignment	not modelled	18.2	16	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
57	d1gesa3	Alignment	not modelled	15.2	12	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
58	d1ekja_	Alignment	not modelled	15.0	16	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
59	d1pm1x_	Alignment	not modelled	14.4	9	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
60	d1lvla3	Alignment	not modelled	13.3	14	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
61	c3p9kD_	Alignment	not modelled	12.5	8	**PDB header:**transferase **Chain:** D: **PDB Molecule:**caffeic acid o-methyltransferase; **PDBTitle:** crystal structure of perennial ryegrass lpomt1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde
62	d1y1xa_	Alignment	not modelled	12.4	9	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Penta-EF-hand proteins
63	c2jsoA_	Alignment	not modelled	11.6	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**polymyxin resistance protein pmrd; **PDBTitle:** antimicrobial resistance protein
64	c3izbO_	Alignment	not modelled	11.6	16	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**40s ribosomal protein rps13 (s15p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
65	d1lpfa3	Alignment	not modelled	10.6	12	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
66	d2i52a1	Alignment	not modelled	10.4	10	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
67	c3lasA_	Alignment	not modelled	10.2	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
68	d2coba1	Alignment	not modelled	9.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
69	d1v59a3	Alignment	not modelled	9.9	12	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
70	d1ixsb1	Alignment	not modelled	9.3	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
71	d1aoga3	Alignment	not modelled	9.3	3	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
72	d1u3em2	Alignment	not modelled	8.9	11	**Fold:**DNA-binding domain of intron-encoded endonucleases **Superfamily:**DNA-binding domain of intron-encoded endonucleases **Family:**DNA-binding domain of intron-encoded endonucleases
73	c2qv5A_	Alignment	not modelled	8.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
74	c1fpqA_	Alignment	not modelled	8.3	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isoliquiritigenin 2'-o-methyltransferase; **PDBTitle:** crystal structure analysis of selenomethionine substituted chalcone o-2 methyltransferase
75	d1onfa3	Alignment	not modelled	8.3	14	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
76	d1ojta3	Alignment	not modelled	8.1	12	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
						PDB header:lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase (carbonate

77	c2a5vB_	Alignment	not modelled	8.0	8	dehydratase) (carbonic **PDBTitle:** crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
78	c2j89A_	Alignment	not modelled	8.0	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine sulfoxide reductase a; **PDBTitle:** functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
79	d1ej5a_	Alignment	not modelled	7.9	20	**Fold:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Superfamily:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Family:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
80	d1ixrc1	Alignment	not modelled	7.8	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
81	d3lada3	Alignment	not modelled	7.6	14	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
82	d1ff3a_	Alignment	not modelled	7.4	18	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
83	d1feca3	Alignment	not modelled	7.4	10	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
84	d1gkab_	Alignment	not modelled	7.3	16	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
85	d1in4a1	Alignment	not modelled	7.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
86	c2k27A_	Alignment	not modelled	7.2	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
87	c1ylkA_	Alignment	not modelled	7.2	4	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv1284/mt1322; **PDBTitle:** crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
88	c1fvaA_	Alignment	not modelled	7.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of bovine methionine sulfoxide reductase
89	c2e4jA_	Alignment	not modelled	7.0	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**prostaglandin-h2 d-isomerase; **PDBTitle:** solution structure of mouse lipocalin-type prostaglandin d2 synthase
90	c1zgaA_	Alignment	not modelled	6.9	9	**PDB header:**plant protein, transferase **Chain:** A: **PDB Molecule:**isoflavanone 4'-o-methyltransferase'; **PDBTitle:** crystal structure of isoflavanone 4'-o-methyltransferase complexed2 with (+)-6a-hydroxymaackiain
91	c3g43F_	Alignment	not modelled	6.9	12	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel subunit **PDBTitle:** crystal structure of the calmodulin-bound cav1.2 c-terminal2 regulatory domain dimer
92	c3elkA_	Alignment	not modelled	6.8	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator ta0346; **PDBTitle:** crystal structure of putative transcriptional regulator ta0346 from2 thermoplasma acidophilum
93	c3klbA_	Alignment	not modelled	6.8	17	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative flavoprotein; **PDBTitle:** crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
94	d1fp2a2	Alignment	not modelled	6.6	5	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
95	c3icrA_	Alignment	not modelled	6.4	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a-disulfide reductase; **PDBTitle:** crystal structure of oxidized bacillus anthracis coadr-rhd
96	c3eyxB_	Alignment	not modelled	6.3	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
97	c2a8cE_	Alignment	not modelled	6.2	5	**PDB header:**lyase **Chain:** E: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** haemophilus influenzae beta-carbonic anhydrase
98	c3ucoB_	Alignment	not modelled	6.1	13	**PDB header:**lyase/lyase inhibitor **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** coccomyxa beta-carbonic anhydrase in complex with iodide
99	c3hhhA_	Alignment	not modelled	5.9	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, padr family; **PDBTitle:** crystal structure of transcriptional regulator, a member of padr2 family, from enterococcus faecalis v583