



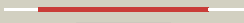
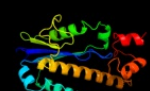


















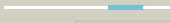
















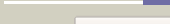

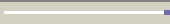






























# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P10442
Date	Thu Jan 5 11:32:18 GMT 2012
Unique Job ID	9e8edf6b7ccedacd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2etja1</a>	 Alignment		100.0	45	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Ribonuclease H
2	<a href="#">c2etjA</a>	 Alignment		100.0	45	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease hii; <b>PDBTitle:</b> crystal structure of ribonuclease hii (ec 3.1.26.4) (rnase hii)2 (tm0915) from thermotoga maritima at 1.74 a resolution
3	<a href="#">c3kioA</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease h2 subunit a; <b>PDBTitle:</b> mouse rnase h2 complex
4	<a href="#">dlio2a</a>	 Alignment		100.0	30	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Ribonuclease H
5	<a href="#">dluaxa</a>	 Alignment		100.0	29	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Ribonuclease H
6	<a href="#">cli3aA</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease hii; <b>PDBTitle:</b> rnase hii from archaeoglobus fulgidus with cobalt hexammine2 chloride
7	<a href="#">dli39a</a>	 Alignment		100.0	30	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Ribonuclease H
8	<a href="#">dlekea</a>	 Alignment		100.0	26	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Ribonuclease H
9	<a href="#">c2d0bA</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease hiii; <b>PDBTitle:</b> crystal structure of bst-rnase hiii in complex with mg2+
10	<a href="#">c3gocB</a>	 Alignment		33.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
11	<a href="#">dlc8ba</a>	 Alignment		32.9	14	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> HybD-like <b>Family:</b> Germination protease

12	<a href="#">c3c6aA_</a>	 Alignment		32.5	33	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> terminase large subunit; <b>PDBTitle:</b> crystal structure of the rb49 gp17 nuclease domain
13	<a href="#">c3ga2A_</a>	 Alignment		32.3	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> crystal structure of the endonuclease_v (bsu36170) from2 bacillus subtilis, northeast structural genomics3 consortium target sr624
14	<a href="#">c2w36B_</a>	 Alignment		29.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
15	<a href="#">c3lhwC_</a>	 Alignment		22.5	60	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m2
16	<a href="#">c3lhwA_</a>	 Alignment		22.5	60	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m2
17	<a href="#">c3lhwB_</a>	 Alignment		22.5	60	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m2
18	<a href="#">c3lhwD_</a>	 Alignment		22.5	60	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> high resolution crystal structure of transmembrane domain of m2
19	<a href="#">c3c9jA_</a>	 Alignment		20.6	54	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> proton channel protein m2, transmembrane segment; <b>PDBTitle:</b> the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
20	<a href="#">c3c9jB_</a>	 Alignment		20.6	54	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> proton channel protein m2, transmembrane segment; <b>PDBTitle:</b> the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
21	<a href="#">d1ttha_</a>	 Alignment	not modelled	18.6	30	<b>Fold:</b> Anti-sigma factor AsiA <b>Superfamily:</b> Anti-sigma factor AsiA <b>Family:</b> Anti-sigma factor AsiA
22	<a href="#">c3c9jC_</a>	 Alignment	not modelled	17.7	54	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> proton channel protein m2, transmembrane segment; <b>PDBTitle:</b> the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
23	<a href="#">c3c9jD_</a>	 Alignment	not modelled	17.7	54	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> proton channel protein m2, transmembrane segment; <b>PDBTitle:</b> the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
24	<a href="#">c2zpaB_</a>	 Alignment	not modelled	15.3	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ypf1; <b>PDBTitle:</b> crystal structure of trna(met) cytidine acetyltransferase
25	<a href="#">c2kqtD_</a>	 Alignment	not modelled	12.4	50	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpe lipid bilayers bound to deuterated3 amantadine
26	<a href="#">c2kqtB_</a>	 Alignment	not modelled	12.4	50	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpe lipid bilayers bound to deuterated3 amantadine
27	<a href="#">c2kqtA_</a>	 Alignment	not modelled	12.4	50	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpe lipid bilayers bound to deuterated3 amantadine

28	<a href="#">c2kqtC</a>	 Alignment	not modelled	12.4	50	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmPC lipid bilayers bound to deuterated3 amantadine
29	<a href="#">d1wfaa</a>	 Alignment	not modelled	12.4	16	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> NifU/IscU domain
30	<a href="#">c1mp6A</a>	 Alignment	not modelled	11.8	50	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein m2; <b>PDBTitle:</b> structure of the transmembrane region of the m2 protein h+2 channel by solid state nmr spectroscopy
31	<a href="#">c1nyjC</a>	 Alignment	not modelled	11.8	50	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> matrix protein m2; <b>PDBTitle:</b> the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
32	<a href="#">c1nyjB</a>	 Alignment	not modelled	11.8	50	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> matrix protein m2; <b>PDBTitle:</b> the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
33	<a href="#">c1nyjA</a>	 Alignment	not modelled	11.8	50	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein m2; <b>PDBTitle:</b> the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
34	<a href="#">c1nyjD</a>	 Alignment	not modelled	11.8	50	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> matrix protein m2; <b>PDBTitle:</b> the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
35	<a href="#">c2z7eB</a>	 Alignment	not modelled	10.1	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> nifu-like protein; <b>PDBTitle:</b> crystal structure of aquifex aeolicus iscu with bound [2Fe-2 Ss] cluster
36	<a href="#">d1jha2</a>	 Alignment	not modelled	9.7	39	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
37	<a href="#">c2qq4A</a>	 Alignment	not modelled	9.5	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-sulfur cluster biosynthesis protein iscu; <b>PDBTitle:</b> crystal structure of iron-sulfur cluster biosynthesis2 protein iscu (tha1736) from thermus thermophilus hb8
38	<a href="#">d1v47a2</a>	 Alignment	not modelled	8.8	28	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
39	<a href="#">d1sddb1</a>	 Alignment	not modelled	8.3	25	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
40	<a href="#">d1sisa</a>	 Alignment	not modelled	8.2	25	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins
41	<a href="#">c2d7cD</a>	 Alignment	not modelled	7.6	31	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> rab11 family-interacting protein 3; <b>PDBTitle:</b> crystal structure of human rab11 in complex with fip3 rab-2 binding domain
42	<a href="#">c3k2gA</a>	 Alignment	not modelled	7.5	22	<b>PDB header:</b> resiniferatoxin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> resiniferatoxin-binding, phosphotriesterase- <b>PDBTitle:</b> crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
43	<a href="#">d1qqga2</a>	 Alignment	not modelled	7.2	50	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Phosphotyrosine-binding domain (PTB)
44	<a href="#">d1chla</a>	 Alignment	not modelled	7.1	33	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins
45	<a href="#">c2ljcA</a>	 Alignment	not modelled	7.0	50	<b>PDB header:</b> transport protein/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> m2 protein, bm2 protein chimera; <b>PDBTitle:</b> structure of the influenza am2-bm2 chimeric channel bound to2 rimantadine
46	<a href="#">c2kadC</a>	 Alignment	not modelled	7.0	50	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> transmembrane peptide of matrix protein 2; <b>PDBTitle:</b> magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
47	<a href="#">c2kadB</a>	 Alignment	not modelled	7.0	50	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> transmembrane peptide of matrix protein 2; <b>PDBTitle:</b> magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
48	<a href="#">c2kadA</a>	 Alignment	not modelled	7.0	50	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane peptide of matrix protein 2; <b>PDBTitle:</b> magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
49	<a href="#">c2kadD</a>	 Alignment	not modelled	7.0	50	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> transmembrane peptide of matrix protein 2; <b>PDBTitle:</b> magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
50	<a href="#">d1xx6a1</a>	 Alignment	not modelled	7.0	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Type II thymidine kinase
51	<a href="#">c2jnhA</a>	 Alignment	not modelled	7.0	54	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase cbl-b; <b>PDBTitle:</b> solution structure of the uba domain from cbl-b
52	<a href="#">d1p5ta</a>	 Alignment	not modelled	6.7	40	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like

						<b>Family:</b> Phosphotyrosine-binding domain (PTB)
53	<a href="#">c2vefB_</a>	Alignment	not modelled	6.5	31	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthase from streptococcus pneumoniae
54	<a href="#">c1jhdA_</a>	Alignment	not modelled	6.4	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate adenyllyltransferase; <b>PDBTitle:</b> crystal structure of bacterial atp sulfurylase from the2 riftia pachyptila symbiont
55	<a href="#">d2arha1</a>	Alignment	not modelled	6.4	40	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> Aq 1966-like
56	<a href="#">d1bm9a_</a>	Alignment	not modelled	6.2	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Replication terminator protein (RTP)
57	<a href="#">c2p2uA_</a>	Alignment	not modelled	5.9	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> host-nuclease inhibitor protein gam, putative; <b>PDBTitle:</b> crystal structure of putative host-nuclease inhibitor2 protein gam from desulfovibrio vulgaris
58	<a href="#">c2d9sA_</a>	Alignment	not modelled	5.7	31	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> cbl e3 ubiquitin protein ligase; <b>PDBTitle:</b> solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
59	<a href="#">d1gota2</a>	Alignment	not modelled	5.5	40	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
60	<a href="#">c2dzaA_</a>	Alignment	not modelled	5.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
61	<a href="#">c2jayA_</a>	Alignment	not modelled	5.3	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proteasome; <b>PDBTitle:</b> proteasome beta subunit prcb from mycobacterium2 tuberculosis
62	<a href="#">c2do6A_</a>	Alignment	not modelled	5.2	54	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase cbl-b; <b>PDBTitle:</b> solution structure of rsgi ruh-065, a uba domain from human2 cdna
63	<a href="#">c1ewrA_</a>	Alignment	not modelled	5.2	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of taq muts