
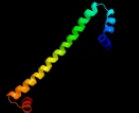
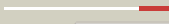












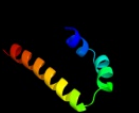










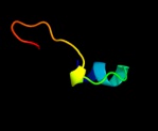






# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0ACG1
Date	Thu Jan 5 11:18:06 GMT 2012
Unique Job ID	8f4b63b57ffcd3ce

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3nr7A_</a>	 Alignment		99.7	54	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> dna-binding protein h-ns; <b>PDBTitle:</b> crystal structure of s. typhimurium h-ns 1-83
2	<a href="#">d1hnra_</a>	 Alignment		99.6	70	<b>Fold:</b> H-NS histone-like proteins <b>Superfamily:</b> H-NS histone-like proteins <b>Family:</b> H-NS histone-like proteins
3	<a href="#">c2levA_</a>	 Alignment		99.3	31	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A; <b>PDB Molecule:</b> ler; <b>PDBTitle:</b> structure of the dna complex of the c-terminal domain of ler
4	<a href="#">c2l92A_</a>	 Alignment		98.7	41	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> histone family protein nucleoid-structuring protein h-ns; <b>PDBTitle:</b> solution structure of the c-terminal domain of h-ns like protein bv3f
5	<a href="#">c2jr1A_</a>	 Alignment		98.6	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> virulence regulator; <b>PDBTitle:</b> solution structure of the dna binding domain of a nucleoid-associated2 protein, h-ns, from the phytopathogen xylella fastidiosa.
6	<a href="#">d1lr1a_</a>	 Alignment		98.5	58	<b>Fold:</b> H-NS histone-like proteins <b>Superfamily:</b> H-NS histone-like proteins <b>Family:</b> H-NS histone-like proteins
7	<a href="#">d1ov9a_</a>	 Alignment		98.4	47	<b>Fold:</b> H-NS histone-like proteins <b>Superfamily:</b> H-NS histone-like proteins <b>Family:</b> H-NS histone-like proteins
8	<a href="#">d1ni8a_</a>	 Alignment		98.3	64	<b>Fold:</b> H-NS histone-like proteins <b>Superfamily:</b> H-NS histone-like proteins <b>Family:</b> H-NS histone-like proteins
9	<a href="#">d1y7ya1</a>	 Alignment		54.8	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
10	<a href="#">d1ayja_</a>	 Alignment		29.9	38	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Plant defensins
11	<a href="#">c3gbhC_</a>	 Alignment		29.8	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> nad(p)h-flavin oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nad(p)h:fmn oxidoreductase (se1966)2 from staphylococcus epidermidis atcc 12228 at 2.00 a resolution

12	<a href="#">c3ivpD_</a>	Alignment		27.2	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative transposon-related dna-binding protein; <b>PDBTitle:</b> the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
13	<a href="#">dli9za_</a>	Alignment		24.5	29	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> Inositol polyphosphate 5-phosphatase (IPP5)
14	<a href="#">c3bpjD_</a>	Alignment		21.8	21	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit j; <b>PDBTitle:</b> crystal structure of human translation initiation factor 3, subunit 12 alpha
15	<a href="#">d1bk8a_</a>	Alignment		21.1	43	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Plant defensins
16	<a href="#">c2eq9C_</a>	Alignment		21.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
17	<a href="#">d2cyua1</a>	Alignment		20.7	9	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
18	<a href="#">c2eq7C_</a>	Alignment		20.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e2 component; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
19	<a href="#">d1f5va_</a>	Alignment		20.2	19	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
20	<a href="#">d1o17a1</a>	Alignment		19.9	20	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
21	<a href="#">d1w4ha1</a>	Alignment	not modelled	19.1	9	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
22	<a href="#">c3dv0L_</a>	Alignment	not modelled	18.8	9	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> I: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
23	<a href="#">d1zcha1</a>	Alignment	not modelled	18.8	26	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
24	<a href="#">c2eq8C_</a>	Alignment	not modelled	17.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
25	<a href="#">c1w3dA_</a>	Alignment	not modelled	17.3	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
26	<a href="#">d1w85i_</a>	Alignment	not modelled	17.1	9	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
27	<a href="#">c2cooA_</a>	Alignment	not modelled	17.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipoamide acyltransferase component of branched-

						<b>PDBTitle:</b> solution structure of the e3_binding domain of 2 dihydrolipoamide branched chaintransacylase <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh dehydrogenase, nadph nitroreductase;
28	<a href="#">c3gagB_</a>	Alignment	not modelled	14.7	20	<b>PDBTitle:</b> crystal structure of a nitroreductase-like protein (smu.346) from2 streptococcus mutans at 1.70 a resolution <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipoamide acyltransferase component of branched-
29	<a href="#">c1zwvA_</a>	Alignment	not modelled	14.1	17	<b>PDBTitle:</b> solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase <b>PDB header:</b> transferase
30	<a href="#">c1w4kA_</a>	Alignment	not modelled	13.8	22	<b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase e2; <b>PDBTitle:</b> peripheral-subunit binding domains from mesophilic, 2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
31	<a href="#">c3d6zA_</a>	Alignment	not modelled	13.6	20	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug-efflux transporter 1 regulator; <b>PDBTitle:</b> crystal structure of r275e mutant of bmrr bound to dna and rhodamine
32	<a href="#">d1brwa1</a>	Alignment	not modelled	13.4	11	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphori bosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphori bosyltransferase N-terminal domain
33	<a href="#">d1ic8a2</a>	Alignment	not modelled	13.3	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
34	<a href="#">c1yw5A_</a>	Alignment	not modelled	13.2	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl prolyl cis/trans isomerase; <b>PDBTitle:</b> peptidyl-prolyl isomerase ess1 from candida albicans
35	<a href="#">d1bala_</a>	Alignment	not modelled	12.9	9	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
36	<a href="#">c1o17A_</a>	Alignment	not modelled	12.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphori bosyltransferase; <b>PDBTitle:</b> anthranilate phosphori bosyl-transferase (trpd)
37	<a href="#">d1iwga5</a>	Alignment	not modelled	12.0	6	<b>Fold:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Superfamily:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Family:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
38	<a href="#">d2ewca1</a>	Alignment	not modelled	11.6	4	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> YjgF-like <b>Family:</b> YjgF/L-PSP
39	<a href="#">c2kpiA_</a>	Alignment	not modelled	11.6	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sos-response transcriptional repressor, lexa; <b>PDBTitle:</b> solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
40	<a href="#">c2xswB_</a>	Alignment	not modelled	11.4	39	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 72 kda inositol polyphosphate 5-phosphatase; <b>PDBTitle:</b> crystal structure of human inpp5e
41	<a href="#">d2a6ca1</a>	Alignment	not modelled	10.8	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
42	<a href="#">c1g6uB_</a>	Alignment	not modelled	10.1	30	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> domain swapped dimer; <b>PDBTitle:</b> crystal structure of a domain swapped dimer
43	<a href="#">c2rpbA_</a>	Alignment	not modelled	9.7	33	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical membrane protein; <b>PDBTitle:</b> the solution structure of membrane protein
44	<a href="#">c2kpoA_</a>	Alignment	not modelled	9.6	36	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> rossmann 2x2 fold protein; <b>PDBTitle:</b> solution nmr structure of de novo designed rossmann 2x2 fold protein,2 northeast structural genomics consortium target or16
45	<a href="#">d1chma1</a>	Alignment	not modelled	9.6	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Creatinase/prolidase N-terminal domain <b>Family:</b> Creatinase/prolidase N-terminal domain
46	<a href="#">d1m5ya3</a>	Alignment	not modelled	9.6	12	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
47	<a href="#">d1k4ta3</a>	Alignment	not modelled	9.4	16	<b>Fold:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment <b>Superfamily:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment <b>Family:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
48	<a href="#">c3bs3A_</a>	Alignment	not modelled	9.4	5	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of a putative dna-binding protein from bacteroides2 fragilis
49	<a href="#">c2jvdA_</a>	Alignment	not modelled	9.3	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0291 protein yncz; <b>PDBTitle:</b> solution nmr structure of the folded n-terminal fragment of2 upf0291 protein yncz from bacillus subtilis. northeast3 structural genomics target sr384-1-46 <b>PDB header:</b> transferase

50	<a href="#">c2jo8B_</a>	Alignment	not modelled	9.3	21	<b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase 4; <b>PDBTitle:</b> solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
51	<a href="#">d1sxic1</a>	Alignment	not modelled	8.9	18	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
52	<a href="#">d1iwga6</a>	Alignment	not modelled	8.6	20	<b>Fold:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Superfamily:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Family:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
53	<a href="#">d2ofya1</a>	Alignment	not modelled	8.6	4	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
54	<a href="#">d1r8ea1</a>	Alignment	not modelled	8.5	20	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
55	<a href="#">d1juba_</a>	Alignment	not modelled	8.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
56	<a href="#">c2l5pA_</a>	Alignment	not modelled	8.1	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipocalin 12; <b>PDBTitle:</b> solution nmr structure of protein lipocalin 12 from rat epididymis
57	<a href="#">c2jeeA_</a>	Alignment	not modelled	8.1	17	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> yiii; <b>PDBTitle:</b> xray structure of e. coli yiii
58	<a href="#">c3hdIA_</a>	Alignment	not modelled	8.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> royal palm tree peroxidase; <b>PDBTitle:</b> crystal structure of highly glycosylated peroxidase from royal palm2 tree
59	<a href="#">d2ifaa1</a>	Alignment	not modelled	7.9	20	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
60	<a href="#">d2ay0a1</a>	Alignment	not modelled	7.8	38	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> PutA pre-N-terminal region-like
61	<a href="#">c3bhpA_</a>	Alignment	not modelled	7.7	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0291 protein yznc; <b>PDBTitle:</b> crystal structure of upf0291 protein yznc from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
62	<a href="#">d2o38a1</a>	Alignment	not modelled	7.5	3	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
63	<a href="#">c2o38A_</a>	Alignment	not modelled	7.5	3	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> putative xre family transcriptional regulator
64	<a href="#">d1r3ha2</a>	Alignment	not modelled	7.4	19	<b>Fold:</b> MHC antigen-recognition domain <b>Superfamily:</b> MHC antigen-recognition domain <b>Family:</b> MHC antigen-recognition domain
65	<a href="#">d1kzyc1</a>	Alignment	not modelled	7.3	5	<b>Fold:</b> BRCT domain <b>Superfamily:</b> BRCT domain <b>Family:</b> 53BP1
66	<a href="#">d1iqpa1</a>	Alignment	not modelled	7.2	18	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
67	<a href="#">c1k5gH_</a>	Alignment	not modelled	7.1	19	<b>PDB header:</b> signaling protein/signaling activator <b>Chain:</b> H: <b>PDB Molecule:</b> ran-specific gtpase-activating protein; <b>PDBTitle:</b> crystal structure of ran-gdp-alfx-ranbp1-rangap complex
68	<a href="#">d1k5db_</a>	Alignment	not modelled	7.1	19	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Ran-binding domain
69	<a href="#">d2r1jl1</a>	Alignment	not modelled	7.1	33	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
70	<a href="#">d1sxb1</a>	Alignment	not modelled	7.0	9	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
71	<a href="#">d1je6a2</a>	Alignment	not modelled	6.8	14	<b>Fold:</b> MHC antigen-recognition domain <b>Superfamily:</b> MHC antigen-recognition domain <b>Family:</b> MHC antigen-recognition domain
72	<a href="#">c3ebwA_</a>	Alignment	not modelled	6.7	5	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> per a 4 allergen; <b>PDBTitle:</b> crystal structure of major allergens, per a 4 from2 cockroaches
73	<a href="#">c3ge6B_</a>	Alignment	not modelled	6.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (exig_2970) from exiguobacterium sibiricum 255-15 at 1.85 a3 resolution
74	<a href="#">c2xstA_</a>	Alignment	not modelled	6.7	5	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipocalin 15; <b>PDBTitle:</b> crystal structure of the human lipocalin 15
75	<a href="#">c3clcC_</a>	Alignment	not modelled	6.6	15	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator

76	<a href="#">c3b7hA</a>	Alignment	not modelled	6.6	7	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> prophage lp1 protein 11; <b>PDBTitle:</b> crystal structure of the prophage lp1 protein 11
77	<a href="#">c3qcD</a>	Alignment	not modelled	6.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative metalloproteinase; <b>PDBTitle:</b> crystal structure of n-terminal domain (creatinase/prolidase like2 domain) of putative metalloproteinase from corynebacterium diphtheriae
78	<a href="#">c3il0B</a>	Alignment	not modelled	6.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> aminopeptidase p; xaa-pro aminopeptidase; <b>PDBTitle:</b> the crystal structure of the aminopeptidase p, xaa-pro aminopeptidase2 from streptococcus thermophilus
79	<a href="#">dlj1va</a>	Alignment	not modelled	6.6	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Chromosomal replication initiation factor DnaA C-terminal domain IV
80	<a href="#">c2q9lA</a>	Alignment	not modelled	6.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
81	<a href="#">dlz3eb1</a>	Alignment	not modelled	6.5	6	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> C-terminal domain of RNA polymerase alpha subunit <b>Family:</b> C-terminal domain of RNA polymerase alpha subunit
82	<a href="#">dlpina2</a>	Alignment	not modelled	6.5	23	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
83	<a href="#">c2k23A</a>	Alignment	not modelled	6.4	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipocalin 2; <b>PDBTitle:</b> solution structure analysis of the rlcn2
84	<a href="#">c3rmrA</a>	Alignment	not modelled	6.4	32	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> avirulence protein; <b>PDBTitle:</b> crystal structure of hyaloperonospora arabidopsidis atr1 effector2 domain
85	<a href="#">c3bemA</a>	Alignment	not modelled	6.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nad(p)h nitroreductase ydfn; <b>PDBTitle:</b> crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution
86	<a href="#">c3ocaB</a>	Alignment	not modelled	6.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide deformylase; <b>PDBTitle:</b> crystal structure of peptide deformylase from ehrlichia chaffeensis
87	<a href="#">dlutxa</a>	Alignment	not modelled	6.4	10	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
88	<a href="#">c2l9vA</a>	Alignment	not modelled	6.3	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-processing factor 40 homolog a; <b>PDBTitle:</b> nmr structure of the ff domain l24a mutant's folding transition state
89	<a href="#">c3gtzA</a>	Alignment	not modelled	6.3	4	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative translation initiation inhibitor; <b>PDBTitle:</b> crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium
90	<a href="#">dlthha</a>	Alignment	not modelled	6.2	16	<b>Fold:</b> Anti-sigma factor AsiA <b>Superfamily:</b> Anti-sigma factor AsiA <b>Family:</b> Anti-sigma factor AsiA
91	<a href="#">d2bjca1</a>	Alignment	not modelled	6.2	7	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
92	<a href="#">c2h0uA</a>	Alignment	not modelled	6.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph-flavin oxidoreductase; <b>PDBTitle:</b> crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
93	<a href="#">c3i7tA</a>	Alignment	not modelled	6.0	8	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of rv2704, a member of highly conserved2 yjgf/yer057c/uk114 family, from mycobacterium tuberculosis
94	<a href="#">c3pvpA</a>	Alignment	not modelled	5.8	18	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
95	<a href="#">c2wl8D</a>	Alignment	not modelled	5.8	19	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> peroxisomal biogenesis factor 19; <b>PDBTitle:</b> x-ray crystal structure of pex19p
96	<a href="#">c2rbfB</a>	Alignment	not modelled	5.8	38	<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)
97	<a href="#">dlr69a</a>	Alignment	not modelled	5.7	26	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
98	<a href="#">dlv8ga1</a>	Alignment	not modelled	5.7	9	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
99	<a href="#">c2kwvA</a>	Alignment	not modelled	5.7	29	<b>PDB header:</b> protein binding/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iota; <b>PDBTitle:</b> solution structure of ubm1 of murine polymerase iota in complex with2 ubiquitin