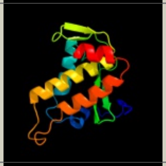
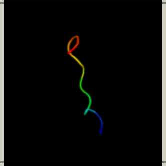
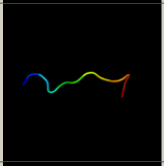
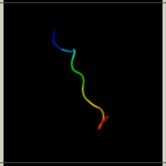
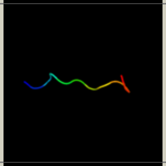
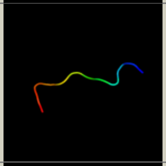
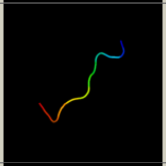
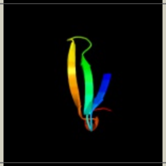
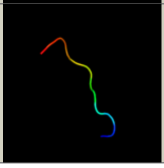
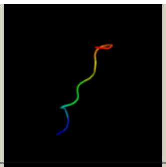
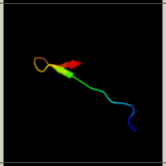
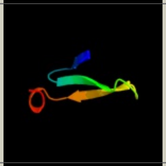
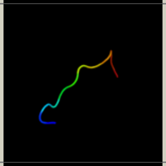
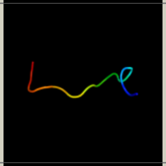
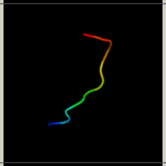
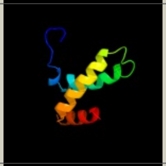
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q9S4W7
Date	Thu Jan 5 12:38:18 GMT 2012
Unique Job ID	cc4d5db6d054106c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kmgA_	Alignment		100.0	38	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**klca; **PDBTitle:** the structure of the klca and ardb proteins show a novel2 fold and antirestriction activity against type i dna3 restriction systems in vivo but not in vitro
2	c2wj9A_	Alignment		100.0	25	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**intergenic-region protein; **PDBTitle:** ardb
3	d2v6ai1	Alignment		48.9	33	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
4	d1gk8i_	Alignment		44.3	33	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
5	d8ruci_	Alignment		38.7	42	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
6	d1uzdc1	Alignment		36.8	42	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
7	d1wdds_	Alignment		36.8	42	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
8	d1ej7s_	Alignment		35.3	42	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
9	d1ueba2	Alignment		33.5	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
10	d1b4ua_	Alignment		32.5	12	**Fold:**LigA subunit of an aromatic-ring-opening dioxygenase LigAB **Superfamily:**LigA subunit of an aromatic-ring-opening dioxygenase LigAB **Family:**LigA subunit of an aromatic-ring-opening dioxygenase LigAB
11	d1uzhc1	Alignment		27.8	25	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit

12	d1ir1s_	Alignment		26.7	42	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
13	d2tssa2	Alignment		24.5	41	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Superantigen toxins, C-terminal domain **Family:**Superantigen toxins, C-terminal domain
14	c1uebB_	Alignment		23.8	18	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**elongation factor p; **PDBTitle:** crystal structure of translation elongation factor p from2 thermus thermophilus hb8
15	d1rbli_	Alignment		19.9	25	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
16	d1svdm1	Alignment		19.1	21	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
17	d1bxni_	Alignment		18.7	25	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
18	d1bwvs_	Alignment		18.1	25	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
19	d1n1ba1	Alignment		15.3	19	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpenoid cyclase N-terminal domain
20	d1m15a1	Alignment		14.7	36	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
21	c3treA_	Alignment	not modelled	13.7	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of a translation elongation factor p (efp) from coxiella2 burnetii
22	c1ybyB_	Alignment	not modelled	12.8	25	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation elongation factor p; **PDBTitle:** conserved hypothetical protein cth-95 from clostridium2 thermocellum
23	c1bkbA_	Alignment	not modelled	12.4	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 5a; **PDBTitle:** initiation factor 5a from archebacterium pyrobaculum2 aerophilum
24	d1qh4a1	Alignment	not modelled	12.1	21	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
25	d1vrpa1	Alignment	not modelled	11.6	21	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
26	d1u6ra1	Alignment	not modelled	11.4	29	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
27	d1i0ea1	Alignment	not modelled	10.8	21	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
28	d1crka1	Alignment	not modelled	10.7	7	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
						Fold: Guanido kinase N-terminal domain

29	d1g0wa1	Alignment	not modelled	10.2	21	**Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
30	c1n20A_	Alignment	not modelled	10.2	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**(+)-bornyl diphosphate synthase; **PDBTitle:** (+)-bornyl diphosphate synthase: complex with mg and 3-aza-2 2,3-dihydrogeranyl diphosphate
31	d1qk1a1	Alignment	not modelled	10.0	21	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
32	d1f3ud_	Alignment	not modelled	9.9	27	**Fold:**triple barrel **Superfamily:**Rap30/74 interaction domains **Family:**Rap30/74 interaction domains
33	c3lo4B_	Alignment	not modelled	9.6	56	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (r24a mutant)
34	c3lo4A_	Alignment	not modelled	9.6	56	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (r24a mutant)
35	d1enfa2	Alignment	not modelled	8.4	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Superantigen toxins, C-terminal domain **Family:**Superantigen toxins, C-terminal domain
36	d1elpa2	Alignment	not modelled	8.2	16	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
37	d1a7ha_	Alignment	not modelled	8.0	21	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
38	d3buxb3	Alignment	not modelled	7.9	50	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
39	c1xxgA_	Alignment	not modelled	7.8	12	**PDB header:**immune system **Chain:** A: **PDB Molecule:**enterotoxin; **PDBTitle:** crystal structure of staphylococcal enterotoxin g
40	c1ck1A_	Alignment	not modelled	6.6	24	**PDB header:**toxin **Chain:** A: **PDB Molecule:**protein (enterotoxin type c-3); **PDBTitle:** structure of staphylococcal enterotoxin c3
41	c3ms6A_	Alignment	not modelled	6.0	36	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hepatitis b virus x-interacting protein; **PDBTitle:** crystal structure of hepatitis b x-interacting protein (hbxip)
42	c3qx3B_	Alignment	not modelled	5.8	15	**PDB header:**isomerase/dna/isomerase inhibitor **Chain:** B: **PDB Molecule:**dna topoisomerase 2-beta; **PDBTitle:** human topoisomerase iibeta in complex with dna and etoposide
43	d1zira2	Alignment	not modelled	5.7	13	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
44	d2z8la2	Alignment	not modelled	5.6	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Superantigen toxins, C-terminal domain **Family:**Superantigen toxins, C-terminal domain
45	d1ha4a_	Alignment	not modelled	5.5	21	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
46	c3bunB_	Alignment	not modelled	5.3	45	**PDB header:**ligase/signaling protein **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase cbl; **PDBTitle:** crystal structure of c-cbl-tkb domain complexed with its2 binding motif in sprouty4
47	c2cblA_	Alignment	not modelled	5.3	45	**PDB header:**complex (proto-oncogene/peptide) **Chain:** A: **PDB Molecule:**proto-oncogene cbl; **PDBTitle:** n-terminal domain of cbl in complex with its binding site2 on zap-70
48	c1d6eC_	Alignment	not modelled	5.2	19	**PDB header:**immune system/peptide inhibitor **Chain:** C: **PDB Molecule:**enterotoxin type b; **PDBTitle:** crystal structure of hla-dr4 complex with peptidomimetic and seb