

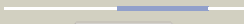

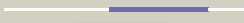







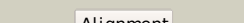





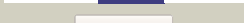

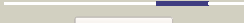



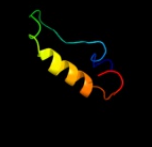


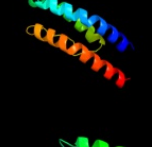
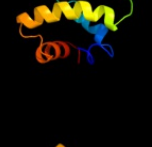
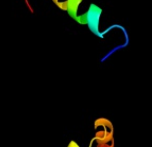
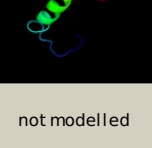


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P21515
Date	Thu Jan 5 11:38:26 GMT 2012
Unique Job ID	0a724e62aee86cb7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1riqa1</a>	 Alignment		27.5	13	<b>Fold:</b> Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) <b>Superfamily:</b> Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) <b>Family:</b> Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
2	<a href="#">dls5qb_</a>	 Alignment		23.8	13	<b>Fold:</b> PAH2 domain <b>Superfamily:</b> PAH2 domain <b>Family:</b> PAH2 domain
3	<a href="#">d1x1na1</a>	 Alignment		16.1	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
4	<a href="#">d1r7ma1</a>	 Alignment		13.5	30	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Homing endonucleases <b>Family:</b> Group I mobile intron endonuclease
5	<a href="#">d1icha_</a>	 Alignment		12.6	12	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> DEATH domain, DD
6	<a href="#">c1ichA_</a>	 Alignment		12.6	12	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor-1; <b>PDBTitle:</b> solution structure of the tumor necrosis factor receptor-12 death domain
7	<a href="#">d1puza_</a>	 Alignment		10.7	17	<b>Fold:</b> YgfY-like <b>Superfamily:</b> YgfY-like <b>Family:</b> YgfY-like
8	<a href="#">c1yfsB_</a>	 Alignment		10.6	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> alanyl-tRNA synthetase; <b>PDBTitle:</b> the crystal structure of alanyl-tRNA synthetase in complex2 with L-alanine
9	<a href="#">d1vhba_</a>	 Alignment		8.9	10	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
10	<a href="#">c2jr5A_</a>	 Alignment		8.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0350 protein vc_2471; <b>PDBTitle:</b> solution structure of upf0350 protein vc_2471. northeast2 structural genomics target vcr36
11	<a href="#">c3hxxA_</a>	 Alignment		8.2	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alanyl-tRNA synthetase; <b>PDBTitle:</b> crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp

12	<a href="#">c1x6iB_</a>	Alignment		7.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ygfy; <b>PDBTitle:</b> crystal structure of ygfy from escherichia coli
13	<a href="#">d1yh2a1</a>	Alignment		7.7	15	<b>Fold:</b> UBC-like <b>Superfamily:</b> UBC-like <b>Family:</b> UBC-related
14	<a href="#">d1muka_</a>	Alignment		7.4	28	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase
15	<a href="#">d2f05a1</a>	Alignment		7.2	21	<b>Fold:</b> PAH2 domain <b>Superfamily:</b> PAH2 domain <b>Family:</b> PAH2 domain
16	<a href="#">c1r7mA_</a>	Alignment		6.6	25	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> intron-encoded endonuclease i-scei; <b>PDBTitle:</b> the homing endonuclease i-scei bound to its dna recognition2 region
17	<a href="#">d2a0ba_</a>	Alignment		6.5	8	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Aerobic respiration control sensor protein, ArcB
18	<a href="#">d1fada_</a>	Alignment		6.4	11	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> DEATH domain, DD
19	<a href="#">c2jynA_</a>	Alignment		6.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0368 protein ypl225w; <b>PDBTitle:</b> a novel solution nmr structure of protein yst0336 from2 saccharomyces cerevisiae. northeast structural genomics3 consortium target yt51/ontario centre for structural4 proteomics target yst0336
20	<a href="#">c4a56A_</a>	Alignment		5.9	14	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> pullulanase secretion protein puls; <b>PDBTitle:</b> crystal structure of the type 2 secretion system pilotin2 from klebsiella oxytoca
21	<a href="#">d1rg6a_</a>	Alignment	not modelled	5.6	24	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> SAM (sterile alpha motif) domain
22	<a href="#">c2yqfA_</a>	Alignment	not modelled	5.3	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin-1; <b>PDBTitle:</b> solution structure of the death domain of ankyrin-1
23	<a href="#">c1ztaA_</a>	Alignment	not modelled	5.2	26	<b>PDB header:</b> dna-binding motif <b>Chain:</b> A: <b>PDB Molecule:</b> leucine zipper monomer; <b>PDBTitle:</b> the solution structure of a leucine-zipper motif peptide
24	<a href="#">d2incc1</a>	Alignment	not modelled	5.2	40	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TmoB-like <b>Family:</b> TmoB-like
25	<a href="#">d1svda2</a>	Alignment	not modelled	5.1	42	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RuBisCO, large subunit, small (N-terminal) domain <b>Family:</b> Ribulose 1,5-bisphosphate carboxylase-oxygenase