




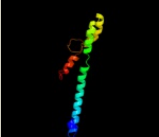

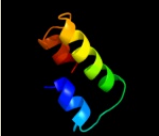





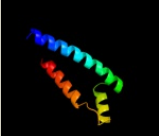





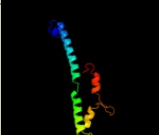


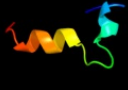




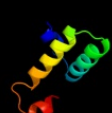





# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8X0
Date	Thu Jan 5 11:08:53 GMT 2012
Unique Job ID	dd335e3edbd2802c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2p0ta1</a>	 Alignment		100.0	41	<b>Fold:</b> PSPTO4464-like <b>Superfamily:</b> PSPTO4464-like <b>Family:</b> PSPTO4464-like
2	<a href="#">c2p0tA</a>	 Alignment		100.0	41	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0307 protein pspto_4464; <b>PDBTitle:</b> structural genomics, the crystal structure of a conserved putative2 protein from pseudomonas syringae pv. tomato str. dc3000
3	<a href="#">c1nafA</a>	 Alignment		60.9	13	<b>PDB header:</b> signaling protein, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylation factor binding protein gga1; <b>PDBTitle:</b> crystal structure of the human gga1 gat domain
4	<a href="#">c2kpgA</a>	 Alignment		50.1	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of agrobacterium tumefaciens protein atu1219:2 northeast structural genomics consortium target att14
5	<a href="#">c2kp6A</a>	 Alignment		42.9	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of protein cv0237 from2 chromobacterium violaceum. northeast structural genomics3 consortium (nesg) target cvt1
6	<a href="#">d1tp6a</a>	 Alignment		40.8	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PA1314-like
7	<a href="#">c3opcB</a>	 Alignment		37.1	18	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of flgn chaperone from bordetella pertussis
8	<a href="#">c3c1dA</a>	 Alignment		26.2	13	<b>PDB header:</b> recombination, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein rexx; <b>PDBTitle:</b> x-ray crystal structure of rexx
9	<a href="#">d1oxza</a>	 Alignment		25.9	13	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> GAT-like domain <b>Family:</b> GAT domain
10	<a href="#">c1oxzA</a>	 Alignment		25.9	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylation factor binding protein gga1; <b>PDBTitle:</b> crystal structure of the human gga1 gat domain
11	<a href="#">c2bcwC</a>	 Alignment		22.2	16	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> coordinates of the n-terminal domain of ribosomal protein2 l11,c-terminal domain of ribosomal protein l7/l12 and a3 portion of the g' domain of elongation factor g, as fitted4 into cryo-em map of an escherichia coli 70s*ef-5 g*gdp*fusidic acid complex

12	<a href="#">d1yt3a2</a>	Alignment		20.2	23	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> RNase D C-terminal domains
13	<a href="#">d2oc6a1</a>	Alignment		18.5	36	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> YdhG-like <b>Family:</b> YdhG-like
14	<a href="#">c2dhyA</a>	Alignment		14.2	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cue domain-containing protein 1; <b>PDBTitle:</b> solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
15	<a href="#">d2i8da1</a>	Alignment		13.2	26	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> YdhG-like <b>Family:</b> YdhG-like
16	<a href="#">d1fs2b1</a>	Alignment		12.9	13	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
17	<a href="#">d1fs1b1</a>	Alignment		12.5	13	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
18	<a href="#">c3k6qB</a>	Alignment		10.5	15	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative ligand binding protein; <b>PDBTitle:</b> crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
19	<a href="#">d1nexa1</a>	Alignment		10.1	11	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
20	<a href="#">d2ovra1</a>	Alignment		9.4	13	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
21	<a href="#">d2izva1</a>	Alignment	not modelled	9.4	12	<b>Fold:</b> SOCS box-like <b>Superfamily:</b> SOCS box-like <b>Family:</b> SOCS box-like
22	<a href="#">c3oq9C</a>	Alignment	not modelled	9.2	9	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> structure of the fas/fadd death domain assembly
23	<a href="#">c2kl4A</a>	Alignment	not modelled	9.1	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2032 protein; <b>PDBTitle:</b> nmr structure of the protein nb7804a
24	<a href="#">d1fkma2</a>	Alignment	not modelled	8.2	17	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> Ypt/Rab-GAP domain of gyp1p <b>Family:</b> Ypt/Rab-GAP domain of gyp1p
25	<a href="#">c3tj3C</a>	Alignment	not modelled	7.9	15	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> nuclear pore complex protein nup50; <b>PDBTitle:</b> structure of importin a5 bound to the n-terminus of nup50
26	<a href="#">d1k91a</a>	Alignment	not modelled	7.7	43	<b>Fold:</b> P-domain of calnexin/calreticulin <b>Superfamily:</b> P-domain of calnexin/calreticulin <b>Family:</b> P-domain of calnexin/calreticulin
27	<a href="#">c2rqpa</a>	Alignment	not modelled	7.2	22	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> heterochromatin protein 1-binding protein 3; <b>PDBTitle:</b> the solution structure of heterochromatin protein 1-binding2 protein 74 histone h1 like domain
28	<a href="#">d2igsal</a>	Alignment	not modelled	6.6	20	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> PA2222-like
						<b>Fold:</b> Ferredoxin-like

29	<a href="#">d1in0a1</a>	Alignment	not modelled	6.6	18	<b>Superfamily:</b> YajQ-like <b>Family:</b> YajQ-like
30	<a href="#">c3dhyC</a>	Alignment	not modelled	6.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
31	<a href="#">d1g8eb</a>	Alignment	not modelled	6.4	11	<b>Fold:</b> Flagellar transcriptional activator FlhD <b>Superfamily:</b> Flagellar transcriptional activator FlhD <b>Family:</b> Flagellar transcriptional activator FlhD
32	<a href="#">d2es9a1</a>	Alignment	not modelled	6.0	45	<b>Fold:</b> YoaC-like <b>Superfamily:</b> YoaC-like <b>Family:</b> YoaC-like
33	<a href="#">c3gehA</a>	Alignment	not modelled	6.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trna modification gtpase mnme; <b>PDBTitle:</b> crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
34	<a href="#">d2choa2</a>	Alignment	not modelled	5.9	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> alpha-D-glucuronidase/Hyaluronidase catalytic domain
35	<a href="#">c2kqrA</a>	Alignment	not modelled	5.8	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> asparaginyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> solution structure of the n-terminal domain (residues 1-111) of brugia2 malayi asparaginyl-trna synthetase
36	<a href="#">d1sm2a</a>	Alignment	not modelled	5.8	24	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
37	<a href="#">d2cbia2</a>	Alignment	not modelled	5.7	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> alpha-D-glucuronidase/Hyaluronidase catalytic domain
38	<a href="#">d1li4a2</a>	Alignment	not modelled	5.6	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> S-adenosylhomocystein hydrolase
39	<a href="#">d1v8ba2</a>	Alignment	not modelled	5.4	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> S-adenosylhomocystein hydrolase
40	<a href="#">c2j8pA</a>	Alignment	not modelled	5.4	17	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> cleavage stimulation factor 64 kda subunit; <b>PDBTitle:</b> nmr structure of c-terminal domain of human cstf-64
41	<a href="#">c1d4fD</a>	Alignment	not modelled	5.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> s-adenosylhomocysteine hydrolase; <b>PDBTitle:</b> crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
42	<a href="#">c3d5IA</a>	Alignment	not modelled	5.4	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein recx; <b>PDBTitle:</b> crystal structure of regulatory protein recx
43	<a href="#">d2edua1</a>	Alignment	not modelled	5.3	10	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> ComEA-like
44	<a href="#">d2esna1</a>	Alignment	not modelled	5.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LysR-like transcriptional regulators
45	<a href="#">d1g8ea</a>	Alignment	not modelled	5.0	11	<b>Fold:</b> Flagellar transcriptional activator FlhD <b>Superfamily:</b> Flagellar transcriptional activator FlhD <b>Family:</b> Flagellar transcriptional activator FlhD