Phyre^2

Email	l.a.kelley@imperial.ac.uk
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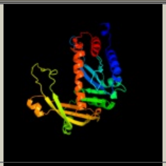
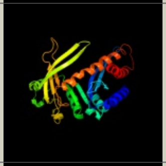
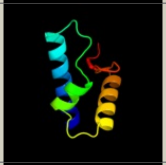
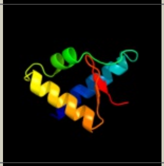
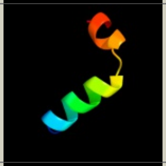
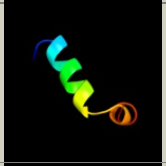
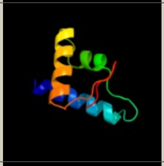
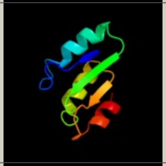
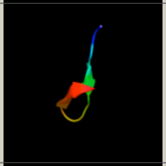
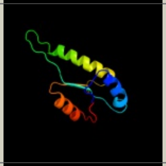
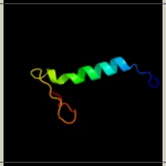
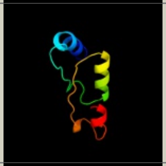
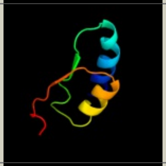
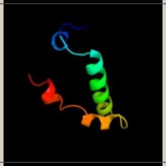
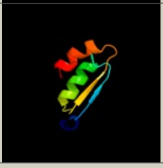
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	Alignment		97.3	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	Alignment		97.1	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
3	d2v9va2	Alignment		82.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
4	c2v9vA_	Alignment		69.1	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** crystal structure of moorella thermoacetica selb(377-511)
5	c3hefB_	Alignment		53.1	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
6	d2ezha_	Alignment		49.2	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
7	d2ezia_	Alignment		48.0	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
8	c6paxA_	Alignment		46.8	24	**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
9	c2plyB_	Alignment		27.5	9	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
10	c2vp8A_	Alignment		22.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
11	d1ajza_	Alignment		21.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase

12	d1pdnc_	Alignment		20.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
13	d1e8qa_	Alignment		19.9	36	**Fold:**Cellulose docking domain, dockering **Superfamily:**Cellulose docking domain, dockering **Family:**Cellulose docking domain, dockering
14	c2pfsA_	Alignment		19.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
15	c2rfpA_	Alignment		18.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
16	d1iyxa1	Alignment		16.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
17	c2y5sA_	Alignment		15.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
18	d1dlwa_	Alignment		13.6	11	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
19	c3e2dB_	Alignment		13.1	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase
20	c3r1iB_	Alignment		12.4	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
21	d2fgga1	Alignment	not modelled	12.2	31	**Fold:**dsRBD-like **Superfamily:**Rv2632c-like **Family:**Rv2632c-like
22	c2kvcA_	Alignment	not modelled	12.0	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
23	c3mx7A_	Alignment	not modelled	12.0	29	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** crystal structure analysis of human faim-ntd
24	c2j4mA_	Alignment	not modelled	11.5	36	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**endoglucanase 45a; **PDBTitle:** double dockerin from piromyces equi cel45a
25	d3bpya1	Alignment	not modelled	11.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
26	d1uuza_	Alignment	not modelled	10.8	20	**Fold:**Inhibitor of vertebrate lysozyme, Ivy **Superfamily:**Inhibitor of vertebrate lysozyme, Ivy **Family:**Inhibitor of vertebrate lysozyme, Ivy
27	c2kzvA_	Alignment	not modelled	10.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of cv_0373(175-257) protein from2 chromobacterium violaceum, northeast structural genomics consortium3 target cvr118a
28	c3emkA_	Alignment	not modelled	10.8	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** 2.5a crystal structure of glucose/ribitol dehydrogenase2

						from brucella melitensis
29	c3pk0B_	Alignment	not modelled	10.5	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
30	c1gmuB_	Alignment	not modelled	10.2	8	**PDB header:**metallochaperone **Chain:** B: **PDB Molecule:**uree; **PDBTitle:** structure of uree
31	c2z1nA_	Alignment	not modelled	9.9	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of ape0912 from aeropyrum pernix k1
32	d1xb4a2	Alignment	not modelled	9.7	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
33	c3ol4B_	Alignment	not modelled	9.7	22	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
34	c3rf7A_	Alignment	not modelled	9.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
35	c3gk0H_	Alignment	not modelled	9.6	24	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
36	c1e17A_	Alignment	not modelled	9.6	9	**PDB header:**dna binding domain **Chain:** A: **PDB Molecule:**afx; **PDBTitle:** solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
37	d1cyda_	Alignment	not modelled	9.6	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
38	d1g9ga_	Alignment	not modelled	9.4	71	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
39	c3aq8A_	Alignment	not modelled	9.1	4	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**group 1 truncated hemoglobin; **PDBTitle:** crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form
40	d1osna_	Alignment	not modelled	9.1	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
41	d2c6ya1	Alignment	not modelled	9.1	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
42	c3n1uA_	Alignment	not modelled	9.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, had superfamily, subfamily iii a; **PDBTitle:** structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
43	d2abka_	Alignment	not modelled	8.9	15	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
44	d1mpga1	Alignment	not modelled	8.8	14	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
45	d1eyea_	Alignment	not modelled	8.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
46	c3ak4C_	Alignment	not modelled	8.8	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-dependent quinuclidinone reductase; **PDBTitle:** crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
47	d3orca_	Alignment	not modelled	8.7	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
48	c3co7C_	Alignment	not modelled	8.7	14	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
49	d1w6ta1	Alignment	not modelled	8.6	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
50	d1s69a_	Alignment	not modelled	8.6	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
51	c2yf3F_	Alignment	not modelled	8.5	20	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**mazg-like nucleoside triphosphate pyrophosphohydrolase; **PDBTitle:** crystal structure of dr2231, the mazg-like protein from2 deinococcus radiodurans, complex with manganese
52	d2ptza1	Alignment	not modelled	8.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
53	d2a22a1	Alignment	not modelled	8.0	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
						PDB header:hydrolase

54	c3a52A_	Alignment	not modelled	7.8	18	**Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
55	d1m5wa_	Alignment	not modelled	7.7	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
56	c1l2aD_	Alignment	not modelled	7.6	57	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
57	d1l1ya_	Alignment	not modelled	7.6	57	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
58	d1g31a_	Alignment	not modelled	7.6	20	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
59	c3ctmH_	Alignment	not modelled	7.5	22	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
60	c1hj0A_	Alignment	not modelled	7.5	17	**PDB header:**actin binding peptide **Chain:** A: **PDB Molecule:**thymosin beta9; **PDBTitle:** thymosin beta9
61	c2iucB_	Alignment	not modelled	7.3	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
62	c1qcrD_	Alignment	not modelled	7.3	8	**PDB header:** **PDB COMPND:**
63	c3othB_	Alignment	not modelled	7.3	11	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**calg1; **PDBTitle:** crystal structure of calg1, calicheamicin glycostyltransferase, tdp2 and calicheamicin alpha3i bound form
64	d1xi8a3	Alignment	not modelled	7.1	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
65	c3g73A_	Alignment	not modelled	7.0	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**forkhead box protein m1; **PDBTitle:** structure of the foxm1 dna binding
66	c1eb0A_	Alignment	not modelled	7.0	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**urease accessory protein uree; **PDBTitle:** crystal structure of bacillus pasteurii uree at 1.85 a,2 phased by siras. type i crystal form.
67	c2giaB_	Alignment	not modelled	7.0	63	**PDB header:**translation **Chain:** B: **PDB Molecule:**mitochondrial rna-binding protein 1; **PDBTitle:** crystal structures of trypanosoma bruciei mrp1/mrp2
68	d2giab1	Alignment	not modelled	7.0	63	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Guide RNA binding protein gBP
69	d1idra_	Alignment	not modelled	6.9	7	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
70	d1bdba_	Alignment	not modelled	6.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
71	c1c94B_	Alignment	not modelled	6.9	63	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**retro-gcn4 leucine zipper; **PDBTitle:** reversing the sequence of the gcn4 leucine zipper does not2 affect its fold.
72	d2o23a1	Alignment	not modelled	6.8	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
73	d1rh6a_	Alignment	not modelled	6.7	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
74	d1ae1a_	Alignment	not modelled	6.7	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
75	d1d1la_	Alignment	not modelled	6.6	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
76	c2x4mD_	Alignment	not modelled	6.6	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
77	c3cxtA_	Alignment	not modelled	6.5	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase with different specificities; **PDBTitle:** quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
78	c2wdzD_	Alignment	not modelled	6.4	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
79	d2gm3a1	Alignment	not modelled	6.4	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
80	c2o2sA_	Alignment	not modelled	6.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase;

80	c2o2sA_	Alignment	not modelled	6.4	12	**PDBTitle:** the structure of t. gondii enoyl acyl carrier protein reductase in2 complex with nad and triclosan
81	c3nswA_	Alignment	not modelled	6.3	60	**PDB header:**immune system **Chain:** A: **PDB Molecule:**excretory-secretory protein 2; **PDBTitle:** crystal structure of ancylostoma ceylanicum excretory-secretory2 protein 2
82	c3hluA_	Alignment	not modelled	6.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf2179; **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 duf2179 from eubacterium ventriosum
83	c3gafF_	Alignment	not modelled	6.2	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**7-alpha-hydroxysteroid dehydrogenase; **PDBTitle:** 2.2a crystal structure of 7-alpha-hydroxysteroid2 dehydrogenase from brucella melitensis
84	c3cwbQ_	Alignment	not modelled	6.1	8	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
85	d1d5va_	Alignment	not modelled	6.1	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
86	c2dkzA_	Alignment	not modelled	6.1	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**hypothetical protein loc64762; **PDBTitle:** solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
87	c2jpiA_	Alignment	not modelled	6.0	17	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
88	c3gdfA_	Alignment	not modelled	6.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nadp-dependent mannitol dehydrogenase; **PDBTitle:** crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
89	d1tx2a_	Alignment	not modelled	5.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
90	c1tx2A_	Alignment	not modelled	5.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
91	d4croa_	Alignment	not modelled	5.9	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
92	d1d7oa_	Alignment	not modelled	5.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
93	c3a44D_	Alignment	not modelled	5.8	0	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
94	d1fmca_	Alignment	not modelled	5.8	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
95	d1gpqa_	Alignment	not modelled	5.7	18	**Fold:**Inhibitor of vertebrate lysozyme, Ivy **Superfamily:**Inhibitor of vertebrate lysozyme, Ivy **Family:**Inhibitor of vertebrate lysozyme, Ivy
96	d2hfha_	Alignment	not modelled	5.7	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
97	c3rihB_	Alignment	not modelled	5.7	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short chain dehydrogenase or reductase; **PDBTitle:** crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
98	c2b99A_	Alignment	not modelled	5.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase; **PDBTitle:** crystal structure of an archaeal pentameric riboflavin2 synthase complex with a substrate analog inhibitor
99	c3rkrC_	Alignment	not modelled	5.6	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short chain oxidoreductase; **PDBTitle:** crystal structure of a metagenomic short-chain oxidoreductase (sdr) in2 complex with nadp