

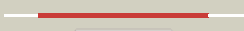










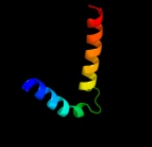







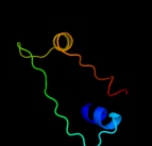



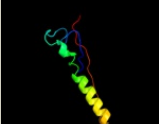


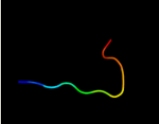
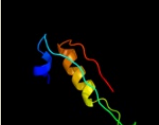



# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P33029
Date	Thu Jan 5 11:51:05 GMT 2012
Unique Job ID	a51684f41d545e72

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1m2wA_</a>	 Alignment		100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mannitol dehydrogenase; <b>PDBTitle:</b> pseudomonas fluorescens mannitol 2-dehydrogenase ternary complex with 2 nad and d-mannitol
2	<a href="#">c3h2zA_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mannitol-1-phosphate 5-dehydrogenase; <b>PDBTitle:</b> the crystal structure of mannitol-1-phosphate dehydrogenase from shigella flexneri
3	<a href="#">d1lj8a4</a>	 Alignment		100.0	43	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
4	<a href="#">d1lj8a3</a>	 Alignment		100.0	33	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Mannitol 2-dehydrogenase
5	<a href="#">c2axqA_</a>	 Alignment		69.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
6	<a href="#">c3mtjA_</a>	 Alignment		42.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> the crystal structure of a homoserine dehydrogenase from thibacillus denitrificans to 2.15Å
7	<a href="#">d1gzsB_</a>	 Alignment		41.2	18	<b>Fold:</b> SopE-like GEF domain <b>Superfamily:</b> SopE-like GEF domain <b>Family:</b> SopE-like GEF domain
8	<a href="#">c3mioA_</a>	 Alignment		38.3	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase; <b>PDBTitle:</b> crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase 2 domain from mycobacterium tuberculosis at pH 6.00
9	<a href="#">d1k4ia_</a>	 Alignment		34.6	12	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
10	<a href="#">c3fggA_</a>	 Alignment		31.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bce2196; <b>PDBTitle:</b> crystal structure of putative ecf-type sigma factor negative effector 2 from bacillus cereus
11	<a href="#">d1snna_</a>	 Alignment		28.2	28	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB

12	<a href="#">c3nt5B_</a>	Alignment		27.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
13	<a href="#">d1qusa_</a>	Alignment		24.7	8	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Bacterial muramidase, catalytic domain
14	<a href="#">c2ph5A_</a>	Alignment		22.8	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homospermidine synthase; <b>PDBTitle:</b> crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
15	<a href="#">c3h8gC_</a>	Alignment		20.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cytosol aminopeptidase; <b>PDBTitle:</b> bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
16	<a href="#">c3euwB_</a>	Alignment		20.3	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> myo-inositol dehydrogenase; <b>PDBTitle:</b> crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
17	<a href="#">c1yy3A_</a>	Alignment		18.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine:trna ribosyltransferase- <b>PDBTitle:</b> structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
18	<a href="#">d2o8ra3</a>	Alignment		18.5	27	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Polyphosphate kinase C-terminal domain
19	<a href="#">c3cwcB_</a>	Alignment		17.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative glycerate kinase 2; <b>PDBTitle:</b> crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
20	<a href="#">d1r0ka2</a>	Alignment		16.3	7	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
21	<a href="#">c2o8rA_</a>	Alignment	not modelled	15.7	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyphosphate kinase; <b>PDBTitle:</b> crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
22	<a href="#">c1ceua_</a>	Alignment	not modelled	15.5	44	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hiv-1 regulatory protein n-terminal <b>PDBTitle:</b> nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
23	<a href="#">c3ceaA_</a>	Alignment	not modelled	15.2	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> myo-inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
24	<a href="#">c1lanA_</a>	Alignment	not modelled	15.1	12	<b>PDB header:</b> hydrolase (alpha-aminoacylpeptide) <b>Chain:</b> A: <b>PDB Molecule:</b> leucine aminopeptidase; <b>PDBTitle:</b> leucine aminopeptidase complex with l-leucinal
25	<a href="#">d1gyta2</a>	Alignment	not modelled	15.1	13	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Leucine aminopeptidase, C-terminal domain
26	<a href="#">c3c7cB_</a>	Alignment	not modelled	14.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> octopine dehydrogenase; <b>PDBTitle:</b> a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
27	<a href="#">c3b20R_</a>	Alignment	not modelled	13.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase (nadp+); <b>PDBTitle:</b> crystal structure analysis of dehydrogenase complexed with nad
28	<a href="#">c3guzB_</a>	Alignment	not modelled	13.2	31	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic

						inhibition3 by pantoate in ps's
29	<a href="#">c1gytG</a>	Alignment	not modelled	13.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> cytosol aminopeptidase; <b>PDBTitle:</b> e. coli aminopeptidase a (pepa)
30	<a href="#">c3egoB</a>	Alignment	not modelled	12.3	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of probable 2-dehydropantoate 2-reductase2 pane from bacillus subtilis
31	<a href="#">d2v0fa1</a>	Alignment	not modelled	11.7	36	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
32	<a href="#">c1z9bA</a>	Alignment	not modelled	11.5	13	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> solution structure of the c1-subdomain of bacillus2 stearothermophilus translation initiation factor if2
33	<a href="#">d1e5qa1</a>	Alignment	not modelled	11.5	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
34	<a href="#">c2d2iO</a>	Alignment	not modelled	11.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of nadp-dependent glyceraldehyde-3-2 phosphate dehydrogenase from synechococcus sp. complexed3 with nadp+
35	<a href="#">c3kzwD</a>	Alignment	not modelled	11.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cytosol aminopeptidase; <b>PDBTitle:</b> crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
36	<a href="#">c1e5lA</a>	Alignment	not modelled	10.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
37	<a href="#">c3bjrA</a>	Alignment	not modelled	10.5	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxylesterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution
38	<a href="#">c1x5bA</a>	Alignment	not modelled	10.3	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducing adaptor molecule 2; <b>PDBTitle:</b> the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
39	<a href="#">c3tbiA</a>	Alignment	not modelled	10.2	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase-associated protein gp33; <b>PDBTitle:</b> crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
40	<a href="#">d1o7fa1</a>	Alignment	not modelled	10.0	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
41	<a href="#">c2qytA</a>	Alignment	not modelled	9.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83
42	<a href="#">c1h6dL</a>	Alignment	not modelled	9.2	13	<b>PDB header:</b> protein translocation <b>Chain:</b> L: <b>PDB Molecule:</b> precursor form of glucose-fructose <b>PDBTitle:</b> oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
43	<a href="#">c1ofgF</a>	Alignment	not modelled	9.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> glucose-fructose oxidoreductase
44	<a href="#">c2c9lZ</a>	Alignment	not modelled	9.0	40	<b>PDB header:</b> viral protein <b>Chain:</b> Z: <b>PDB Molecule:</b> bzlf1 trans-activator protein; <b>PDBTitle:</b> structure of the epstein-barr virus zebra protein
45	<a href="#">d1r6ea</a>	Alignment	not modelled	8.6	21	<b>Fold:</b> SopE-like GEF domain <b>Superfamily:</b> SopE-like GEF domain <b>Family:</b> SopE-like GEF domain
46	<a href="#">c2hc9A</a>	Alignment	not modelled	8.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine aminopeptidase 1; <b>PDBTitle:</b> structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
47	<a href="#">d1to6a</a>	Alignment	not modelled	8.2	20	<b>Fold:</b> Glycerate kinase I <b>Superfamily:</b> Glycerate kinase I <b>Family:</b> Glycerate kinase I
48	<a href="#">c2cu2A</a>	Alignment	not modelled	8.2	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mannose-1-phosphate guanylyl transferase; <b>PDBTitle:</b> crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
49	<a href="#">d1dvpA1</a>	Alignment	not modelled	8.2	14	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ENTH/VHS domain <b>Family:</b> VHS domain
50	<a href="#">c3ingA</a>	Alignment	not modelled	8.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
51	<a href="#">c3omdB</a>	Alignment	not modelled	8.2	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of unknown function protein from leptospirillum2 rubarum
52	<a href="#">c1dvpA</a>	Alignment	not modelled	8.1	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine <b>PDBTitle:</b> crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
53	<a href="#">c3q2kB</a>	Alignment	not modelled	8.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxi doreductase; <b>PDBTitle:</b> crystal structure of the wlba dehydrogenase from

						<p>bordeetella pertussis2 in complex with nadh and udp-glcnac</p> <p><b>Fold:</b>S-adenosyl-L-methionine-dependent methyltransferases</p> <p><b>Superfamily:</b>S-adenosyl-L-methionine-dependent methyltransferases</p> <p><b>Family:</b>FkbM-like</p>
54	<a href="#">d2py6a1</a>	Alignment	not modelled	8.0	25	<p><b>PDB header:</b>signaling</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>hepatocyte growth factor-regulated tyrosine kinase</p> <p><b>PDBTitle:</b> crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution</p>
55	<a href="#">c3zyqA</a>	Alignment	not modelled	7.7	12	<p><b>PDB header:</b>oxidoreductase</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>diaminopimelic acid dehydrogenase;</p> <p><b>PDBTitle:</b> c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline</p>
56	<a href="#">c3dapB</a>	Alignment	not modelled	7.6	17	<p><b>Fold:</b>NAD(P)-binding Rossmann-fold domains</p> <p><b>Superfamily:</b>NAD(P)-binding Rossmann-fold domains</p> <p><b>Family:</b>Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain</p>
57	<a href="#">d1q0qa2</a>	Alignment	not modelled	7.1	13	<p><b>PDB header:</b>cell cycle</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>chromosome partition protein mukf;</p> <p><b>PDBTitle:</b> crystal structure of the muke-mukf complex</p>
58	<a href="#">c3euhB</a>	Alignment	not modelled	6.9	15	<p><b>Fold:</b>Heme-dependent peroxidases</p> <p><b>Superfamily:</b>Heme-dependent peroxidases</p> <p><b>Family:</b>Catalase-peroxidase KatG</p>
59	<a href="#">d1u2ka</a>	Alignment	not modelled	6.8	29	<p><b>Fold:</b>Phospholipase D/nuclease</p> <p><b>Superfamily:</b>Phospholipase D/nuclease</p> <p><b>Family:</b>Polyphosphate kinase C-terminal domain</p>
60	<a href="#">d1xdpa3</a>	Alignment	not modelled	6.8	50	<p><b>PDB header:</b>transferase</p> <p><b>Chain:</b> C: <b>PDB Molecule:</b>succinyl-coa:3-ketoacid-coenzyme a transferase subunit a;</p> <p><b>PDBTitle:</b> complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695</p>
61	<a href="#">c3rrlC</a>	Alignment	not modelled	6.6	24	<p><b>Fold:</b>NAD(P)-binding Rossmann-fold domains</p> <p><b>Superfamily:</b>NAD(P)-binding Rossmann-fold domains</p> <p><b>Family:</b>Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain</p>
62	<a href="#">d1f06a1</a>	Alignment	not modelled	6.6	17	<p><b>PDB header:</b>transcription</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>putative apha-like transcription factor;</p> <p><b>PDBTitle:</b> crystal structure of a putative apha-like transcription factor2 (zp_00208345.1) from magnetospirillum magnetotacticum ms-1 at 2.00 a3 resolution</p>
63	<a href="#">c2rkha</a>	Alignment	not modelled	6.5	44	<p><b>Fold:</b>Nucleotide-diphospho-sugar transferases</p> <p><b>Superfamily:</b>Nucleotide-diphospho-sugar transferases</p> <p><b>Family:</b>mannose-1-phosphate guanylyl transferase</p>
64	<a href="#">d2cu2a2</a>	Alignment	not modelled	6.5	15	<p><b>Fold:</b>Spectrin repeat-like</p> <p><b>Superfamily:</b>Spectrin repeat</p> <p><b>Family:</b>Spectrin repeat</p>
65	<a href="#">d1hcia1</a>	Alignment	not modelled	6.5	23	<p><b>PDB header:</b>cell cycle</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>sfi1 peptide;</p> <p><b>PDBTitle:</b> nmr solution structure of the c-terminal domain (t94-y172)2 of the human centrin 2 in complex with a repeat sequence of3 human sfi1 (r641-t660)</p>
66	<a href="#">c2k2iB</a>	Alignment	not modelled	6.3	50	<p><b>Fold:</b>Another 3-helical bundle</p> <p><b>Superfamily:</b>IscX-like</p> <p><b>Family:</b>IscX-like</p>
67	<a href="#">d1uj8a1</a>	Alignment	not modelled	6.2	16	<p><b>PDB header:</b>viral protein</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>vrp protein;</p> <p><b>PDBTitle:</b> solution structure of hiv-1 vrp (13-33) peptide in micells</p>
68	<a href="#">c1fi0A</a>	Alignment	not modelled	6.2	44	<p><b>Fold:</b>NAD(P)-binding Rossmann-fold domains</p> <p><b>Superfamily:</b>NAD(P)-binding Rossmann-fold domains</p> <p><b>Family:</b>6-phosphogluconate dehydrogenase-like, N-terminal domain</p>
69	<a href="#">d1mv8a2</a>	Alignment	not modelled	6.1	24	<p><b>PDB header:</b>oxidoreductase</p> <p><b>Chain:</b> C: <b>PDB Molecule:</b>peroxidase/catalase hpi;</p> <p><b>PDBTitle:</b> crystal structure of the c-terminal domain from the2 catalase-peroxidase katg of escherichia coli (p21 21 21)</p>
70	<a href="#">c1u2jC</a>	Alignment	not modelled	5.9	29	<p><b>PDB header:</b>structural genomics, unknown function</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>agr_c_984p;</p> <p><b>PDBTitle:</b> x-ray crystal structure of protein agr_c_984 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr120.</p>
71	<a href="#">c2o8sA</a>	Alignment	not modelled	5.9	24	<p><b>PDB header:</b>transcription</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>protein doublesex;</p> <p><b>PDBTitle:</b> dsx_long</p>
72	<a href="#">c2jz1A</a>	Alignment	not modelled	5.8	23	<p><b>PDB header:</b>hydrolase</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>probable cytosol aminopeptidase;</p> <p><b>PDBTitle:</b> crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331</p>
73	<a href="#">c3jruB</a>	Alignment	not modelled	5.7	17	<p><b>PDB header:</b>metal binding protein/protein binding</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>ca2+/calmodulin dependent kinase kinase;</p> <p><b>PDBTitle:</b> calmodulin/nematode ca2+/calmodulin dependent kinase kinase2 fragment</p>
74	<a href="#">cliq5B</a>	Alignment	not modelled	5.7	67	<p><b>Fold:</b>NAD(P)-binding Rossmann-fold domains</p> <p><b>Superfamily:</b>NAD(P)-binding Rossmann-fold domains</p> <p><b>Family:</b>6-phosphogluconate dehydrogenase-like, N-terminal domain</p>
75	<a href="#">d1txga2</a>	Alignment	not modelled	5.7	25	<p><b>Fold:</b>NAD(P)-binding Rossmann-fold domains</p> <p><b>Superfamily:</b>NAD(P)-binding Rossmann-fold domains</p> <p><b>Family:</b>Transcriptional repressor Rex, C-terminal domain</p>
76	<a href="#">d2dt5a2</a>	Alignment	not modelled	5.6	19	<p><b>PDB header:</b>hydrolase</p> <p><b>Chain:</b> E: <b>PDB Molecule:</b>m17 leucyl aminopeptidase;</p> <p><b>PDBTitle:</b> structure of a protease 4</p>
77	<a href="#">c3kr5E</a>	Alignment	not modelled	5.6	17	<p><b>PDB header:</b>transcription/dna</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>redox-sensing transcriptional repressor</p>

78	<a href="#">c3ketA_</a>	Alignment	not modelled	5.5	23	rex; <b>PDBTitle:</b> crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
79	<a href="#">c1s6cB_</a>	Alignment	not modelled	5.5	38	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily d member 2; <b>PDBTitle:</b> crystal structure of the complex between kchip1 and kv4.2 n1-30
80	<a href="#">c3ij3A_</a>	Alignment	not modelled	5.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosol aminopeptidase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
81	<a href="#">c3ktwA_</a>	Alignment	not modelled	5.4	26	<b>PDB header:</b> rna/rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle 19 kda protein; <b>PDBTitle:</b> crystal structure of the srp19/s-domain srp rna complex of sulfolobus2 solfataricus
82	<a href="#">c3ghyA_</a>	Alignment	not modelled	5.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ketopantoate reductase protein; <b>PDBTitle:</b> crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
83	<a href="#">d1k8kg_</a>	Alignment	not modelled	5.2	6	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Arp2/3 complex 16 kDa subunit ARPC5 <b>Family:</b> Arp2/3 complex 16 kDa subunit ARPC5
84	<a href="#">d2hiqa1</a>	Alignment	not modelled	5.1	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Hypothetical protein YdhR