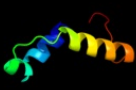
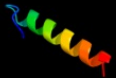
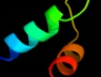


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A7A7
Date	Thu Jan 5 11:05:13 GMT 2012
Unique Job ID	9c74607744eb9073

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1iuga_	 Alignment		97.5	16	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
2	d2a07f1	 Alignment		31.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
3	c3hqdB_	 Alignment		29.7	20	PDB header: motor protein Chain: B: PDB Molecule: kinesin-like protein kif11; PDBTitle: human kinesin eg5 motor domain in complex with amppnp and2 mg2+
4	c2jlhA_	 Alignment		28.3	18	PDB header: protein transport Chain: A: PDB Molecule: yop proteins translocation protein u; PDBTitle: crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant
5	d2dpwa1	 Alignment		28.0	25	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
6	c3tevA_	 Alignment		26.7	22	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 3; PDBTitle: the crystal structure of glycosyl hydrolase from deinococcus2 radiodurans r1
7	d1tr9a_	 Alignment		25.8	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
8	d2p6ra1	 Alignment		25.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RecQ helicase DNA-binding domain-like
9	d1t3la2	 Alignment		21.7	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
10	c1e17A_	 Alignment		20.8	19	PDB header: dna binding domain Chain: A: PDB Molecule: afx; PDBTitle: solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
11	c3s2wB_	 Alignment		19.7	18	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the crystal structure of a marr transcriptional regulator from2 methanosarcina maezi go1

12	d1vyva2	Alignment		18.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
13	d1t0hb_	Alignment		18.3	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
14	d1vyua2	Alignment		17.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
15	d1ry6a_	Alignment		16.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Motor proteins
16	c1ry6A_	Alignment		16.9	14	PDB header: transport protein Chain: A: PDB Molecule: internal kinesin; PDBTitle: crystal structure of internal kinesin motor domain
17	d1wj5a_	Alignment		16.3	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: An Obfc1 domain
18	d1z6ra1	Alignment		16.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
19	d2c6ya1	Alignment		15.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
20	d1mvoa_	Alignment		15.5	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
21	c1sfeA_	Alignment	not modelled	15.2	57	PDB header: dna-binding protein Chain: A: PDB Molecule: ada o6-methylguanine-dna methyltransferase; PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli
22	c2jk1A_	Alignment	not modelled	14.7	7	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
23	c3t6aB_	Alignment	not modelled	14.5	15	PDB header: signaling protein Chain: B: PDB Molecule: breast cancer anti-estrogen resistance protein 3; PDBTitle: structure of the c-terminal domain of bcar3
24	c3c00B_	Alignment	not modelled	14.4	11	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: escu; PDBTitle: crystal structural of the mutated g247t escu/spas c-terminal domain
25	c2k29A_	Alignment	not modelled	14.1	13	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
26	c2wbeC_	Alignment	not modelled	14.0	17	PDB header: structural protein Chain: C: PDB Molecule: bipolar kinesin krp-130; PDBTitle: kinesin-5-tubulin complex with amppnp
27	d1x88a1	Alignment	not modelled	13.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Motor proteins
28	c3lk6A_	Alignment	not modelled	13.2	25	PDB header: hydrolase Chain: A: PDB Molecule: lipoprotein ybbd; PDBTitle: beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis

29	d2qzga1	Alignment	not modelled	13.0	12	Fold: Bromodomain-like Superfamily: Ta0600-like Family: Ta0600-like
30	c1wrjA_	Alignment	not modelled	12.9	57	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
31	c3g73A_	Alignment	not modelled	12.5	11	PDB header: transcription/dna Chain: A: PDB Molecule: forkhead box protein m1; PDBTitle: structure of the foxm1 dna binding
32	c3sqlB_	Alignment	not modelled	12.2	17	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3; PDBTitle: crystal structure of glycoside hydrolase from synechococcus
33	d1q42a_	Alignment	not modelled	12.2	39	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
34	c2vt1B_	Alignment	not modelled	12.1	17	PDB header: membrane protein Chain: B: PDB Molecule: surface presentation of antigens protein spas; PDBTitle: crystal structure of the cytoplasmic domain of spa40, the2 specificity switch for the shigella flexneri type iii3 secretion system
35	c2ctuA_	Alignment	not modelled	11.9	50	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 483; PDBTitle: solution structure of zinc finger domain from human zn2 finger protein 483
36	c2byvE_	Alignment	not modelled	11.3	13	PDB header: regulation Chain: E: PDB Molecule: rap guanine nucleotide exchange factor 4; PDBTitle: structure of the camp responsive exchange factor epac2 in2 its auto-inhibited state
37	d2cqna1	Alignment	not modelled	11.3	27	Fold: Another 3-helical bundle Superfamily: FF domain Family: FF domain
38	c1t39A_	Alignment	not modelled	11.0	57	PDB header: transferase/dna Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
39	d1lj5a_	Alignment	not modelled	10.8	9	Fold: Serpins Superfamily: Serpins Family: Serpins
40	c3nwrA_	Alignment	not modelled	10.7	16	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
41	c3i71B_	Alignment	not modelled	10.1	28	PDB header: unknown function Chain: B: PDB Molecule: ethanolamine utilization protein eutk; PDBTitle: ethanolamine utilization microcompartment shell subunit, eutk c-2 terminal domain
42	c3r4kD_	Alignment	not modelled	10.1	16	PDB header: dna binding protein Chain: D: PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
43	c2ijeS_	Alignment	not modelled	10.1	18	PDB header: signaling protein Chain: S: PDB Molecule: guanine nucleotide-releasing protein; PDBTitle: crystal structure of the cdc25 domain of rasgrf1
44	c2fyuE_	Alignment	not modelled	10.1	64	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
45	c3bmxB_	Alignment	not modelled	9.9	25	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized lipoprotein ybbd; PDBTitle: beta-n-hexosaminidase (ybbd) from bacillus subtilis
46	c3ndaA_	Alignment	not modelled	9.9	16	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: serpin-2; PDBTitle: crystal structure of serpin from tick ixodes ricinus
47	d1whna_	Alignment	not modelled	9.8	18	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
48	c3co7C_	Alignment	not modelled	9.6	16	PDB header: transcription/dna Chain: C: PDB Molecule: forkhead box protein o1; PDBTitle: crystal structure of foxo1 dbd bound to dbe2 dna
49	d1seka_	Alignment	not modelled	9.5	14	Fold: Serpins Superfamily: Serpins Family: Serpins
50	d1dqna_	Alignment	not modelled	9.4	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
51	c3ozqA_	Alignment	not modelled	9.2	16	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: serpin48; PDBTitle: crystal structure of serpin48, which is a highly specific serpin in2 the insect tenebrio molitor
52	c1p84E_	Alignment	not modelled	8.9	50	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
53	d2qsba1	Alignment	not modelled	8.8	17	Fold: Bromodomain-like Superfamily: Ta0600-like Family: Ta0600-like
54	d2hfha_	Alignment	not modelled	8.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

						Family: Forkhead DNA-binding domain
55	d1ykwa1	Alignment	not modelled	8.7	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
56	c3c01H_	Alignment	not modelled	8.5	20	PDB header: membrane protein, protein transport Chain: H: PDB Molecule: surface presentation of antigens protein spas; PDBTitle: crystal structural of native spas c-terminal domain
57	c3psfA_	Alignment	not modelled	8.0	19	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
58	c2l25A_	Alignment	not modelled	7.9	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: np_888769.1
59	d8ruca1	Alignment	not modelled	7.8	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
60	d1kcfa2	Alignment	not modelled	7.7	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Mitochondrial resolvase ydc2 catalytic domain
61	d1jm6a1	Alignment	not modelled	7.7	19	Fold: Bromodomain-like Superfamily: alpha-ketoacid dehydrogenase kinase, N-terminal domain Family: alpha-ketoacid dehydrogenase kinase, N-terminal domain
62	c2h4qA_	Alignment	not modelled	7.5	15	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: heterochromatin-associated protein ment; PDBTitle: crystal structure of a m-loop deletion variant of ment in2 the cleaved conformation
63	c3kcna_	Alignment	not modelled	7.4	5	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylate cyclase from2 rhodopirellula baltica
64	c1mgtA_	Alignment	not modelled	7.4	71	PDB header: transferase Chain: A: PDB Molecule: protein (o6-methylguanine-dna methyltransferase); PDBTitle: crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1
65	c3t7yB_	Alignment	not modelled	7.3	17	PDB header: protein transport Chain: B: PDB Molecule: yop proteins translocation protein u; PDBTitle: structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
66	c2kk6A_	Alignment	not modelled	7.3	22	PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase fer; PDBTitle: solution structure of sh2 domain of proto-oncogene tyrosine-2 protein kinase fer from homo sapiens, northeast structural3 genomics consortium (nesg) target hr3461d
67	c3igzB_	Alignment	not modelled	7.3	22	PDB header: isomerase Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
68	d1ej7l1	Alignment	not modelled	7.3	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
69	d1svda1	Alignment	not modelled	7.2	18	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
70	c2vh4B_	Alignment	not modelled	7.2	13	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: tengpin; PDBTitle: structure of a loop c-sheet serpin polymer
71	d1d7ka2	Alignment	not modelled	7.2	24	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
72	d3bzra1	Alignment	not modelled	7.1	12	Fold: EscU C-terminal domain-like Superfamily: EscU C-terminal domain-like Family: EscU C-terminal domain-like
73	c3bzra_	Alignment	not modelled	7.1	12	PDB header: membrane protein, protein transport Chain: A: PDB Molecule: escu; PDBTitle: crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
74	c2fynO_	Alignment	not modelled	7.1	50	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
75	d3bpya1	Alignment	not modelled	7.1	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
76	d1k9oi_	Alignment	not modelled	7.0	14	Fold: Serpins Superfamily: Serpins Family: Serpins
77	c1hleA_	Alignment	not modelled	6.9	17	PDB header: hydrolase inhibitor(serine proteinase) Chain: A: PDB Molecule: horse leukocyte elastase inhibitor; PDBTitle: crystal structure of cleaved equine leukocyte elastase2 inhibitor determined at 1.95 angstroms resolution
78	c2imgA_	Alignment	not modelled	6.9	33	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 23; PDBTitle: crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
						Fold: DNA/RNA-binding 3-helical bundle

79	d1kq8a_	Alignment	not modelled	6.6	27	Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
80	c1kq8A_	Alignment	not modelled	6.6	27	PDB header: transcription Chain: A: PDB Molecule: hepatocyte nuclear factor 3 forkhead homolog 1; PDBTitle: solution structure of winged helix protein hfh-1
81	c2hxcC_	Alignment	not modelled	6.5	19	PDB header: transport protein Chain: C: PDB Molecule: kinesin-like protein kif1a; PDBTitle: kif1a head-microtubule complex structure in adp-form
82	c3euhB_	Alignment	not modelled	6.5	18	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of the muke-mukf complex
83	c1sngA_	Alignment	not modelled	6.4	22	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: cog4826: serine protease inhibitor; PDBTitle: structure of a thermophilic serpin in the native state
84	d1imva_	Alignment	not modelled	6.3	19	Fold: Serpins Superfamily: Serpins Family: Serpins
85	d2doea1	Alignment	not modelled	6.2	14	Fold: Another 3-helical bundle Superfamily: FF domain Family: FF domain
86	d2qlvb1	Alignment	not modelled	6.0	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: AMPK-beta glycogen binding domain-like
87	c3rggA_	Alignment	not modelled	6.0	22	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
88	d1x38a1	Alignment	not modelled	5.9	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
89	d1riea_	Alignment	not modelled	5.9	64	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
90	c3qfwB_	Alignment	not modelled	5.8	20	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodopseudomonas2 palustris
91	c1t5cA_	Alignment	not modelled	5.7	12	PDB header: contractile protein Chain: A: PDB Molecule: centromeric protein e; PDBTitle: crystal structure of the motor domain of human kinetochore2 protein cenp-e
92	d2z15a1	Alignment	not modelled	5.7	10	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
93	c3fcnA_	Alignment	not modelled	5.7	18	PDB header: unknown function Chain: A: PDB Molecule: an alpha-helical protein of unknown function (pfam01724); PDBTitle: crystal structure of an alpha-helical protein of unknown function2 (rru_a3208) from rhodospirillum rubrum atcc 11170 at 1.45 a3 resolution
94	d3e9va1	Alignment	not modelled	5.6	14	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
95	d1sfea1	Alignment	not modelled	5.6	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
96	c2k7rA_	Alignment	not modelled	5.5	11	PDB header: replication Chain: A: PDB Molecule: primosomal protein dnaI; PDBTitle: n-terminal domain of the bacillus subtilis helicase-loading2 protein dnaI
97	c2ia2D_	Alignment	not modelled	5.5	12	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
98	c2nvgA_	Alignment	not modelled	5.4	45	PDB header: oxidoreductase Chain: A: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: soluble domain of rieske iron sulfur protein.
99	d2bsqe1	Alignment	not modelled	5.4	29	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like