




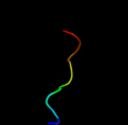

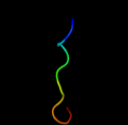

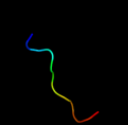



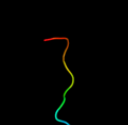

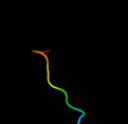

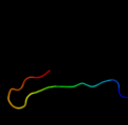

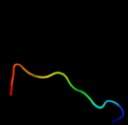


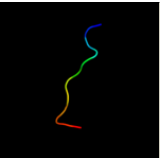
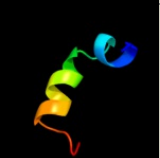
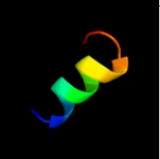

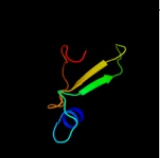
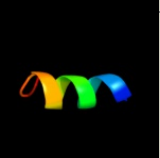
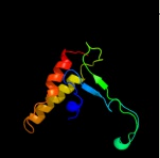

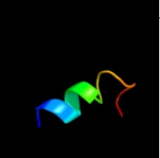


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P52139
Date	Thu Jan 5 12:05:44 GMT 2012
Unique Job ID	3f98229b86d44963

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2kmgA_</a>	 Alignment		100.0	38	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> klca; <b>PDBTitle:</b> the structure of the klca and ardb proteins show a novel 2 fold and antirestriction activity against type i dna3 restriction systems in vivo but not in vitro
2	<a href="#">c2wj9A_</a>	 Alignment		100.0	73	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> intergenic-region protein; <b>PDBTitle:</b> ardb
3	<a href="#">d2v6ai1</a>	 Alignment		42.9	25	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
4	<a href="#">d1gk8i_</a>	 Alignment		38.2	25	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
5	<a href="#">d8ruc1_</a>	 Alignment		33.0	33	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
6	<a href="#">d1wdds_</a>	 Alignment		31.7	33	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
7	<a href="#">d1uzdc1</a>	 Alignment		31.4	33	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
8	<a href="#">d1ej7s_</a>	 Alignment		30.1	33	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
9	<a href="#">d2tssa2</a>	 Alignment		25.3	29	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Superantigen toxins, C-terminal domain <b>Family:</b> Superantigen toxins, C-terminal domain
10	<a href="#">d1uzhc1</a>	 Alignment		23.9	17	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
11	<a href="#">d1x3zb1</a>	 Alignment		23.4	25	<b>Fold:</b> XPC-binding domain <b>Superfamily:</b> XPC-binding domain <b>Family:</b> XPC-binding domain

12	<a href="#">dlir1s_</a>	Alignment		23.2	33	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
13	<a href="#">c2qsgX_</a>	Alignment		23.0	25	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> X: <b>PDB Molecule:</b> uv excision repair protein rad23; <b>PDBTitle:</b> crystal structure of rad4-rad23 bound to a uv-damaged dna
14	<a href="#">dlm15a1</a>	Alignment		22.1	36	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
15	<a href="#">dlqh4a1</a>	Alignment		19.5	21	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
16	<a href="#">c2otnB_</a>	Alignment		18.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelate epimerase; <b>PDBTitle:</b> crystal structure of the catalytically active form of diaminopimelate2 epimerase from bacillus anthracis
17	<a href="#">dlvrpa1</a>	Alignment		18.6	21	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
18	<a href="#">dlks8a_</a>	Alignment		18.6	7	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
19	<a href="#">dlu6ra1</a>	Alignment		18.4	21	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
20	<a href="#">dli0ea1</a>	Alignment		17.6	21	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
21	<a href="#">dlcrka1</a>	Alignment	not modelled	17.6	14	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
22	<a href="#">dlg0wa1</a>	Alignment	not modelled	17.5	21	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
23	<a href="#">dlrbli_</a>	Alignment	not modelled	17.4	17	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
24	<a href="#">dlqk1a1</a>	Alignment	not modelled	17.0	21	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
25	<a href="#">dlsvdm1</a>	Alignment	not modelled	16.3	14	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
26	<a href="#">dlbxni_</a>	Alignment	not modelled	16.2	17	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
27	<a href="#">dlbwvs_</a>	Alignment	not modelled	15.9	17	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
28	<a href="#">dla7ha_</a>	Alignment	not modelled	13.3	19	<b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Crystallins/Ca-binding development proteins
29	<a href="#">c3lo4B_</a>	Alignment	not modelled	13.1	44	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (r24a

					mutant)
30	<a href="#">c3lo4A_</a>	Alignment	not modelled	13.1	44 <b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (r24a mutant)
31	<a href="#">c3cinA_</a>	Alignment	not modelled	12.2	23 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> myo-inositol-1-phosphate synthase-related protein; <b>PDBTitle:</b> crystal structure of a myo-inositol-1-phosphate synthase-related2 protein (tm_1419) from thermotoga maritima msb8 at 1.70 a resolution
32	<a href="#">d1elpa2</a>	Alignment	not modelled	11.5	22 <b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Crystallins/Ca-binding development proteins
33	<a href="#">c3aq3A_</a>	Alignment	not modelled	11.4	39 <b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> 6b protein; <b>PDBTitle:</b> molecular insights into plant cell proliferation disturbance by2 agrobacterium protein 6b
34	<a href="#">d1zira2</a>	Alignment	not modelled	10.7	19 <b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Crystallins/Ca-binding development proteins
35	<a href="#">d1enfa2</a>	Alignment	not modelled	10.2	18 <b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Superantigen toxins, C-terminal domain <b>Family:</b> Superantigen toxins, C-terminal domain
36	<a href="#">d1kfia3</a>	Alignment	not modelled	9.8	18 <b>Fold:</b> Phosphoglucumutase, first 3 domains <b>Superfamily:</b> Phosphoglucumutase, first 3 domains <b>Family:</b> Phosphoglucumutase, first 3 domains
37	<a href="#">d1ia9a_</a>	Alignment	not modelled	9.5	18 <b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> MHCK/EF2 kinase
38	<a href="#">d1bi5a2</a>	Alignment	not modelled	9.5	15 <b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
39	<a href="#">d1amma2</a>	Alignment	not modelled	9.4	16 <b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Crystallins/Ca-binding development proteins
40	<a href="#">c1xxgA_</a>	Alignment	not modelled	9.1	29 <b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> enterotoxin; <b>PDBTitle:</b> crystal structure of staphylococcal enterotoxin g
41	<a href="#">d1y0ua_</a>	Alignment	not modelled	8.1	28 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
42	<a href="#">c1ck1A_</a>	Alignment	not modelled	8.1	41 <b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> protein (enterotoxin type c-3); <b>PDBTitle:</b> structure of staphylococcal enterotoxin c3
43	<a href="#">c2xjgA_</a>	Alignment	not modelled	7.6	16 <b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> flocculation protein flo5; <b>PDBTitle:</b> x-ray structure of the n-terminal domain of the flocculin2 flo5 from saccharomyces cerevisiae
44	<a href="#">d2hg7a1</a>	Alignment	not modelled	7.5	30 <b>Fold:</b> gpW/XkdW-like <b>Superfamily:</b> XkdW-like <b>Family:</b> XkdW-like
45	<a href="#">c2hg7A_</a>	Alignment	not modelled	7.5	30 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phage-like element pbsx protein xkdw; <b>PDBTitle:</b> solution nmr structure of phage-like element pbsx protein2 xkdw, northeast structural genomics consortium target sr355
46	<a href="#">c1d6eC_</a>	Alignment	not modelled	7.4	31 <b>PDB header:</b> immune system/peptide inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> enterotoxin type b; <b>PDBTitle:</b> crystal structure of hla-dr4 complex with peptidomimetic and seb
47	<a href="#">d1uaya_</a>	Alignment	not modelled	7.4	19 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
48	<a href="#">d3pmga3</a>	Alignment	not modelled	7.3	21 <b>Fold:</b> Phosphoglucumutase, first 3 domains <b>Superfamily:</b> Phosphoglucumutase, first 3 domains <b>Family:</b> Phosphoglucumutase, first 3 domains
49	<a href="#">d1j83a_</a>	Alignment	not modelled	7.2	19 <b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Family 17 carbohydrate binding module, CBM17
50	<a href="#">d1okia2</a>	Alignment	not modelled	6.8	13 <b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Crystallins/Ca-binding development proteins
51	<a href="#">d1ytqa2</a>	Alignment	not modelled	6.5	8 <b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Crystallins/Ca-binding development proteins
52	<a href="#">d1ueba2</a>	Alignment	not modelled	6.2	7 <b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
53	<a href="#">c2k1wA_</a>	Alignment	not modelled	6.1	23 <b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta/gama crystallin family protein; <b>PDBTitle:</b> nmr solution structure of m-crystallin in calcium loaded2 form(holo).
54	<a href="#">c2j4xA_</a>	Alignment	not modelled	6.1	12 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitogen; <b>PDBTitle:</b> streptococcus dysgalactiae-derived mitogen (sdm)
55	<a href="#">d1h4ax1</a>	Alignment	not modelled	6.1	13 <b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Crystallins/Ca-binding development proteins

56	<a href="#">d2z8la2</a>	Alignment	not modelled	6.1	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Superantigen toxins, C-terminal domain <b>Family:</b> Superantigen toxins, C-terminal domain
57	<a href="#">c1et9A_</a>	Alignment	not modelled	6.1	24	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> superantigen spe-h; <b>PDBTitle:</b> crystal structure of the superantigen spe-h from2 streptococcus pyogenes
58	<a href="#">d1amma1</a>	Alignment	not modelled	6.0	13	<b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Crystallins/Ca-binding development proteins
59	<a href="#">c1bxtA_</a>	Alignment	not modelled	5.8	35	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> protein (streptococcal superantigen); <b>PDBTitle:</b> streptococcal superantigen (ssa) from streptococcus pyogenes
60	<a href="#">d1x4ka2</a>	Alignment	not modelled	5.7	50	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
61	<a href="#">c1js4B_</a>	Alignment	not modelled	5.5	8	<b>PDB header:</b> glycosyl hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo/exocellulase e4; <b>PDBTitle:</b> endo/exocellulase:cellobiose from thermomonospora
62	<a href="#">d3buxb3</a>	Alignment	not modelled	5.2	38	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain