

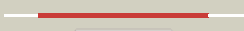





















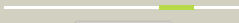


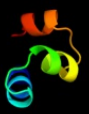




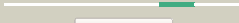


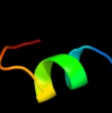






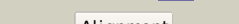
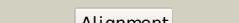
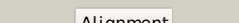


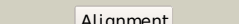


# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P45767
Date	Thu Jan 5 12:03:42 GMT 2012
Unique Job ID	86deb16a2ca29c8c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d3dhwa1</a>	 Alignment		99.9	27	<b>Fold:</b> Metl-like <b>Superfamily:</b> Metl-like <b>Family:</b> Metl-like
2	<a href="#">c2onkC_</a>	 Alignment		99.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> molybdate/tungstate abc transporter, permease <b>PDBTitle:</b> abc transporter modbc in complex with its binding protein2 moda
3	<a href="#">d2onkc1</a>	 Alignment		99.9	14	<b>Fold:</b> Metl-like <b>Superfamily:</b> Metl-like <b>Family:</b> Metl-like
4	<a href="#">d2r6gf2</a>	 Alignment		99.8	18	<b>Fold:</b> Metl-like <b>Superfamily:</b> Metl-like <b>Family:</b> Metl-like
5	<a href="#">d3d31c1</a>	 Alignment		99.8	21	<b>Fold:</b> Metl-like <b>Superfamily:</b> Metl-like <b>Family:</b> Metl-like
6	<a href="#">c3d31D_</a>	 Alignment		99.8	21	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> sulfate/molybdate abc transporter, permease <b>PDBTitle:</b> modbc from methanosarcina acetivorans
7	<a href="#">c3fh6F_</a>	 Alignment		99.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> maltose transport system permease protein malF; <b>PDBTitle:</b> crystal structure of the resting state maltose transporter from e.2 coli
8	<a href="#">c2r6gF_</a>	 Alignment		99.8	16	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> maltose transport system permease protein malF; <b>PDBTitle:</b> the crystal structure of the e. coli maltose transporter
9	<a href="#">d2r6gg1</a>	 Alignment		99.7	17	<b>Fold:</b> Metl-like <b>Superfamily:</b> Metl-like <b>Family:</b> Metl-like
10	<a href="#">d1umqa_</a>	 Alignment		67.6	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
11	<a href="#">c1umqA_</a>	 Alignment		67.6	22	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity

12	<a href="#">d1ntca_</a>	 Alignment		64.7	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
13	<a href="#">d1fipa_</a>	 Alignment		64.7	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
14	<a href="#">d1etob_</a>	 Alignment		63.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
15	<a href="#">c3e7lD_</a>	 Alignment		61.0	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain
16	<a href="#">d1etxa_</a>	 Alignment		55.5	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
17	<a href="#">d1g2ha_</a>	 Alignment		42.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
18	<a href="#">c2cw1A_</a>	 Alignment		35.6	47	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> sn4m; <b>PDBTitle:</b> solution structure of the de novo-designed lambda cro fold2 protein
19	<a href="#">c2auwB_</a>	 Alignment		24.4	16	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ne0471; <b>PDBTitle:</b> crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
20	<a href="#">d1igna2</a>	 Alignment		18.5	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> DNA-binding domain of rap1
21	<a href="#">c2h51B_</a>	 Alignment	not modelled	18.3	22	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> caspase-1; <b>PDBTitle:</b> crystal structure of human caspase-1 (glu390->asp and arg286->lys) in2 complex with 3-[2-(2-benzoyloxycarbonylamino-3-methyl-butylamino)-3 propionylamino]-4-oxo-pentanoic acid (z-vad-fmk)
22	<a href="#">d2auwa1</a>	 Alignment	not modelled	16.0	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE0471 C-terminal domain-like
23	<a href="#">d3orca_</a>	 Alignment	not modelled	15.6	29	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
24	<a href="#">d1puca_</a>	 Alignment	not modelled	14.4	40	<b>Fold:</b> Cell cycle regulatory proteins <b>Superfamily:</b> Cell cycle regulatory proteins <b>Family:</b> Cell cycle regulatory proteins
25	<a href="#">c1qb3B_</a>	 Alignment	not modelled	14.1	40	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cyclin-dependent kinases regulatory subunit; <b>PDBTitle:</b> crystal structure of the cell cycle regulatory protein cks1
26	<a href="#">c2d7dB_</a>	 Alignment	not modelled	13.4	21	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> 40-mer from uvrabc system protein b; <b>PDBTitle:</b> structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
27	<a href="#">d1a8ra_</a>	 Alignment	not modelled	12.1	24	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> GTP cyclohydrolase I
28	<a href="#">c1is7F_</a>	 Alignment	not modelled	12.0	35	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> gtp cyclohydrolase i; <b>PDBTitle:</b> crystal structure of rat gtpchi/gfrp stimulatory complex

29	<a href="#">d1wpla_</a>	Alignment	not modelled	12.0	35	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> GTP cyclohydrolase I
30	<a href="#">c3e8gB_</a>	Alignment	not modelled	11.6	3	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> potassium channel protein; <b>PDBTitle:</b> crystal structure of the the open nak channel-na+/ca2+ complex
31	<a href="#">d1wura1</a>	Alignment	not modelled	11.6	24	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> GTP cyclohydrolase I
32	<a href="#">c1wm9D_</a>	Alignment	not modelled	11.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> gtp cyclohydrolase i; <b>PDBTitle:</b> structure of gtp cyclohydrolase i from thermus thermophilus hb8
33	<a href="#">d1cksa_</a>	Alignment	not modelled	11.1	33	<b>Fold:</b> Cell cycle regulatory proteins <b>Superfamily:</b> Cell cycle regulatory proteins <b>Family:</b> Cell cycle regulatory proteins
34	<a href="#">c2jwaA_</a>	Alignment	not modelled	11.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> erbb2 transmembrane segment dimer spatial structure
35	<a href="#">d1qb3a_</a>	Alignment	not modelled	10.8	40	<b>Fold:</b> Cell cycle regulatory proteins <b>Superfamily:</b> Cell cycle regulatory proteins <b>Family:</b> Cell cycle regulatory proteins
36	<a href="#">c2vn2B_</a>	Alignment	not modelled	10.7	25	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome replication initiation protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
37	<a href="#">c2c1eB_</a>	Alignment	not modelled	9.6	35	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> caspase-3 subunit p12; <b>PDBTitle:</b> crystal structures of caspase-3 in complex with aza-peptide michael2 acceptor inhibitors.
38	<a href="#">d2astc1</a>	Alignment	not modelled	9.1	27	<b>Fold:</b> Cell cycle regulatory proteins <b>Superfamily:</b> Cell cycle regulatory proteins <b>Family:</b> Cell cycle regulatory proteins
39	<a href="#">d2axtz1</a>	Alignment	not modelled	9.1	25	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> PsbZ-like <b>Family:</b> PsbZ-like
40	<a href="#">d1w96a2</a>	Alignment	not modelled	7.2	4	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
41	<a href="#">d2j9ga2</a>	Alignment	not modelled	7.0	25	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
42	<a href="#">d1ulza2</a>	Alignment	not modelled	6.9	29	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
43	<a href="#">c2c2zB_</a>	Alignment	not modelled	6.8	31	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> caspase-8 p10 subunit; <b>PDBTitle:</b> crystal structure of caspase-8 in complex with aza-peptide michael2 acceptor inhibitor
44	<a href="#">c2v79B_</a>	Alignment	not modelled	6.8	17	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna replication protein dnad; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
45	<a href="#">d1jhfa1</a>	Alignment	not modelled	6.7	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
46	<a href="#">d3c07a2</a>	Alignment	not modelled	6.6	20	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
47	<a href="#">c3iz5C_</a>	Alignment	not modelled	6.6	53	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> 60s ribosomal protein l3 (l3p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
48	<a href="#">d1d1la_</a>	Alignment	not modelled	6.5	31	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
49	<a href="#">c3sipB_</a>	Alignment	not modelled	6.4	43	<b>PDB header:</b> hydrolase/ligase/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> caspase; <b>PDBTitle:</b> crystal structure of drice and diap1-bir1 complex
50	<a href="#">d1mzja2</a>	Alignment	not modelled	6.4	25	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
51	<a href="#">c2gutA_</a>	Alignment	not modelled	6.4	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> arc/mediator, positive cofactor 2 glutamine/q- <b>PDBTitle:</b> solution structure of the trans-activation domain of the2 human co-activator arc105
52	<a href="#">c2p22D_</a>	Alignment	not modelled	6.3	50	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical 12.0 kda protein in ade3-ser2 <b>PDBTitle:</b> structure of the yeast escrt-i heterotetramer core
53	<a href="#">d1zk8a2</a>	Alignment	not modelled	6.2	26	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
54	<a href="#">d1i3ja_</a>	Alignment	not modelled	6.2	19	<b>Fold:</b> DNA-binding domain of intron-encoded endonucleases <b>Superfamily:</b> DNA-binding domain of intron-encoded endonucleases <b>Family:</b> DNA-binding domain of intron-encoded endonucleases
55	<a href="#">d2cg4a1</a>	Alianment	not modelled	6.1	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain

					<b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
56	<a href="#">c3mkyP_</a>	Alignment	not modelled	6.1	7 <b>PDB header:</b> dna binding protein/dna <b>Chain:</b> P: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-323)-18mer dna complex, i23 form
57	<a href="#">d1i1ga1</a>	Alignment	not modelled	6.1	19 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
58	<a href="#">d4croa_</a>	Alignment	not modelled	6.1	31 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
59	<a href="#">c2zihC_</a>	Alignment	not modelled	6.1	16 <b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 74; <b>PDBTitle:</b> crystal structure of yeast vps74
60	<a href="#">c2qljB_</a>	Alignment	not modelled	6.1	35 <b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> caspase-7; <b>PDBTitle:</b> crystal structure of caspase-7 with inhibitor ac-wehd-cho
61	<a href="#">c2ziiA_</a>	Alignment	not modelled	6.0	16 <b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 74; <b>PDBTitle:</b> crystal structure of yeast vps74-n-term truncation variant
62	<a href="#">c2w7nA_</a>	Alignment	not modelled	5.9	33 <b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> trfb transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of kora bound to operator dna: insight2 into repressor cooperation in rp4 gene regulation
63	<a href="#">d2cyya1</a>	Alignment	not modelled	5.9	16 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
64	<a href="#">d2coba1</a>	Alignment	not modelled	5.9	26 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
65	<a href="#">c3natB_</a>	Alignment	not modelled	5.8	20 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function ef_19772 from enterococcus faecalis
66	<a href="#">c3mkzU_</a>	Alignment	not modelled	5.7	9 <b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> U: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-272)-18mer complex, p21 form
67	<a href="#">c1mhmB_</a>	Alignment	not modelled	5.7	18 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosylmethionine decarboxylase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine decarboxylase2 from potato
68	<a href="#">c2ijlB_</a>	Alignment	not modelled	5.6	15 <b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> molybdenum-binding transcriptional repressor; <b>PDBTitle:</b> the structure of a putative mode from agrobacterium tumefaciens.
69	<a href="#">d2cfxa1</a>	Alignment	not modelled	5.6	22 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
70	<a href="#">d1bxya_</a>	Alignment	not modelled	5.4	35 <b>Fold:</b> Ribosomal protein L30p/L7e <b>Superfamily:</b> Ribosomal protein L30p/L7e <b>Family:</b> Ribosomal protein L30p/L7e
71	<a href="#">d2apob1</a>	Alignment	not modelled	5.4	15 <b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Nop10-like SnoRNP <b>Family:</b> Nucleolar RNA-binding protein Nop10-like
72	<a href="#">c2rbfB_</a>	Alignment	not modelled	5.3	27 <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)
73	<a href="#">d1cy9a_</a>	Alignment	not modelled	5.2	29 <b>Fold:</b> Prokaryotic type I DNA topoisomerase <b>Superfamily:</b> Prokaryotic type I DNA topoisomerase <b>Family:</b> Prokaryotic type I DNA topoisomerase
74	<a href="#">d2ey4e1</a>	Alignment	not modelled	5.2	31 <b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Nop10-like SnoRNP <b>Family:</b> Nucleolar RNA-binding protein Nop10-like