



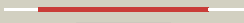






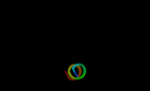









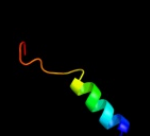
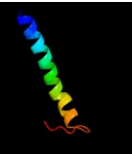






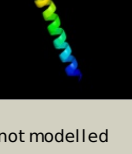
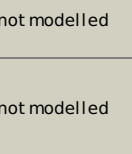


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P15078
Date	Thu Jan 5 11:34:36 GMT 2012
Unique Job ID	418770152a832dd9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3giaA_</a>	 Alignment		97.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj0609; <b>PDBTitle:</b> crystal structure of apct transporter
2	<a href="#">c2jlnA_</a>	 Alignment		96.9	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
3	<a href="#">c3lrcC_</a>	 Alignment		94.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> arginine/agmatine antiporter; <b>PDBTitle:</b> structure of e. coli adic (p1)
4	<a href="#">c2xq2A_</a>	 Alignment		94.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> structure of the k294a mutant of vsglT
5	<a href="#">c3dh4A_</a>	 Alignment		87.2	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
6	<a href="#">c3a8qB_</a>	 Alignment		42.1	70	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> t-lymphoma invasion and metastasis-inducing <b>PDBTitle:</b> low-resolution crystal structure of the tiam2 phccex domain
7	<a href="#">c3a8nA_</a>	 Alignment		40.7	58	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> t-lymphoma invasion and metastasis-inducing <b>PDBTitle:</b> crystal structure of the tiam1 phccex domain
8	<a href="#">c3pl0B_</a>	 Alignment		38.2	44	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution
9	<a href="#">d2axtj1</a>	 Alignment		27.7	36	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein J, Psbj <b>Family:</b> Psbj-like
10	<a href="#">d2bfdb2</a>	 Alignment		27.3	4	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
11	<a href="#">d1rp4a_</a>	 Alignment		26.8	36	<b>Fold:</b> ERO1-like <b>Superfamily:</b> ERO1-like <b>Family:</b> ERO1-like

12	<a href="#">c3hd6A_</a>	Alignment		26.3	14	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter rh type c; <b>PDBTitle:</b> crystal structure of the human rhesus glycoprotein rhcg
13	<a href="#">c2k9pA_</a>	Alignment		26.3	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> pheromone alpha factor receptor; <b>PDBTitle:</b> structure of tm1_tm2 in lppg micelles
14	<a href="#">d1h5pa_</a>	Alignment		24.8	33	<b>Fold:</b> SAND domain-like <b>Superfamily:</b> SAND domain-like <b>Family:</b> SAND domain
15	<a href="#">c2ktlA_</a>	Alignment		24.5	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> structure of c-terminal domain from mtyrrs of a. nidulans
16	<a href="#">d1qs0b2</a>	Alignment		24.1	15	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
17	<a href="#">d2jeka1</a>	Alignment		23.7	19	<b>Fold:</b> Rv1873-like <b>Superfamily:</b> Rv1873-like <b>Family:</b> Rv1873-like
18	<a href="#">d1oqja_</a>	Alignment		23.6	20	<b>Fold:</b> SAND domain-like <b>Superfamily:</b> SAND domain-like <b>Family:</b> SAND domain
19	<a href="#">d1s6la1</a>	Alignment		23.5	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MerB N-terminal domain-like
20	<a href="#">c3b9yA_</a>	Alignment		23.3	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter family rh-like protein; <b>PDBTitle:</b> crystal structure of the nitrosomonas europaea rh protein
21	<a href="#">d1afra_</a>	Alignment	not modelled	23.0	30	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
22	<a href="#">d1ufna_</a>	Alignment	not modelled	22.4	27	<b>Fold:</b> SAND domain-like <b>Superfamily:</b> SAND domain-like <b>Family:</b> SAND domain
23	<a href="#">c3zy6A_</a>	Alignment	not modelled	22.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative gdp-fucose protein o-fucosyltransferase 1; <b>PDBTitle:</b> crystal structure of pofut1 in complex with gdp-fucose2 (crystal-form-ii) <b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
24	<a href="#">dlik6a2</a>	Alignment	not modelled	21.2	12	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
25	<a href="#">d2awia1</a>	Alignment	not modelled	20.7	29	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> PrgX N-terminal domain-like
26	<a href="#">c3iymA_</a>	Alignment	not modelled	20.6	35	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> backbone trace of the capsid protein dimer of a fungal partitiivirus2 from electron cryomicroscopy and homology modeling
27	<a href="#">c2qx5B_</a>	Alignment	not modelled	19.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoporin nic96; <b>PDBTitle:</b> structure of nucleoporin nic96
28	<a href="#">d2ozlb2</a>	Alignment	not modelled	19.5	10	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain

29	<a href="#">c3ahrA</a>	Alignment	not modelled	19.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ero1-like protein alpha; <b>PDBTitle:</b> inactive human ero1
30	<a href="#">c3pppA</a>	Alignment	not modelled	18.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/carnitine/choline-binding protein; <b>PDBTitle:</b> structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
31	<a href="#">d1w85b2</a>	Alignment	not modelled	17.5	28	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
32	<a href="#">d2fug61</a>	Alignment	not modelled	17.3	36	<b>Fold:</b> HydA/Nqo6-like <b>Superfamily:</b> HydA/Nqo6-like <b>Family:</b> Nqo6-like
33	<a href="#">d1i0za2</a>	Alignment	not modelled	17.2	21	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
34	<a href="#">d1llda2</a>	Alignment	not modelled	17.0	29	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
35	<a href="#">d2yrka1</a>	Alignment	not modelled	16.8	27	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> HkH motif-containing C2H2 finger
36	<a href="#">d9lta2</a>	Alignment	not modelled	16.7	25	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
37	<a href="#">c2lbfA</a>	Alignment	not modelled	16.6	43	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 60s acidic ribosomal protein p1; <b>PDBTitle:</b> solution structure of the dimerization domain of human ribosomal2 protein p1/p2 heterodimer
38	<a href="#">d1nekd</a>	Alignment	not modelled	16.6	13	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
39	<a href="#">c2k42A</a>	Alignment	not modelled	16.4	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> wiskott-aldrich syndrome protein; <b>PDBTitle:</b> solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehcc effector
40	<a href="#">c2elnA</a>	Alignment	not modelled	16.2	50	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 406; <b>PDBTitle:</b> solution structure of the 11th c2h2 zinc finger of human2 zinc finger protein 406
41	<a href="#">c3iz5t</a>	Alignment	not modelled	15.8	43	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 60s ribosomal protein l19 (l19e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
42	<a href="#">c3nctC</a>	Alignment	not modelled	15.8	22	<b>PDB header:</b> dna binding protein, chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> protein psib; <b>PDBTitle:</b> x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
43	<a href="#">c2etjA</a>	Alignment	not modelled	15.7	67	<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
44	<a href="#">d2etja1</a>	Alignment	not modelled	15.7	67	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Ribonuclease H
45	<a href="#">d1fvka</a>	Alignment	not modelled	15.7	29	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
46	<a href="#">d1i10a2</a>	Alignment	not modelled	15.7	25	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
47	<a href="#">d1umdb2</a>	Alignment	not modelled	15.6	19	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
48	<a href="#">c1x4rA</a>	Alignment	not modelled	15.2	29	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> parp14 protein; <b>PDBTitle:</b> solution structure of wwe domain in parp14 protein
49	<a href="#">d1oeya</a>	Alignment	not modelled	15.0	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
50	<a href="#">d1d4va1</a>	Alignment	not modelled	14.9	38	<b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> TNF receptor-like
51	<a href="#">c2k1aA</a>	Alignment	not modelled	14.8	45	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iiB) transmembrane segment
52	<a href="#">c3es4B</a>	Alignment	not modelled	14.2	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein duf861 with a rmlc-like cupin fold; <b>PDBTitle:</b> crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
53	<a href="#">c3o66A</a>	Alignment	not modelled	14.2	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine betaine/carnitine/choline abc transporter; <b>PDBTitle:</b> crystal structure of glycine betaine/carnitine/choline abc transporter
						<b>PDB header:</b> oxidoreductase, membrane protein

54	<a href="#">c1yewl_</a>	Alignment	not modelled	14.1	40	<b>Chain:</b> I: <b>PDB Molecule:</b> particulate methane monooxygenase, b subunit; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase
55	<a href="#">c2dnfA_</a>	Alignment	not modelled	14.0	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> doublecortin domain-containing protein 2; <b>PDBTitle:</b> solution structure of rsgr ruh-062, a dcx domain from human
56	<a href="#">d1hyha2</a>	Alignment	not modelled	14.0	13	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
57	<a href="#">d5csma_</a>	Alignment	not modelled	14.0	20	<b>Fold:</b> Chorismate mutase II <b>Superfamily:</b> Chorismate mutase II <b>Family:</b> Allosteric chorismate mutase
58	<a href="#">d1rxwa1</a>	Alignment	not modelled	13.9	20	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain
59	<a href="#">c2j8lB_</a>	Alignment	not modelled	13.9	43	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> coagulation factor xi; <b>PDBTitle:</b> fxi apple 4 domain loop-out conformation
60	<a href="#">d1i39a_</a>	Alignment	not modelled	13.7	56	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Ribonuclease H
61	<a href="#">cli3aA_</a>	Alignment	not modelled	13.7	56	<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
62	<a href="#">c3k1qS_</a>	Alignment	not modelled	13.6	22	<b>PDB header:</b> virus <b>Chain:</b> S: <b>PDB Molecule:</b> vp7: protector protein (outer shell); <b>PDBTitle:</b> backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics
63	<a href="#">c2hx6A_</a>	Alignment	not modelled	13.6	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease; <b>PDBTitle:</b> solution structure analysis of the phage t42 endoribonuclease regb
64	<a href="#">c2j8lA_</a>	Alignment	not modelled	13.6	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> coagulation factor xi; <b>PDBTitle:</b> fxi apple 4 domain loop-out conformation
65	<a href="#">c2j8jA_</a>	Alignment	not modelled	13.6	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> coagulation factor xi; <b>PDBTitle:</b> solution structure of the a4 domain of blood coagulation2 factor xi
66	<a href="#">d1k1ga_</a>	Alignment	not modelled	13.5	32	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
67	<a href="#">d2ldxa2</a>	Alignment	not modelled	13.5	25	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
68	<a href="#">c2kn6A_</a>	Alignment	not modelled	13.5	16	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> apoptosis-associated speck-like protein containing a card; <b>PDBTitle:</b> structure of full-length human asc (apoptosis-associated speck-like2 protein containing a card)
69	<a href="#">d2j0111</a>	Alignment	not modelled	13.4	40	<b>Fold:</b> L28p-like <b>Superfamily:</b> L28p-like <b>Family:</b> Ribosomal protein L28
70	<a href="#">d1ekea_</a>	Alignment	not modelled	13.4	67	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Ribonuclease H
71	<a href="#">c2h8bB_</a>	Alignment	not modelled	13.4	50	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> B: <b>PDB Molecule:</b> insulin-like 3; <b>PDBTitle:</b> solution structure of insl3
72	<a href="#">d2axtc1</a>	Alignment	not modelled	13.3	18	<b>Fold:</b> Photosystem II antenna protein-like <b>Superfamily:</b> Photosystem II antenna protein-like <b>Family:</b> Photosystem II antenna protein-like
73	<a href="#">c2axtc_</a>	Alignment	not modelled	13.3	18	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> photosystem ii cp43 protein; <b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus
74	<a href="#">c2jrpA_</a>	Alignment	not modelled	13.2	44	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
75	<a href="#">d2oara1</a>	Alignment	not modelled	13.2	14	<b>Fold:</b> Gated mechanosensitive channel <b>Superfamily:</b> Gated mechanosensitive channel <b>Family:</b> Gated mechanosensitive channel
76	<a href="#">clsazA_</a>	Alignment	not modelled	13.2	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable butyrate kinase 2; <b>PDBTitle:</b> membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
77	<a href="#">d2csba1</a>	Alignment	not modelled	13.1	71	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Topoisomerase V repeat domain
78	<a href="#">c2rejA_</a>	Alignment	not modelled	13.1	8	<b>PDB header:</b> choline-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycine betaine abc transporter protein; <b>PDBTitle:</b> abc-transporter choline binding protein in unliganded semi-2 closed conformation
79	<a href="#">c2yguA_</a>	Alignment	not modelled	13.0	20	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> venom allergen 2; <b>PDBTitle:</b> crystal structure of fire ant venom allergen, sol i 2

80	<a href="#">c2jo1A_</a>	Alignment	not modelled	13.0	2	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
81	<a href="#">d2axti1</a>	Alignment	not modelled	13.0	23	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein I, Psbl <b>Family:</b> Psbl-like
82	<a href="#">c3kioA_</a>	Alignment	not modelled	13.0	67	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease h2 subunit a; <b>PDBTitle:</b> mouse rnase h2 complex
83	<a href="#">d1l7la_</a>	Alignment	not modelled	13.0	14	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> PA-IL, galactose-binding lectin 1
84	<a href="#">d1m98a1</a>	Alignment	not modelled	13.0	26	<b>Fold:</b> Orange carotenoid protein, N-terminal domain <b>Superfamily:</b> Orange carotenoid protein, N-terminal domain <b>Family:</b> Orange carotenoid protein, N-terminal domain
85	<a href="#">c3g9rF_</a>	Alignment	not modelled	12.9	36	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> fusion complex of hiv-1 envelope glycoprotein <b>PDBTitle:</b> structure of the hiv-1 gp41 membrane-proximal ectodomain2 region in a putative prefusion conformation
86	<a href="#">c2bbjB_</a>	Alignment	not modelled	12.9	15	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein; <b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
87	<a href="#">d1uaxa_</a>	Alignment	not modelled	12.8	67	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Ribonuclease H
88	<a href="#">d1c9ka_</a>	Alignment	not modelled	12.8	55	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
89	<a href="#">c2j8jB_</a>	Alignment	not modelled	12.8	43	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> coagulation factor xi; <b>PDBTitle:</b> solution structure of the a4 domain of blood coagulation2 factor xi
90	<a href="#">d1uf0a_</a>	Alignment	not modelled	12.7	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Doublecortin (DC) <b>Family:</b> Doublecortin (DC)
91	<a href="#">c2p58C_</a>	Alignment	not modelled	12.7	45	<b>PDB header:</b> transport protein/chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> putative type iii secretion protein yscg; <b>PDBTitle:</b> structure of the yersinia pestis type iii secretion system2 needle protein yscf in complex with its chaperones3 ysce/yscg
92	<a href="#">c1rr7A_</a>	Alignment	not modelled	12.6	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> middle operon regulator; <b>PDBTitle:</b> crystal structure of the middle operon regulator protein of2 bacteriophage mu
93	<a href="#">d1rr7a_</a>	Alignment	not modelled	12.6	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Middle operon regulator, Mor
94	<a href="#">d1j5pa4</a>	Alignment	not modelled	12.6	14	<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
95	<a href="#">c3s0xB_</a>	Alignment	not modelled	12.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidase a24b, flak domain protein; <b>PDBTitle:</b> the crystal structure of gxgd membrane protease flak
96	<a href="#">c2d0bA_</a>	Alignment	not modelled	12.6	44	<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 +
97	<a href="#">c2jpmA_</a>	Alignment	not modelled	12.6	40	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin lactococcin-g subunit beta; <b>PDBTitle:</b> lactococcin g-b in tfe
98	<a href="#">d1io2a_</a>	Alignment	not modelled	12.5	67	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Ribonuclease H
99	<a href="#">c2oarA_</a>	Alignment	not modelled	12.4	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> large-conductance mechanosensitive channel; <b>PDBTitle:</b> mechanosensitive channel of large conductance (mscl)