








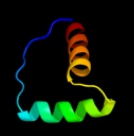
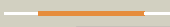



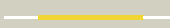

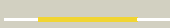

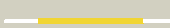


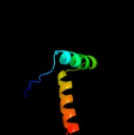
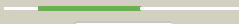
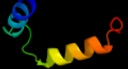

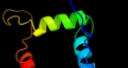

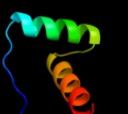





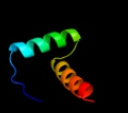






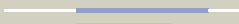

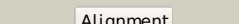
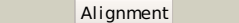
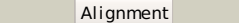

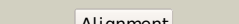
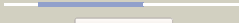


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	POC079
Date	Thu Jan 5 11:29:49 GMT 2012
Unique Job ID	064dcf99beb1a18e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k29A_	 Alignment		99.7	100	PDB header: transcription Chain: A; PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
2	c2kc8B_	 Alignment		94.4	100	PDB header: toxin/toxin repressor Chain: B; PDB Molecule: antitoxin relb; PDBTitle: structure of e. coli toxin rele (r81a/r83a) mutant in2 complex with antitoxin relbc (k47-l79) peptide
3	d2bj7a1	 Alignment		90.6	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
4	c1q5vB_	 Alignment		87.0	26	PDB header: transcription Chain: B; PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
5	c2bj3D_	 Alignment		84.1	20	PDB header: transcription Chain: D; PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
6	d1p94a_	 Alignment		80.7	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
7	c2keba_	 Alignment		79.6	8	PDB header: dna binding protein Chain: A; PDB Molecule: dna polymerase subunit alpha b; PDBTitle: nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
8	c2ca9B_	 Alignment		77.4	17	PDB header: transcriptional regulation Chain: B; PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
9	d2hzaa1	 Alignment		75.6	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
10	d2hza1	 Alignment		74.2	26	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
11	c2k5jB_	 Alignment		58.9	18	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

12	d1sxd1	 Alignment		50.7	20	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
13	d1mnta_	 Alignment		42.0	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
14	d1y9ba1	 Alignment		39.5	15	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like
15	d2hsga1	 Alignment		36.0	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
16	d1myla_	 Alignment		35.9	19	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
17	c1u9pA_	 Alignment		35.2	17	PDB header: unknown function Chain: A: PDB Molecule: parc; PDBTitle: permuted single-chain arc
18	d1b28a_	 Alignment		30.1	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
19	d1u5ta1	 Alignment		29.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
20	c1u5tA_	 Alignment		28.0	10	PDB header: transport protein Chain: A: PDB Molecule: appears to be functionally related to snf7; PDBTitle: structure of the escrt-ii endosomal trafficking complex
21	c2kwpA_	 Alignment	not modelled	27.0	18	PDB header: transcription Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: solution structure of the aminoterminal domain of e. coli nusa
22	c3cuqA_	 Alignment	not modelled	26.7	21	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
23	c2zmeA_	 Alignment	not modelled	26.4	21	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
24	c1vbiA_	 Alignment	not modelled	26.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: type 2 malate/lactate dehydrogenase; PDBTitle: crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
25	c3ltiA_	 Alignment	not modelled	25.8	25	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-betai4 domains
26	d1mylb_	 Alignment	not modelled	24.5	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
27	c3cqrB_	 Alignment	not modelled	23.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: violaxanthin de-epoxidase, chloroplast; PDBTitle: crystal structure of the lipocalin domain of violaxanthin2 de-epoxidase (vde) at ph5
28	d2cpga_	 Alignment	not modelled	23.5	13	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like

29	dli4ua_	Alignment	not modelled	23.3	19	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
30	d1qpza1	Alignment	not modelled	22.8	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
31	d2bsqe1	Alignment	not modelled	22.6	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
32	c2h1rA_	Alignment	not modelled	22.5	19	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase, putative; PDBTitle: crystal structure of a dimethyladenosine transferase from <i>Plasmodium falciparum</i>
33	c3ebwA_	Alignment	not modelled	22.3	24	PDB header: allergen Chain: A: PDB Molecule: per a 4 allergen; PDBTitle: crystal structure of major allergens, per a 4 from 2 cockroaches
34	d2ff4a2	Alignment	not modelled	20.4	26	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: BTAD-like
35	c3oopA_	Alignment	not modelled	20.3	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2960 protein; PDBTitle: the structure of a protein with unknown function from <i>Listeria innocua</i> 2 clip11262
36	d1efaa1	Alignment	not modelled	20.3	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
37	c2jucA_	Alignment	not modelled	20.2	9	PDB header: unknown function Chain: A: PDB Molecule: pre-mrna-splicing factor urn1; PDBTitle: urn1 ff domain yeast
38	d1cuka1	Alignment	not modelled	20.1	31	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
39	d2bjca1	Alignment	not modelled	19.1	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
40	d1luxca_	Alignment	not modelled	18.1	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
41	c3nrwA_	Alignment	not modelled	18.1	18	PDB header: recombination Chain: A: PDB Molecule: phage integrase/site-specific recombinase; PDBTitle: crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from <i>Haloarcula marismortui</i> , northeast3 structural genomics consortium target hmr208a
42	d1lcda_	Alignment	not modelled	17.1	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
43	d2vqca1	Alignment	not modelled	16.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: F112-like
44	c2vqcA_	Alignment	not modelled	16.8	11	PDB header: dna-binding protein Chain: A: PDB Molecule: hypothetical 13.2 kda protein; PDBTitle: structure of a dna binding winged-helix protein, f-112.2 from <i>Sulfolobus spindle-shaped virus 1</i> .
45	d1sxb1	Alignment	not modelled	16.6	8	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
46	d1gkab_	Alignment	not modelled	16.5	24	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
47	d1qwda_	Alignment	not modelled	16.4	33	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
48	c2hzqA_	Alignment	not modelled	16.1	10	PDB header: transport protein Chain: A: PDB Molecule: apolipoprotein d; PDBTitle: crystal structure of human apolipoprotein d (apod) in 2 complex with progesterone
49	c3h87D_	Alignment	not modelled	16.0	28	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from <i>Mycobacterium tuberculosis</i>
50	d1l6ja1	Alignment	not modelled	16.0	27	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
51	c3ecoB_	Alignment	not modelled	15.4	24	PDB header: transcription Chain: B: PDB Molecule: mepR; PDBTitle: crystal structure of mepR, a transcription regulator of the 2 <i>Staphylococcus aureus</i> multidrug efflux pump mepA
52	c2lcvA_	Alignment	not modelled	14.2	19	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate 2 calculation
53	c2q37A_	Alignment	not modelled	13.9	24	PDB header: plant protein, lyase Chain: A: PDB Molecule: ohcu decarboxylase; PDBTitle: crystal structure of ohcu decarboxylase in the presence of 2 (s)-allantoin
54	d2q37a1	Alignment	not modelled	13.9	24	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
						PDB header: ligand binding protein

55	c3by0B_	Alignment	not modelled	13.6	19	Chain: B: PDB Molecule: neutrophil gelatinase-associated lipocalin; PDBTitle: crystal structure of siderocalin (ngal, lipocalin 2) w79a-r81a2 complexed with ferric enterobactin
56	c2l8nA_	Alignment	not modelled	13.2	19	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
57	c2k23A_	Alignment	not modelled	12.8	29	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 2; PDBTitle: solution structure analysis of the rlcn2
58	c2xstA_	Alignment	not modelled	12.6	5	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 15; PDBTitle: crystal structure of the human lipocalin 15
59	c2qwwB_	Alignment	not modelled	12.5	10	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
60	d1a0pa1	Alignment	not modelled	12.3	14	Fold: SAM domain-like Superfamily: lambda integrase-like, N-terminal domain Family: lambda integrase-like, N-terminal domain
61	d2d0ob1	Alignment	not modelled	11.9	14	Fold: Anti codon-binding domain-like Superfamily: B12-dependent dehydratase associated subunit Family: Dehydratase-reactivating factor beta subunit
62	c3l4rA_	Alignment	not modelled	11.5	10	PDB header: allergen, lipid binding protein Chain: A: PDB Molecule: minor allergen can f 2; PDBTitle: crystal structure of the dog lipocalin allergen can f 2 and2 implications for cross-reactivity to the cat allergen fel d 4
63	d2pb9a1	Alignment	not modelled	11.4	21	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: Phosphomethylpyrimidine kinase C-terminal domain-like
64	d1epba_	Alignment	not modelled	11.3	10	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
65	c2l5pA_	Alignment	not modelled	10.9	18	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 12; PDBTitle: solution nmr structure of protein lipocalin 12 from rat epididymis
66	d1jhfa1	Alignment	not modelled	10.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
67	d1v92a_	Alignment	not modelled	10.8	30	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TAP-C domain-like
68	c1avoA_	Alignment	not modelled	10.5	17	PDB header: proteasome activator Chain: A: PDB Molecule: 11s regulator; PDBTitle: proteasome activator reg(alpha)
69	c2rdpA_	Alignment	not modelled	10.5	24	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator marr; PDBTitle: the structure of a marr family protein from bacillus2 stearothermophilus
70	c2rn7A_	Alignment	not modelled	10.4	23	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tpe protein from shigella2 flexneri. northeast structural genomics target sfr125
71	d1gm6a_	Alignment	not modelled	10.4	14	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
72	d2ieaa3	Alignment	not modelled	10.3	15	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
73	d1ew3a_	Alignment	not modelled	9.9	19	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
74	c3jw4C_	Alignment	not modelled	9.9	18	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, marr/emrr family; PDBTitle: the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
75	d1mkma1	Alignment	not modelled	9.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator ICLR, N-terminal domain
76	d1iqpa1	Alignment	not modelled	9.7	14	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
77	c3k0lA_	Alignment	not modelled	9.7	16	PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
78	d1uxda_	Alignment	not modelled	9.6	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
79	c2pexA_	Alignment	not modelled	9.5	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator ohrr; PDBTitle: structure of reduced c22s ohrr from xanthomonas campestris
80	d1g7oa1	Alignment	not modelled	9.4	9	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
						Fold: Ribbon-helix-helix

81	d1bazb_	Alignment	not modelled	9.2	23	Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
82	c2jxnA_	Alignment	not modelled	9.2	6	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein ymr074c; PDBTitle: solution structure of s. cerevisiae pdcd5-like protein ymr074cp
83	d1znda1	Alignment	not modelled	9.2	19	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
84	d1x71a1	Alignment	not modelled	9.1	19	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
85	d1iwqa5	Alignment	not modelled	8.9	17	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
86	c2g8yB_	Alignment	not modelled	8.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: malate/l-lactate dehydrogenases; PDBTitle: the structure of a putative malate/lactate dehydrogenase from e. coli.
87	d2o8ia1	Alignment	not modelled	8.8	14	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
88	d2o70a1	Alignment	not modelled	8.7	17	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
89	d2doda1	Alignment	not modelled	8.7	18	Fold: Another 3-helical bundle Superfamily: FF domain Family: FF domain
90	d1uzca_	Alignment	not modelled	8.3	18	Fold: Another 3-helical bundle Superfamily: FF domain Family: FF domain
91	d1xkia_	Alignment	not modelled	8.1	16	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
92	d2jn6a1	Alignment	not modelled	8.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
93	c2kobA_	Alignment	not modelled	8.0	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of clolep_01837 (fragment 61-160)2 from clostridium leptum. northeast structural genomics3 consortium target qlr8a
94	d1avsa_	Alignment	not modelled	7.9	14	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
95	d1baza_	Alignment	not modelled	7.8	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
96	d1xl3c1	Alignment	not modelled	7.7	6	Fold: Type III secretion system domain Superfamily: Type III secretion system domain Family: TyeA-like
97	c1bdhA_	Alignment	not modelled	7.7	19	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
98	d1yupa1	Alignment	not modelled	7.5	26	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
99	d2isya1	Alignment	not modelled	7.5	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein