



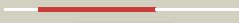



















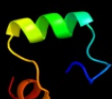



Phyre2


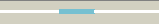
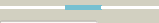



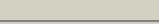



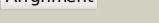
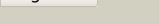

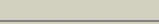
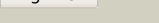
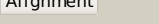
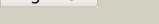
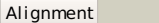



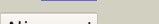
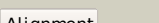
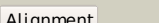
Email	I.a.kelley@imperial.ac.uk
Description	P75869
Date	Thu Jan 5 12:15:17 GMT 2012
Unique Job ID	93eccfda05a188b2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2od0a1	 Alignment		100.0	32	Fold: Secretion chaperone-like Superfamily: YgaC/TfoX-N like Family: TfoX N-terminal domain-like
2	c3bqsB_	 Alignment		100.0	37	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form
3	d2a1va1	 Alignment		96.4	14	Fold: Secretion chaperone-like Superfamily: YjbR-like Family: YjbR-like
4	d2fkia1	 Alignment		96.2	18	Fold: Secretion chaperone-like Superfamily: YjbR-like Family: YjbR-like
5	c1t3nB_	 Alignment		94.0	26	PDB header: replication/dna Chain: B: PDB Molecule: polymerase (dna directed) iota; PDBTitle: structure of the catalytic core of dna polymerase iota in2 complex with dna and dttp
6	d1pzna1	 Alignment		93.7	21	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
7	c2flIA_	 Alignment		93.6	26	PDB header: replication/dna Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: ternary complex of human dna polymerase iota with dna and dttp
8	c3gqcB_	 Alignment		92.3	21	PDB header: transferase/dna Chain: B: PDB Molecule: dna repair protein rev1; PDBTitle: structure of human rev1-dna-dntp ternary complex
9	c2oh2B_	 Alignment		92.1	17	PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase kappa; PDBTitle: ternary complex of human dna polymerase
10	c1k1qA_	 Alignment		91.7	16	PDB header: transcription Chain: A: PDB Molecule: dbh protein; PDBTitle: crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
11	d2ilqa1	 Alignment		91.5	24	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain

12	d1t94a2	Alignment		91.4	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
13	c2aq4A_	Alignment		91.4	23	PDB header: transferase Chain: A: PDB Molecule: dna repair protein rev1; PDBTitle: ternary complex of the catalytic core of rev1 with dna and dctp.
14	d1zeta2	Alignment		91.0	26	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
15	d1jx4a2	Alignment		91.0	13	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
16	c1s97D_	Alignment		90.8	13	PDB header: transferase/dna Chain: D: PDB Molecule: dna polymerase iv; PDBTitle: dpo4 with gt mismatch
17	d1gm5a2	Alignment		90.5	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain
18	c1t94B_	Alignment		90.4	17	PDB header: replication Chain: B: PDB Molecule: polymerase (dna directed) kappa; PDBTitle: crystal structure of the catalytic core of human dna2 polymerase kappa
19	d1k1sa2	Alignment		90.3	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
20	c1wcnA_	Alignment		89.9	18	PDB header: rna-binding protein Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: nmr structure of the carboxyterminal domains of escherichia2 coli nusa
21	c8icZA_	Alignment	not modelled	88.9	15	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase beta (e.c.2.7.7.7)); PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 dna base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
22	c3mr2A_	Alignment	not modelled	87.9	11	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)
23	d1lb2b_	Alignment	not modelled	87.7	16	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
24	d1z3eb1	Alignment	not modelled	86.4	22	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
25	c2bcuA_	Alignment	not modelled	86.4	7	PDB header: transferase, lyase/dna Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
26	c2w9mB_	Alignment	not modelled	86.3	15	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
27	d1doqa_	Alignment	not modelled	86.3	41	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
						PDB header: transferase/dna Chain: A: PDB Molecule: terminal deoxynucleotidyltransferase

28	c1kdhA	Alignment	not modelled	85.5	5	short PDBTitle: binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
29	dlim4a	Alignment	not modelled	85.2	28	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
30	c1nomA	Alignment	not modelled	84.4	25	PDB header: nucleotidyltransferase Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mncl2 (5 millimolar)
31	dlcooa	Alignment	not modelled	83.6	16	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
32	dlszpa1	Alignment	not modelled	83.5	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
33	d2p6ra2	Alignment	not modelled	83.3	14	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain
34	c2ihmA	Alignment	not modelled	82.6	11	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide
35	c1gm5A	Alignment	not modelled	80.6	18	PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
36	c1t4ga	Alignment	not modelled	78.1	24	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: atpase in complex with amp-pnp
37	d1lmb3	Alignment	not modelled	75.0	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
38	c2va8A	Alignment	not modelled	74.2	19	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
39	c1jihA	Alignment	not modelled	74.0	21	PDB header: translation Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: yeast dna polymerase eta
40	dlszpb1	Alignment	not modelled	73.5	18	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
41	d2q0zx1	Alignment	not modelled	72.2	18	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Sec63 N-terminal domain
42	c2r8kB	Alignment	not modelled	68.3	21	PDB header: replication, transferase/dna Chain: B: PDB Molecule: dna polymerase eta; PDBTitle: structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna
43	d1jmsa3	Alignment	not modelled	67.6	4	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
44	d1b22a	Alignment	not modelled	66.0	21	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
45	c1b22A	Alignment	not modelled	66.0	21	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
46	d2bcqa2	Alignment	not modelled	59.5	8	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
47	c3h9xB	Alignment	not modelled	58.5	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein pspto_3016; PDBTitle: crystal structure of the pspto_3016 protein from2 pseudomonas syringae, northeast structural genomics3 consortium target psr293
48	d2fmpa2	Alignment	not modelled	58.3	19	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
49	c2p6uA	Alignment	not modelled	56.6	14	PDB header: dna binding protein Chain: A: PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
50	d2vana1	Alignment	not modelled	53.3	23	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
51	c2df1A	Alignment	not modelled	51.3	24	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament
52	c3iwcD	Alignment	not modelled	46.4	18	PDB header: lyase Chain: D: PDB Molecule: s-adenosylmethionine decarboxylase; PDBTitle: t. maritima adometdc complex with s-adenosylmethionine2 methyl ester
53	d1jiha2	Alignment	not modelled	45.5	21	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
54	c2kz3A	Alignment	not modelled	40.5	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein rad51l3; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83

55	c3im2A	 Alignment	not modelled	39.9	7	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: structure of the c-terminal sec63 unit of yeast brr2, p41212 form
56	d1ci4a	 Alignment	not modelled	37.5	19	Fold: SAM domain-like Superfamily: Barrier-to-autointegration factor, BAF Family: Barrier-to-autointegration factor, BAF
57	d1kfta	 Alignment	not modelled	32.8	12	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
58	c1kfta	 Alignment	not modelled	32.8	12	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc subunit c; PDBTitle: solution nmr structure of the c-terminal domain of uvrC from e-2 coli
59	c1zg2A	 Alignment	not modelled	26.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0213 protein bh0048; PDBTitle: solution nmr structure of the upf0213 protein bh0048 from2 bacillus halodurans. northeast structural genomics target3 bhr2.
60	c3f42A	 Alignment	not modelled	25.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hp0035; PDBTitle: crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
61	d1iufa1	 Alignment	not modelled	24.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
62	d1wfla	 Alignment	not modelled	20.9	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
63	c2iiiA	 Alignment	not modelled	19.4	18	PDB header: lyase Chain: A: PDB Molecule: s-adenosylmethionine decarboxylase proenzyme; PDBTitle: crystal structure of the adenosylmethionine decarboxylase (aq_254)2 from aquifex aeolicus vf5
64	d3bzka1	 Alignment	not modelled	18.4	14	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
65	d2axtu1	 Alignment	not modelled	17.6	6	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
66	c1s5lu	 Alignment	not modelled	17.6	9	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
67	d1pugb	 Alignment	not modelled	17.2	17	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
68	c1vr7A	 Alignment	not modelled	16.3	18	PDB header: lyase Chain: A: PDB Molecule: s-adenosylmethionine decarboxylase proenzyme; PDBTitle: crystal structure of s-adenosylmethionine decarboxylase proenzyme2 (tm0655) from thermotoga maritima at 1.2 a resolution
69	d1dgsa1	 Alignment	not modelled	16.0	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
70	d1vr7a1	 Alignment	not modelled	15.9	18	Fold: S-adenosylmethionine decarboxylase Superfamily: S-adenosylmethionine decarboxylase Family: Bacterial S-adenosylmethionine decarboxylase
71	d1nzpa	 Alignment	not modelled	15.7	8	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
72	c1ixrA	 Alignment	not modelled	15.6	14	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
73	c2qguA	 Alignment	not modelled	14.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable signal peptide protein; PDBTitle: three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
74	c1vddC	 Alignment	not modelled	14.6	25	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
75	c2kp7A	 Alignment	not modelled	14.5	29	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
76	d1wyua1	 Alignment	not modelled	14.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
77	d2edua1	 Alignment	not modelled	13.8	8	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
78	d1us7b	 Alignment	not modelled	13.7	7	Fold: Hsp90 co-chaperone CDC37 Superfamily: Hsp90 co-chaperone CDC37 Family: Hsp90 co-chaperone CDC37
79	c1us7B	 Alignment	not modelled	13.7	7	PDB header: chaperone Chain: B: PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: complex of hsp90 and p50
80	d1j3xa	 Alignment	not modelled	13.3	8	Fold: HMG-box Superfamily: HMG-box Family: HMG-box

81	c1j3xA_	Alignment	not modelled	13.3	8	PDB header: dna binding protein Chain: A: PDB Molecule: high mobility group protein 2; PDBTitle: solution structure of the n-terminal domain of the hmgb2
82	c2csdB_	Alignment	not modelled	13.1	14	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
83	d1vdda_	Alignment	not modelled	13.1	25	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
84	d2bcqa1	Alignment	not modelled	12.9	8	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
85	c2hldH_	Alignment	not modelled	12.3	8	PDB header: hydrolase Chain: H: PDB Molecule: atp synthase delta chain, mitochondrial; PDBTitle: crystal structure of yeast mitochondrial f1-atpase
86	d1hlwa_	Alignment	not modelled	11.9	11	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
87	d1k44a_	Alignment	not modelled	11.8	21	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
88	c3bs7A_	Alignment	not modelled	11.8	11	PDB header: signaling protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
89	d1ep3a_	Alignment	not modelled	11.3	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
90	d1l1la_	Alignment	not modelled	11.3	18	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
91	d2a1jb1	Alignment	not modelled	10.9	16	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
92	d1iyka2	Alignment	not modelled	10.7	20	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-myristoyl transferase, NMT
93	c1xbsA_	Alignment	not modelled	10.3	13	PDB header: transcription, cell cycle Chain: A: PDB Molecule: dim1-like protein; PDBTitle: crystal structure of human dim2: a dim1-like protein
94	c1fi4A_	Alignment	not modelled	10.0	43	PDB header: lyase Chain: A: PDB Molecule: mevalonate 5-diphosphate decarboxylase; PDBTitle: the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
95	c2w0gA_	Alignment	not modelled	9.7	7	PDB header: chaperone Chain: A: PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: hsp90 co-chaperone cdc37
96	d1jmsa1	Alignment	not modelled	9.6	10	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
97	d1ej5a_	Alignment	not modelled	9.5	23	Fold: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain Superfamily: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain Family: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
98	c2q0zX_	Alignment	not modelled	9.3	18	PDB header: protein transport Chain: X: PDB Molecule: protein pro2281; PDBTitle: crystal structure of q9p172/sec63 from homo sapiens.2 northeast structural genomics target hr1979.
99	c3r9lA_	Alignment	not modelled	9.0	19	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: crystal structure of nucleoside diphosphate kinase from giardia lamblia featuring a disordered dinucleotide binding site