







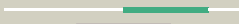




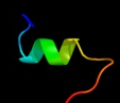








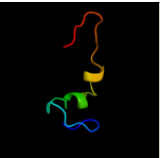
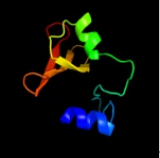
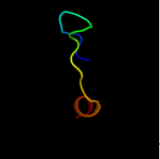
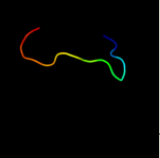
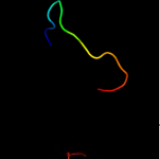
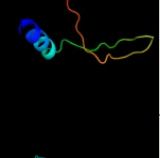
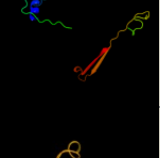
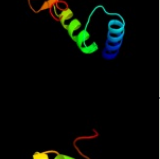
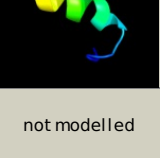


# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P46856
Date	Thu Jan 5 12:04:28 GMT 2012
Unique Job ID	2b263dbb77c05392

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2paga1</a>	 Alignment		66.1	19	<b>Fold:</b> SMI1/KNR4-like <b>Superfamily:</b> SMI1/KNR4-like <b>Family:</b> SMI1/KNR4-like
2	<a href="#">dlyfna1</a>	 Alignment		60.1	19	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
3	<a href="#">dlou9a_</a>	 Alignment		55.2	20	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
4	<a href="#">dlzszc1</a>	 Alignment		45.4	20	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
5	<a href="#">dlou8a_</a>	 Alignment		42.3	19	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
6	<a href="#">c1ponB_</a>	 Alignment		23.7	33	<b>PDB header:</b> calcium-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> troponin c; <b>PDBTitle:</b> site iii-site iv troponin c heterodimer, nmr
7	<a href="#">dle7la1</a>	 Alignment		20.7	28	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> Recombination endonuclease VII, C-terminal and dimerization domains <b>Family:</b> Recombination endonuclease VII, C-terminal and dimerization domains
8	<a href="#">d2f05a1</a>	 Alignment		19.4	19	<b>Fold:</b> PAH2 domain <b>Superfamily:</b> PAH2 domain <b>Family:</b> PAH2 domain
9	<a href="#">d2icga1</a>	 Alignment		13.7	21	<b>Fold:</b> SMI1/KNR4-like <b>Superfamily:</b> SMI1/KNR4-like <b>Family:</b> SMI1/KNR4-like
10	<a href="#">dljvra_</a>	 Alignment		11.9	29	<b>Fold:</b> Retroviral matrix proteins <b>Superfamily:</b> Retroviral matrix proteins <b>Family:</b> HTLV-II matrix protein
11	<a href="#">c2hw2A_</a>	 Alignment		11.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rifampin adp-ribosyl transferase; <b>PDBTitle:</b> crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin

12	<a href="#">c1zd1B_</a>	Alignment		11.8	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfotransferase 4a1; <b>PDBTitle:</b> human sulfortransferase sult4a1
13	<a href="#">d2prva1</a>	Alignment		10.0	11	<b>Fold:</b> SMI1/KNR4-like <b>Superfamily:</b> SMI1/KNR4-like <b>Family:</b> SMI1/KNR4-like
14	<a href="#">c2a8vA_</a>	Alignment		9.3	19	<b>PDB header:</b> protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> rna binding domain of rho transcription <b>PDBTitle:</b> rho transcription termination factor/rna complex
15	<a href="#">d2i5ha1</a>	Alignment		9.3	27	<b>Fold:</b> AF1531-like <b>Superfamily:</b> AF1531-like <b>Family:</b> AF1531-like
16	<a href="#">c2i5hA_</a>	Alignment		9.3	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein af1531; <b>PDBTitle:</b> crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
17	<a href="#">c3lfaA_</a>	Alignment		9.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein fto; <b>PDBTitle:</b> crystal structure of the fat mass and obesity associated (fto) protein2 reveals basis for its substrate specificity
18	<a href="#">c1w63P_</a>	Alignment		8.9	22	<b>PDB header:</b> endocytosis <b>Chain:</b> P: <b>PDB Molecule:</b> adaptor-related protein complex 1, mu 1 subunit; <b>PDBTitle:</b> ap1 clathrin adaptor core
19	<a href="#">c2r1fB_</a>	Alignment		8.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> predicted aminodeoxychorismate lyase; <b>PDBTitle:</b> crystal structure of predicted aminodeoxychorismate lyase from2 escherichia coli
20	<a href="#">d1vaza_</a>	Alignment		8.2	23	<b>Fold:</b> NSFL1 (p97 ATPase) cofactor p47, SEP domain <b>Superfamily:</b> NSFL1 (p97 ATPase) cofactor p47, SEP domain <b>Family:</b> NSFL1 (p97 ATPase) cofactor p47, SEP domain
21	<a href="#">d1vpza_</a>	Alignment	not modelled	8.1	24	<b>Fold:</b> CsrA-like <b>Superfamily:</b> CsrA-like <b>Family:</b> CsrA-like
22	<a href="#">c1qmoG_</a>	Alignment	not modelled	7.8	30	<b>PDB header:</b> lectin <b>Chain:</b> G: <b>PDB Molecule:</b> mannose binding lectin, fril; <b>PDBTitle:</b> structure of fril, a legume lectin that delays2 hematopoietic progenitor maturation
23	<a href="#">d1a62a2</a>	Alignment	not modelled	7.8	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
24	<a href="#">d1tdja2</a>	Alignment	not modelled	7.7	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Allosteric threonine deaminase C-terminal domain
25	<a href="#">c3csqC_</a>	Alignment	not modelled	7.5	31	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> morphogenesis protein 1; <b>PDBTitle:</b> crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
26	<a href="#">d1a9xa3</a>	Alignment	not modelled	7.4	22	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
27	<a href="#">d1kshb_</a>	Alignment	not modelled	7.3	31	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> RhoGDI-like
28	<a href="#">d2f2ab1</a>	Alignment	not modelled	7.1	11	<b>Fold:</b> GatB/YqeY motif <b>Superfamily:</b> GatB/YqeY motif <b>Family:</b> GatB/GatE C-terminal domain-like
29	<a href="#">d1qtma1</a>	Alignment	not modelled	6.9	47	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like

					<b>Family:</b> DnaQ-like 3'-5' exonuclease
30	<a href="#">dlss6a_</a>	Alignment	not modelled	6.6	23 <b>Fold:</b> NSFL1 (p97 ATPase) cofactor p47, SEP domain <b>Superfamily:</b> NSFL1 (p97 ATPase) cofactor p47, SEP domain <b>Family:</b> NSFL1 (p97 ATPase) cofactor p47, SEP domain
31	<a href="#">c2f4qA_</a>	Alignment	not modelled	6.5	23 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> type i topoisomerase, putative; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans topoisomerase ib
32	<a href="#">c3fbyC_</a>	Alignment	not modelled	6.3	26 <b>PDB header:</b> cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> cartilage oligomeric matrix protein; <b>PDBTitle:</b> the crystal structure of the signature domain of cartilage oligomeric2 matrix protein.
33	<a href="#">dl066a_</a>	Alignment	not modelled	6.3	14 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
34	<a href="#">c1vpzB_</a>	Alignment	not modelled	6.1	24 <b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> carbon storage regulator homolog; <b>PDBTitle:</b> crystal structure of a putative carbon storage regulator protein2 (csra, pa0905) from pseudomonas aeruginosa at 2.05 a resolution
35	<a href="#">c1c8m2_</a>	Alignment	not modelled	6.1	25 <b>PDB header:</b> virus <b>Chain:</b> 2: <b>PDB Molecule:</b> human rhinovirus 16 coat protein; <b>PDB Fragment:</b> residues 2-78; <b>PDBTitle:</b> refined crystal structure of human rhinovirus 16 complexed2 with vp63843 (pleconaril), an anti-picornaviral drug3 currently in clinical trials
36	<a href="#">dl1elka_</a>	Alignment	not modelled	6.0	16 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ENTH/VHS domain <b>Family:</b> VHS domain
37	<a href="#">c2b1uA_</a>	Alignment	not modelled	5.9	10 <b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calmodulin-like protein 5; <b>PDBTitle:</b> solution structure of calmodulin-like skin protein c2 terminal domain
38	<a href="#">dl1d8ua_</a>	Alignment	not modelled	5.6	6 <b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
39	<a href="#">c2jppB_</a>	Alignment	not modelled	5.4	32 <b>PDB header:</b> translation/rna <b>Chain:</b> B: <b>PDB Molecule:</b> translational repressor; <b>PDBTitle:</b> structural basis of rsma/csra rna recognition: structure of2 rsme bound to the shine-dalgarno sequence of hcna mrna
40	<a href="#">dl1hdsa_</a>	Alignment	not modelled	5.2	13 <b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
41	<a href="#">c2amiA_</a>	Alignment	not modelled	5.2	13 <b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> caltractin; <b>PDBTitle:</b> solution structure of the calcium-loaded n-terminal sensor2 domain of centrin
42	<a href="#">dl1zgha1</a>	Alignment	not modelled	5.1	22 <b>Fold:</b> FMT C-terminal domain-like <b>Superfamily:</b> FMT C-terminal domain-like <b>Family:</b> Post formyltransferase domain