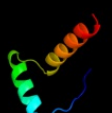
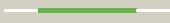
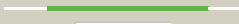
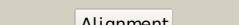
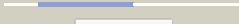
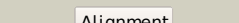


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	Q47150
Date	Thu Jan 5 12:36:25 GMT 2012
Unique Job ID	092353bcc562d3fa

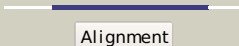
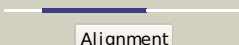
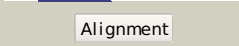
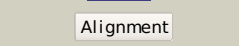
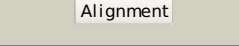
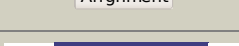
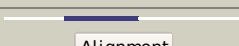
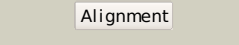
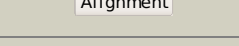
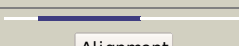
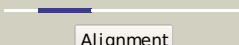
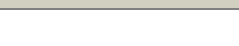
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k29A_	 Alignment		99.7	33	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
2	d2bj7a1	 Alignment		83.3	12	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
3	d1y9ba1	 Alignment		83.2	27	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like
4	d1p94a_	 Alignment		82.6	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
5	c2kebA_	 Alignment		80.2	9	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
6	c2bj3D_	 Alignment		74.2	13	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
7	d2bsqe1	 Alignment		74.2	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
8	c1q5vB_	 Alignment		73.5	22	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
9	d2hzab1	 Alignment		68.8	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
10	d2hzaa1	 Alignment		68.7	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
11	c2ca9B_	 Alignment		59.3	18	PDB header: transcriptional regulation Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation

12	c3bq3A_	 Alignment		56.9	9	PDB header: cell cycle, ligase Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: crystal structure of s. cerevisiae dcn1
13	d1mnta_	 Alignment		41.2	5	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
14	d1u5ta1	 Alignment		35.6	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
15	c2fe3B_	 Alignment		31.6	13	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
16	c1u5ta_	 Alignment		31.0	15	PDB header: transport protein Chain: A: PDB Molecule: appears to be functionally related to snf7; PDBTitle: structure of the escrt-ii endosomal trafficking complex
17	c3cuqA_	 Alignment		29.7	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
18	c2zmeA_	 Alignment		29.6	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
19	c2h1rA_	 Alignment		28.1	24	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase, putative; PDBTitle: crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum
20	c3ltiA_	 Alignment		25.5	19	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-beta14 domains
21	c3g5oA_	 Alignment	not modelled	25.5	19	PDB header: toxin/antitoxin Chain: A: PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
22	c3cqrB_	 Alignment	not modelled	23.7	10	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
23	c1vbiA_	 Alignment	not modelled	22.1	12	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
24	c3ebwA_	 Alignment	not modelled	21.5	29	PDB header: allergen Chain: A: PDB Molecule: per a 4 allergen; PDBTitle: crystal structure of major allergens, per a 4 from2 cockroaches
25	d1i4ua_	 Alignment	not modelled	21.2	0	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
26	c3h87D_	 Alignment	not modelled	20.2	22	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
27	c1u9pA_	 Alignment	not modelled	20.1	5	PDB header: unknown function Chain: A: PDB Molecule: parc; PDBTitle: permuted single-chain arc
28	c1avoA_	 Alignment	not modelled	18.3	11	PDB header: proteasome activator Chain: A: PDB Molecule: 11s regulator; PDBTitle: proteasome activator reg(alpha)
						Fold: lambda repressor-like DNA-binding domains

29	d2hsqa1	Alignment	not modelled	17.4	7	Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
30	c1rr7A_	Alignment	not modelled	17.2	11	PDB header: transcription Chain: A: PDB Molecule: middle operon regulator; PDBTitle: crystal structure of the middle operon regulator protein of2 bacteriophage mu
31	d1rr7a_	Alignment	not modelled	17.2	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Middle operon regulator, Mor
32	c2g8yB_	Alignment	not modelled	16.4	8	PDB header: oxidoreductase Chain: B: PDB Molecule: malate/l-lactate dehydrogenases; PDBTitle: the structure of a putative malate/lactate dehydrogenase from e. coli.
33	d1b28a_	Alignment	not modelled	16.1	12	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
34	d1gkab_	Alignment	not modelled	16.0	19	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
35	c2hzqa_	Alignment	not modelled	15.9	5	PDB header: transport protein Chain: A: PDB Molecule: apolipoprotein d; PDBTitle: crystal structure of human apolipoprotein d (apod) in2 complex with progesterone
36	d1qwda_	Alignment	not modelled	15.8	24	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
37	c2k5jB_	Alignment	not modelled	15.5	14	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
38	c3oopA_	Alignment	not modelled	15.2	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2960 protein; PDBTitle: the structure of a protein with unknown function from listeria innocua2 clip11262
39	d1sxjd1	Alignment	not modelled	15.0	5	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
40	c2fu4B_	Alignment	not modelled	14.7	14	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)
41	d2idba2	Alignment	not modelled	14.4	10	Fold: UbiD C-terminal domain-like Superfamily: UbiD C-terminal domain-like Family: UbiD C-terminal domain-like
42	d2ff4a2	Alignment	not modelled	14.0	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: BTAD-like
43	c2jucA_	Alignment	not modelled	13.4	14	PDB header: unknown function Chain: A: PDB Molecule: pre-mrna-splicing factor urn1; PDBTitle: urn1 ff domain yeast
44	d1mzba_	Alignment	not modelled	13.3	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FUR-like
45	d1iwga5	Alignment	not modelled	12.5	22	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
46	d2vqa1	Alignment	not modelled	12.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: F112-like
47	c2vqaA_	Alignment	not modelled	12.3	20	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 sulfolobus spindle-shaped virus 1.
48	d1v92a_	Alignment	not modelled	10.9	13	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TAP-C domain-like
49	c2kp6A_	Alignment	not modelled	10.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein cv0237 from2 chromobacterium violaceum. northeast structural genomics3 consortium (nesg) target cvt1
50	d1l6ja1	Alignment	not modelled	10.4	17	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
51	c2l5pA_	Alignment	not modelled	10.4	14	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 12; PDBTitle: solution nmr structure of protein lipocalin 12 from rat epididymis
52	c2vzaD_	Alignment	not modelled	10.3	12	PDB header: cell adhesion Chain: D: PDB Molecule: cell filamentation protein; PDBTitle: type iv secretion system effector protein bepa
53	c2xstA_	Alignment	not modelled	10.2	14	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 15; PDBTitle: crystal structure of the human lipocalin 15
54	c3by0B_	Alignment	not modelled	10.1	19	PDB header: ligand binding protein Chain: B: PDB Molecule: neutrophil gelatinase-associated lipocalin; PDBTitle: crystal structure of siderocalin (ngal, lipocalin 2) w79a-r81a2 complexed with ferric enterobactin

55	c3l4rA_	Alignment	not modelled	9.8	19	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
56	c2qwwB_	Alignment	not modelled	9.5	31	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
57	c2k23A_	Alignment	not modelled	9.1	19	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 2; PDBTitle: solution structure analysis of the rlcn2
58	dlepba_	Alignment	not modelled	9.0	5	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
59	c1a11A_	Alignment	not modelled	8.8	15	PDB header: acetylcholine receptor Chain: A: PDB Molecule: acetylcholine receptor m2; PDBTitle: nmr structure of membrane spanning segment 2 of the2 acetylcholine receptor in dpc micelles, 10 structures
60	d2ohwa1	Alignment	not modelled	8.7	13	Fold: Bacillus chorismate mutase-like Superfamily: Yuel-like Family: Yuel-like
61	c1eq8A_	Alignment	not modelled	8.7	15	PDB header: signaling protein Chain: A: PDB Molecule: acetylcholine receptor protein; PDBTitle: three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
62	c1eq8E_	Alignment	not modelled	8.7	15	PDB header: signaling protein Chain: E: PDB Molecule: acetylcholine receptor protein; PDBTitle: three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
63	c1eq8C_	Alignment	not modelled	8.7	15	PDB header: signaling protein Chain: C: PDB Molecule: acetylcholine receptor protein; PDBTitle: three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
64	c1eq8B_	Alignment	not modelled	8.7	15	PDB header: signaling protein Chain: B: PDB Molecule: acetylcholine receptor protein; PDBTitle: three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
65	c1eq8D_	Alignment	not modelled	8.7	15	PDB header: signaling protein Chain: D: PDB Molecule: acetylcholine receptor protein; PDBTitle: three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
66	dlew3a_	Alignment	not modelled	8.1	10	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
67	d1gm6a_	Alignment	not modelled	8.0	14	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
68	d1znda1	Alignment	not modelled	7.7	19	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
69	c1z4hA_	Alignment	not modelled	7.6	13	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
70	d2pb9a1	Alignment	not modelled	7.5	8	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: Phosphomethylpyrimidine kinase C-terminal domain-like
71	d12asa_	Alignment	not modelled	7.5	12	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
72	d1uxca_	Alignment	not modelled	7.4	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
73	c3nrwA_	Alignment	not modelled	7.3	17	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 haloarcula marismortui, northeast3 structural genomics consortium target hmr208a
74	d1cuka1	Alignment	not modelled	7.2	18	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
75	c2rn7A_	Alignment	not modelled	7.2	18	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
76	d1xkia_	Alignment	not modelled	7.1	11	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
77	c2jyaA_	Alignment	not modelled	7.0	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1810; PDBTitle: nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
78	c3czcA_	Alignment	not modelled	6.9	14	PDB header: transferase Chain: A: PDB Molecule: rmpb; PDBTitle: the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
79	c3ld1A_	Alignment	not modelled	6.8	24	PDB header: hydrolase Chain: A: PDB Molecule: replicase polyprotein 1a; PDBTitle: crystal structure of ibv nsp2a

80	c2w57A	 Alignment	not modelled	6.6	14	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
81	c2rdpA	 Alignment	not modelled	6.6	22	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator marr; PDBTitle: the structure of a marr family protein from bacillus2 steaerothermophilus
82	c3iukB	 Alignment	not modelled	6.6	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative bacterial protein of unknown function2 (duf885, pf05960.1,) from arthrobacter aureus tc1, reveals fold3 similar to that of m32 carboxypeptidases
83	c3ecoB	 Alignment	not modelled	6.5	17	PDB header: transcription Chain: B: PDB Molecule: mepr; PDBTitle: crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
84	d1efaa1	 Alignment	not modelled	6.3	4	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
85	c1viqB	 Alignment	not modelled	6.3	30	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
86	d1yupa1	 Alignment	not modelled	6.3	11	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
87	d1oqya2	 Alignment	not modelled	6.3	18	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
88	d1qpza1	 Alignment	not modelled	6.2	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
89	c3mr2A	 Alignment	not modelled	6.2	15	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
90	d2ieaa3	 Alignment	not modelled	6.2	12	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
91	c1vzmB	 Alignment	not modelled	6.1	25	PDB header: calcium-binding protein Chain: B: PDB Molecule: osteocalcin; PDBTitle: osteocalcin from fish argyrosomus regius
92	c3bx6A	 Alignment	not modelled	6.0	10	PDB header: signaling protein Chain: A: PDB Molecule: alpha-1-acid glycoprotein; PDBTitle: crystal structure of human alpha 1 acid glycoprotein
93	d1bw6a	 Alignment	not modelled	6.0	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
94	d1i94m	 Alignment	not modelled	6.0	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
95	d1mkma1	 Alignment	not modelled	5.9	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain
96	d1zj8a1	 Alignment	not modelled	5.8	17	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
97	d1q9ja2	 Alignment	not modelled	5.7	9	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
98	d1dv0a	 Alignment	not modelled	5.7	18	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
99	c2idbB	 Alignment	not modelled	5.6	10	PDB header: lyase Chain: B: PDB Molecule: 3-octaprenyl-4-hydroxybenzoate carboxy-lyase; PDBTitle: crystal structure of 3-octaprenyl-4-hydroxybenzoate decarboxylase2 (ubid) from escherichia coli, northeast structural genomics target3 er459.