



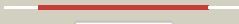









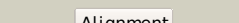
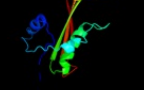






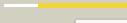











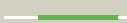


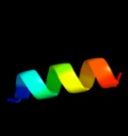





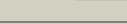
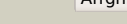






Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P52061
Date	Wed Jan 25 15:20:57 GMT 2012
Unique Job ID	699ecdc8ef1e6ff2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k7ka_	 Alignment		100.0	99	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
2	c3tquD_	 Alignment		100.0	53	PDB header: hydrolase Chain: D: PDB Molecule: non-canonical purine ntp pyrophosphatase; PDBTitle: structure of a ham1 protein from coxiella burnetii
3	d1v7ra_	 Alignment		100.0	36	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
4	d1vp2a_	 Alignment		100.0	34	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
5	d2cara1	 Alignment		100.0	26	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
6	d1b78a_	 Alignment		100.0	33	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
7	d2amha1	 Alignment		97.5	14	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: Maf-like
8	d1ex2a_	 Alignment		93.3	20	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: Maf-like
9	c2p5xB_	 Alignment		89.6	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: n-acetylserotonin o-methyltransferase-like protein; PDBTitle: crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
10	d1u5wa1	 Alignment		81.5	21	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: YjjX-like
11	c3brcA_	 Alignment		73.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum

12	d1nn4a_	 Alignment		72.6	15	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
13	c3m1pA_	 Alignment		69.4	18	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with alloose-6-phosphate
14	c3k7pA_	 Alignment		69.4	18	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
15	d1zwyal	 Alignment		67.1	18	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: YjjX-like
16	c3crgA_	 Alignment		64.8	19	PDB header: transferase Chain: A: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: structure of trna dimethylallyltransferase: rna2 modification through a channel
17	c3c5yD_	 Alignment		59.8	18	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
18	c3fozB_	 Alignment		56.4	17	PDB header: transferase/rna Chain: B: PDB Molecule: trna delta(2)-isopentenylpyrophosphate transferase; PDBTitle: structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
19	c3c5tB_	 Alignment		46.8	38	PDB header: signaling protein/signaling protein Chain: B: PDB Molecule: exendin-4; PDBTitle: crystal structure of the ligand-bound glucagon-like peptide-1 receptor2 extracellular domain
20	c3onoA_	 Alignment		39.8	21	PDB header: isomerase Chain: A: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase lacab_rpiB from2 vibrio parahaemolyticus
21	c2ppwA_	 Alignment	not modelled	38.9	17	PDB header: isomerase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpiB from streptococcus pneumoniae
22	d2vvpa1	 Alignment	not modelled	29.4	18	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
23	d1u14a_	 Alignment	not modelled	29.2	17	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: YjjX-like
24	c2jrlA_	 Alignment	not modelled	26.8	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
25	c1nm3B_	 Alignment	not modelled	26.7	25	PDB header: electron transport Chain: B: PDB Molecule: protein hi0572; PDBTitle: crystal structure of heamophilus influenza hybrid-prx5
26	d1rlka_	 Alignment	not modelled	26.5	18	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
27	d2pc6a1	 Alignment	not modelled	26.2	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
28	d2fgca1	 Alignment	not modelled	26.0	26	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
		 Alignment				PDB header: transferase Chain: B: PDB Molecule: trna delta(2)-isopentenylpyrophosphate

29	c3d3qB_	Alignment	not modelled	25.6	22	PDBTitle: crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
30	c1d0rA_	Alignment	not modelled	25.4	38	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon-like peptide-1-(7-36)-amide; PDBTitle: solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
31	c3exaD_	Alignment	not modelled	24.9	20	PDB header: transferase Chain: D: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: crystal structure of the full-length trna2 isopentenylpyrophosphate transferase (bh2366) from3 bacillus halodurans, northeast structural genomics4 consortium target bhr41.
32	d1vbva1	Alignment	not modelled	24.6	22	Fold: SH3-like barrel Superfamily: YccV-like Family: YccV-like
33	c1jrjA_	Alignment	not modelled	24.1	38	PDB header: hormone/growth factor Chain: A: PDB Molecule: exendin-4; PDBTitle: solution structure of exendin-4 in 30-vol% trifluoroethanol
34	d1ixra2	Alignment	not modelled	23.2	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
35	c3i42A_	Alignment	not modelled	23.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey- PDBTitle: structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
36	d2f1fa2	Alignment	not modelled	22.9	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
37	d1l8na1	Alignment	not modelled	22.5	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
38	c3rh0A_	Alignment	not modelled	22.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
39	d1rp3a2	Alignment	not modelled	21.5	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
40	c1mqra_	Alignment	not modelled	20.3	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-d-glucuronidase; PDBTitle: the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 stearotherophilus t-6
41	c3crnA_	Alignment	not modelled	19.8	7	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, chey-like; PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
42	c3he8A_	Alignment	not modelled	19.6	18	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
43	d2eyqa2	Alignment	not modelled	19.1	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
44	d1o1xa_	Alignment	not modelled	18.4	16	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
45	d1c01a_	Alignment	not modelled	17.8	21	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Plant antimicrobial protein MIAMP1
46	d3ehwa1	Alignment	not modelled	16.2	50	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
47	d2nn6h3	Alignment	not modelled	15.4	14	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
48	d1smyf2	Alignment	not modelled	15.1	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
49	d1q7sa_	Alignment	not modelled	14.8	20	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
50	c3jteA_	Alignment	not modelled	13.7	12	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
51	c3a8tA_	Alignment	not modelled	13.3	24	PDB header: transferase Chain: A: PDB Molecule: adenylate isopentenyltransferase; PDBTitle: plant adenylate isopentenyltransferase in complex with atp
52	c3mzyA_	Alignment	not modelled	12.8	15	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
53	c2wmpB_	Alignment	not modelled	12.4	33	PDB header: chaperone Chain: B: PDB Molecule: pagp protein; PDBTitle: structure of the e. coli chaperone pagp in complex with the pilin2 domain of the pagpii adhesin
						Fold: Peptidyl-tRNA hydrolase II

54	d3erja1	Alignment	not modelled	12.0	20	Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
55	d2f06a2	Alignment	not modelled	11.9	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
56	c3f4fB_	Alignment	not modelled	11.3	50	PDB header: hydrolase Chain: B: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of dut1p, a dutpase from saccharomyces cerevisiae
57	c3kc2A_	Alignment	not modelled	11.2	19	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
58	d1dq3a4	Alignment	not modelled	10.7	17	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
59	c2zv3E_	Alignment	not modelled	10.7	22	PDB header: hydrolase Chain: E: PDB Molecule: peptidyl-tRNA hydrolase; PDBTitle: crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
60	d1ku7a_	Alignment	not modelled	10.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
61	c2qr3A_	Alignment	not modelled	10.6	13	PDB header: transcription Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
62	c3hugA_	Alignment	not modelled	10.3	22	PDB header: transcription/membrane protein Chain: A: PDB Molecule: RNA polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigl
63	c1xtyD_	Alignment	not modelled	10.0	16	PDB header: hydrolase Chain: D: PDB Molecule: peptidyl-tRNA hydrolase; PDBTitle: crystal structure of sulfobolus solfataricus peptidyl-tRNA2 hydrolase
64	c1or7A_	Alignment	not modelled	9.3	12	PDB header: transcription Chain: A: PDB Molecule: RNA polymerase sigma-e factor; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rseA
65	c2rpbA_	Alignment	not modelled	8.9	18	PDB header: membrane protein Chain: A: PDB Molecule: hypothetical membrane protein; PDBTitle: the solution structure of membrane protein
66	c3c3mA_	Alignment	not modelled	8.9	10	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
67	c3s5pA_	Alignment	not modelled	8.9	20	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
68	c1yd2A_	Alignment	not modelled	8.8	18	PDB header: DNA binding protein Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the giv-yig n-terminal endonuclease domain of2 uvrC from thermotoga maritima: point mutant y19f bound to the3 catalytic divalent cation
69	d2ix0a2	Alignment	not modelled	8.6	35	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
70	c3qd5B_	Alignment	not modelled	8.6	24	PDB header: isomerase Chain: B: PDB Molecule: putative ribose-5-phosphate isomerase; PDBTitle: crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
71	d1or7a1	Alignment	not modelled	8.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
72	c3cg0A_	Alignment	not modelled	8.4	17	PDB header: lyase Chain: A: PDB Molecule: response regulator receiver modulated diguanylate cyclase PDBTitle: crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
73	c1upiA_	Alignment	not modelled	8.3	21	PDB header: epimerase Chain: A: PDB Molecule: dtddp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: mycobacterium tuberculosis rmlC epimerase (rv3465)
74	d1j9ba_	Alignment	not modelled	7.7	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: ArsC-like
75	c3ehwA_	Alignment	not modelled	7.7	50	PDB header: hydrolase Chain: A: PDB Molecule: dutp pyrophosphatase; PDBTitle: human dutpase in complex with alpha,beta-imido-dutp and mg2+:2 visualization of the full-length c-termini in all monomers and3 suggestion for an additional metal ion binding site
76	d1cuka3	Alignment	not modelled	7.7	28	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
77	c1y7xA_	Alignment	not modelled	7.5	10	PDB header: structural protein, protein binding Chain: A: PDB Molecule: major vault protein; PDBTitle: solution structure of a two-repeat fragment of major vault2 protein
78	c3b0dB_	Alignment	not modelled	7.5	38	PDB header: transcription/dna Chain: B: PDB Molecule: cts;

78	c3lv0b	Alignment	not modelled	7.5	38	PDBTitle: crystal structure of ctsr in complex with a 26bp dna duplex PDB header: dna binding protein Chain: A: PDB Molecule: uvrc; PDBTitle: crystal structure of the gty-yig n-terminal endonuclease2 domain of uvrc from bacillus caldotenax
79	c1yd6A	Alignment	not modelled	7.5	45	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: structural study on project id ph1539 from pyrococcus2 horikoshii ot3
80	c2d3kA	Alignment	not modelled	7.4	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
81	d1muma	Alignment	not modelled	7.2	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
82	d1ku3a	Alignment	not modelled	6.9	21	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
83	c2h5xA	Alignment	not modelled	6.9	23	PDB header: transferase/rna Chain: A: PDB Molecule: trna isopentenyltransferase; PDBTitle: crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
84	c3eplA	Alignment	not modelled	6.7	18	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
85	c3b8iF	Alignment	not modelled	6.5	33	PDB header: de novo protein Chain: A: PDB Molecule: protein or36; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or36 (casd3 target)
86	c2lciA	Alignment	not modelled	6.3	19	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
87	d1jvaa3	Alignment	not modelled	6.2	27	PDB header: hydrolase inhibitor/hydrolase Chain: B: PDB Molecule: bowman-birk type bran trypsin inhibitor; PDBTitle: crystal structure and functional study of the bowman-birk2 inhibitor from rice bran in complex with bovine trypsin
88	c2qn5B	Alignment	not modelled	6.1	36	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
89	d1mvoa	Alignment	not modelled	5.8	24	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setdb1; PDBTitle: crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
90	c3dlmA	Alignment	not modelled	5.8	15	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
91	c3nhzA	Alignment	not modelled	5.7	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
92	d1h41a1	Alignment	not modelled	5.7	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
93	d1bvsa3	Alignment	not modelled	5.6	28	PDB header: transcription Chain: B: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: n-terminal gaf domain of transcriptional pleiotropic repressor cody
94	c2gx5B	Alignment	not modelled	5.4	11	PDB header: translation Chain: P: PDB Molecule: mitochondrial rna-binding protein 2; PDBTitle: crystal structures of trypanosoma brucei mrp1/mrp2
95	c2gidP	Alignment	not modelled	5.3	36	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: PG0945 N-terminal domain-like
96	d2p0sa1	Alignment	not modelled	5.2	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein purs; PDBTitle: structure of thermus thermophilus purs in the p21 form
97	c2dgbA	Alignment	not modelled	5.1	18	PDB header: transferase/dna Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
98	c1t39A	Alignment	not modelled	5.1	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
99	d1s7oa	Alignment	not modelled	5.0	16	