
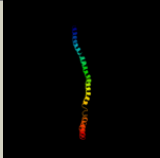

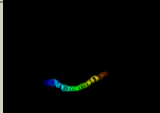



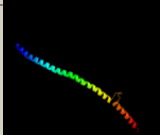

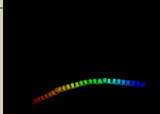



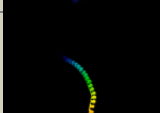








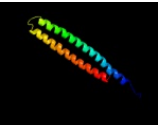
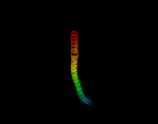
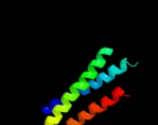
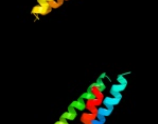

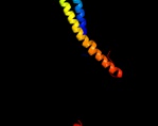

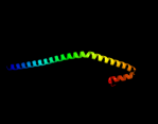
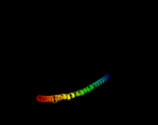


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0PK00
Date	Fri May 25 09:38:31 BST 2012
Unique Job ID	9897288fcc7d7a4c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1deqO_</a>	 Alignment		97.4	7	<b>PDB header:</b> <b>PDB COMPND:</b>
2	<a href="#">c3ghgK_</a>	 Alignment		97.4	5	<b>PDB header:</b> blood clotting <b>Chain:</b> K: <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
3	<a href="#">c1ei3E_</a>	 Alignment		97.3	7	<b>PDB header:</b> <b>PDB COMPND:</b>
4	<a href="#">c3dtpA_</a>	 Alignment		97.0	12	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain chimera of smooth and <b>PDBTitle:</b> tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
5	<a href="#">c3u59C_</a>	 Alignment		97.0	5	<b>PDB header:</b> contractile protein <b>Chain:</b> C: <b>PDB Molecule:</b> tropomyosin beta chain; <b>PDBTitle:</b> n-terminal 98-aa fragment of smooth muscle tropomyosin beta
6	<a href="#">c3ojaB_</a>	 Alignment		96.9	13	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anopheles plasmodium-responsive leucine-rich repeat protein <b>PDBTitle:</b> crystal structure of Irim1/apl1c complex
7	<a href="#">c1ei3C_</a>	 Alignment		96.8	6	<b>PDB header:</b> <b>PDB COMPND:</b>
8	<a href="#">c2dq3A_</a>	 Alignment		96.7	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of aq_298
9	<a href="#">c3vkgB_</a>	 Alignment		96.4	9	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> crystal structure of an motor protein
10	<a href="#">c1deqF_</a>	 Alignment		96.4	10	<b>PDB header:</b> <b>PDB COMPND:</b>
11	<a href="#">c2fxmB_</a>	 Alignment		96.2	12	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> myosin heavy chain, cardiac muscle beta isoform; <b>PDBTitle:</b> structure of the human beta-myosin s2 fragment

12	<a href="#">c2y3aB_</a>	Alignment		96.1	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit beta; <b>PDBTitle:</b> crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
13	<a href="#">c3q8tB_</a>	Alignment		96.0	12	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> beclin-1; <b>PDBTitle:</b> crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
14	<a href="#">c1s94A_</a>	Alignment		96.0	15	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> s-syntaxin; <b>PDBTitle:</b> crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
15	<a href="#">d1s94a_</a>	Alignment		96.0	15	<b>Fold:</b> STAT-like <b>Superfamily:</b> t-snare proteins <b>Family:</b> t-snare proteins
16	<a href="#">c1bf5A_</a>	Alignment		95.7	9	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> tyrosine phosphorylated stat-1/dna complex
17	<a href="#">c3hnwB_</a>	Alignment		95.7	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
18	<a href="#">c3na7A_</a>	Alignment		95.7	9	<b>PDB header:</b> gene regulation, chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hp0958; <b>PDBTitle:</b> 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
19	<a href="#">c2d3eD_</a>	Alignment		95.3	15	<b>PDB header:</b> contractile protein <b>Chain:</b> D: <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1 <b>PDBTitle:</b> crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
20	<a href="#">c2efrB_</a>	Alignment		95.1	17	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1 alpha chain; <b>PDBTitle:</b> crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
21	<a href="#">c3hizB_</a>	Alignment	not modelled	94.9	17	<b>PDB header:</b> transferase/oncoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit <b>PDBTitle:</b> crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
22	<a href="#">c3ol1A_</a>	Alignment	not modelled	94.7	7	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
23	<a href="#">c2dq0A_</a>	Alignment	not modelled	94.7	6	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
24	<a href="#">c2b9cA_</a>	Alignment	not modelled	94.7	16	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> striated-muscle alpha tropomyosin; <b>PDBTitle:</b> structure of tropomyosin's mid-region: bending and binding2 sites for actin
25	<a href="#">c3cwgA_</a>	Alignment	not modelled	94.5	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> unphosphorylated mouse stat3 core fragment
26	<a href="#">c3ipkA_</a>	Alignment	not modelled	94.5	8	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> agi/ii; <b>PDBTitle:</b> crystal structure of a3vp1 of agi/ii of streptococcus mutans
27	<a href="#">c2wpgA_</a>	Alignment	not modelled	94.5	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> trimeric autotransporter adhesin fragment; <b>PDBTitle:</b> salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion)
28	<a href="#">c1bg1A_</a>	Alignment	not modelled	94.4	8	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (transcription factor stat3b);

						<b>PDBTitle:</b> transcription factor stat3b/dna complex
29	<a href="#">c1y4cA</a>	Alignment	not modelled	94.4	12	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose binding protein fused with designed <b>PDBTitle:</b> designed helical protein fusion mbp
30	<a href="#">c3vkhD</a>	Alignment	not modelled	94.2	9	<b>PDB header:</b> motor protein <b>Chain:</b> D: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> crystal structure of an motor protein
31	<a href="#">c1c1gA</a>	Alignment	not modelled	94.1	7	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> tropomyosin; <b>PDBTitle:</b> crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
32	<a href="#">c1l8dB</a>	Alignment	not modelled	93.6	19	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> dna double-strand break repair rad50 atpase; <b>PDBTitle:</b> rad50 coiled-coil zn hook
33	<a href="#">c2gl2B</a>	Alignment	not modelled	93.3	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> adhesion a; <b>PDBTitle:</b> crystal structure of the tetra mutant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
34	<a href="#">d1seta1</a>	Alignment	not modelled	93.2	9	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> tRNA-binding arm <b>Family:</b> Seryl-tRNA synthetase (SerRS)
35	<a href="#">c3l9oA</a>	Alignment	not modelled	92.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> crystal structure of mtr4, a co-factor of the nuclear exosome
36	<a href="#">c4a55B</a>	Alignment	not modelled	92.2	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
37	<a href="#">c3lssA</a>	Alignment	not modelled	91.7	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> trypanosoma brucei seryl-trna synthetase in complex with atp
38	<a href="#">d1gqea</a>	Alignment	not modelled	91.4	11	<b>Fold:</b> Release factor <b>Superfamily:</b> Release factor <b>Family:</b> Release factor
39	<a href="#">c1jchC</a>	Alignment	not modelled	91.2	15	<b>PDB header:</b> ribosome inhibitor, hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin e3; <b>PDBTitle:</b> crystal structure of colicin e3 in complex with its immunity protein
40	<a href="#">c2oevA</a>	Alignment	not modelled	91.1	14	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death 6-interacting protein; <b>PDBTitle:</b> crystal structure of alix/aip1
41	<a href="#">c1sryB</a>	Alignment	not modelled	90.7	10	<b>PDB header:</b> ligase(synthetase) <b>Chain:</b> B: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> refined crystal structure of the seryl-trna synthetase from2 thermus thermophilus at 2.5 angstroms resolution
42	<a href="#">c3o0zD</a>	Alignment	not modelled	90.5	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> rho-associated protein kinase 1; <b>PDBTitle:</b> crystal structure of a coiled-coil domain from human rock i
43	<a href="#">c3a7pB</a>	Alignment	not modelled	90.2	20	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> autophagy protein 16; <b>PDBTitle:</b> the crystal structure of saccharomyces cerevisiae atg16
44	<a href="#">c1ciiA</a>	Alignment	not modelled	90.0	11	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
45	<a href="#">c3vkhB</a>	Alignment	not modelled	89.9	6	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> crystal structure of an motor protein
46	<a href="#">c2v71A</a>	Alignment	not modelled	88.9	12	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear distribution protein nude-like 1; <b>PDBTitle:</b> coiled-coil region of nudel
47	<a href="#">c3qo8A</a>	Alignment	not modelled	88.8	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase from candida albicans
48	<a href="#">c2zdiA</a>	Alignment	not modelled	88.8	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> prefoldin subunit beta; <b>PDBTitle:</b> crystal structure of prefoldin from pyrococcus horikoshii2 ot3
49	<a href="#">c2eqbC</a>	Alignment	not modelled	88.6	11	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> C: <b>PDB Molecule:</b> rab guanine nucleotide exchange factor sec2; <b>PDBTitle:</b> crystal structure of the rab gtpase sec4p, the sec2p gef2 domain, and phosphate complex
50	<a href="#">c2dfsA</a>	Alignment	not modelled	88.5	17	<b>PDB header:</b> contractile protein/transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin-5a; <b>PDBTitle:</b> 3-d structure of myosin-v inhibited state
51	<a href="#">c2rd0B</a>	Alignment	not modelled	88.2	16	<b>PDB header:</b> transferase/oncoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> structure of a human p110alpha/p85alpha complex
52	<a href="#">c1m1jA</a>	Alignment	not modelled	87.0	9	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> fibrinogen alpha subunit; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen with two different2 bound ligands
53	<a href="#">c3ojaA</a>	Alignment	not modelled	86.9	6	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> leucine-rich immune molecule 1; <b>PDBTitle:</b> crystal structure of lrim1/ap1c complex
						<b>PDB header:</b> metal transport, hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> pneumococcal surface protein a (pspa);

54	<a href="#">c2pmsD_</a>	Alignment	not modelled	86.6	20	<b>PDBTitle:</b> crystal structure of the complex of human lactoferrin n-lobe and2 lactoferrin-binding domain of pneumococcal surface protein a
55	<a href="#">c2e7sM_</a>	Alignment	not modelled	86.3	11	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> M: <b>PDB Molecule:</b> rab guanine nucleotide exchange factor sec2; <b>PDBTitle:</b> crystal structure of the yeast sec2p gef domain
56	<a href="#">c2xgiA_</a>	Alignment	not modelled	86.2	7	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
57	<a href="#">c2v66C_</a>	Alignment	not modelled	86.1	14	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> nuclear distribution protein nude-like 1; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of ndel1 (a.a.2 58 to 169)c
58	<a href="#">c1g8xB_</a>	Alignment	not modelled	85.9	3	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> myosin ii heavy chain fused to alpha-actinin 3; <b>PDBTitle:</b> structure of a genetically engineered molecular motor
59	<a href="#">c1f5nA_</a>	Alignment	not modelled	85.5	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> interferon-induced guanylate-binding protein 1; <b>PDBTitle:</b> human guanylate binding protein-1 in complex with the gtp2 analogue, gmppnp.
60	<a href="#">c1cz7C_</a>	Alignment	not modelled	85.5	10	<b>PDB header:</b> contractile protein <b>Chain:</b> C: <b>PDB Molecule:</b> microtubule motor protein ncd; <b>PDBTitle:</b> the crystal structure of a minus-end directed microtubule2 motor protein ncd reveals variable dimer conformations
61	<a href="#">c1i84V_</a>	Alignment	not modelled	84.6	14	<b>PDB header:</b> contractile protein <b>Chain:</b> V: <b>PDB Molecule:</b> smooth muscle myosin heavy chain; <b>PDBTitle:</b> cryo-em structure of the heavy meromyosin subfragment of2 chicken gizzard smooth muscle myosin with regulatory light3 chain in the dephosphorylated state. only c alphas4 provided for regulatory light chain. only backbone atoms5 provided for s2 fragment
62	<a href="#">c2i1jA_</a>	Alignment	not modelled	84.1	12	<b>PDB header:</b> cell adhesion, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> moesin; <b>PDBTitle:</b> moesin from spodoptera frugiperda at 2.1 angstroms resolution
63	<a href="#">c4dndA_</a>	Alignment	not modelled	83.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> syntaxin-10; <b>PDBTitle:</b> crystal structure of syntaxin 10 from homo sapiens
64	<a href="#">c2ch7A_</a>	Alignment	not modelled	82.6	10	<b>PDB header:</b> chemotaxis <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
65	<a href="#">c1hciB_</a>	Alignment	not modelled	81.9	7	<b>PDB header:</b> triple-helix coiled coil <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-actinin 2; <b>PDBTitle:</b> crystal structure of the rod domain of alpha-actinin
66	<a href="#">d1fxkc_</a>	Alignment	not modelled	81.9	16	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Prefoldin <b>Family:</b> Prefoldin
67	<a href="#">c4dylA_</a>	Alignment	not modelled	81.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase fes/fps; <b>PDBTitle:</b> f-bar domain of human fes tyrosine kinase
68	<a href="#">d1ez3a_</a>	Alignment	not modelled	80.4	13	<b>Fold:</b> STAT-like <b>Superfamily:</b> t-snare proteins <b>Family:</b> t-snare proteins
69	<a href="#">c1sijB_</a>	Alignment	not modelled	80.4	6	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> actinin; <b>PDBTitle:</b> cryo-em structure of chicken gizzard smooth muscle alpha-2 actinin
70	<a href="#">c1ik9B_</a>	Alignment	not modelled	79.8	10	<b>PDB header:</b> gene regulation/ligase <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein xrcc4; <b>PDBTitle:</b> crystal structure of a xrcc4-dna ligase iv complex
71	<a href="#">c2dnxA_</a>	Alignment	not modelled	79.1	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> syntaxin-12; <b>PDBTitle:</b> solution structure of rsgi ruh-063, an n-terminal domain of2 syntaxin 12 from human cdna
72	<a href="#">c2v1yB_</a>	Alignment	not modelled	77.7	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
73	<a href="#">c1n73C_</a>	Alignment	not modelled	77.2	13	<b>PDB header:</b> blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> fibrin gamma chain; <b>PDBTitle:</b> fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
74	<a href="#">c1wleB_</a>	Alignment	not modelled	77.2	9	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
75	<a href="#">c2zdiC_</a>	Alignment	not modelled	76.2	19	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> prefoldin subunit alpha; <b>PDBTitle:</b> crystal structure of prefoldin from pyrococcus horikoshii2 ot3
76	<a href="#">c3pe0B_</a>	Alignment	not modelled	76.1	13	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> plectin; <b>PDBTitle:</b> structure of the central region of the plakin domain of plectin
77	<a href="#">c3i2wB_</a>	Alignment	not modelled	75.8	11	<b>PDB header:</b> endocytosis <b>Chain:</b> B: <b>PDB Molecule:</b> syndapin; <b>PDBTitle:</b> crystal structure of efc/f-bar domain of drosophila2 syndapin/pacsin
78	<a href="#">c3hajA_</a>	Alignment	not modelled	74.4	12	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> human pacsin2 f-bar; <b>PDBTitle:</b> crystal structure of human pacsin2 f-bar domain

						(p2121212 lattice)
79	<a href="#">c3ghgD_</a>	Alignment	not modelled	73.4	12	<b>PDB header:</b> blood clotting <b>Chain:</b> D: <b>PDB Molecule:</b> fibrinogen alpha chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
80	<a href="#">d1ykhb1</a>	Alignment	not modelled	72.9	17	<b>Fold:</b> Mediator hinge subcomplex-like <b>Superfamily:</b> Mediator hinge subcomplex-like <b>Family:</b> CSE2-like
81	<a href="#">c1deqD_</a>	Alignment	not modelled	72.9	16	<b>PDB header:</b> <b>PDB COMPND:</b>
82	<a href="#">c1yvlB_</a>	Alignment	not modelled	72.7	7	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> structure of unphosphorylated stat1
83	<a href="#">c3m9bK_</a>	Alignment	not modelled	72.5	19	<b>PDB header:</b> chaperone <b>Chain:</b> K: <b>PDB Molecule:</b> proteasome-associated atpase; <b>PDBTitle:</b> crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
84	<a href="#">c3kltB_</a>	Alignment	not modelled	72.0	9	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of a vimentin fragment
85	<a href="#">d1fioa_</a>	Alignment	not modelled	72.0	8	<b>Fold:</b> STAT-like <b>Superfamily:</b> t-snare proteins <b>Family:</b> t-snare proteins
86	<a href="#">c4aniA_</a>	Alignment	not modelled	71.7	12	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> protein grpe; <b>PDBTitle:</b> structural basis for the intermolecular communication between2 dnak and grpe in the dnak chaperone system from3 geobacillus kaustophilus hta426
87	<a href="#">c3errB_</a>	Alignment	not modelled	71.3	12	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> fusion protein of microtubule binding domain from <b>PDBTitle:</b> microtubule binding domain from mouse cytoplasmic dynein as2 a fusion with seryl-trna synthetase
88	<a href="#">c3u0cA_</a>	Alignment	not modelled	70.8	11	<b>PDB header:</b> cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> invasin ipab; <b>PDBTitle:</b> crystal structure of n-terminal region of type iii secretion first2 translocator ipab (residues 74-224)
89	<a href="#">c3q0xA_</a>	Alignment	not modelled	69.4	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> centriole protein; <b>PDBTitle:</b> n-terminal coiled-coil dimer domain of c. reinhardtii sas-6 homolog2 bld12p
90	<a href="#">c3oa7A_</a>	Alignment	not modelled	68.4	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> head morphogenesis protein, chaotic nuclear migration <b>PDBTitle:</b> structure of the c-terminal domain of cnm67, a core component of the2 spindle pole body of saccharomyces cerevisiae
91	<a href="#">c3peuB_</a>	Alignment	not modelled	67.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoporin gle1; <b>PDBTitle:</b> s. cerevisiae dbp5 l327v c-terminal domain bound to gle1 h337r and ip6
92	<a href="#">c2qjhA_</a>	Alignment	not modelled	66.6	7	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> protein uspa1; <b>PDBTitle:</b> crystal structure of 527-665 fragment of uspa1 protein from2 moraxella catarrhalis
93	<a href="#">d1lvfa_</a>	Alignment	not modelled	64.3	15	<b>Fold:</b> STAT-like <b>Superfamily:</b> t-snare proteins <b>Family:</b> t-snare proteins
94	<a href="#">d1ivsa1</a>	Alignment	not modelled	64.2	15	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> tRNA-binding arm <b>Family:</b> Valyl-tRNA synthetase (ValRS) C-terminal domain
95	<a href="#">d2ap3a1</a>	Alignment	not modelled	64.1	8	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> MW0975(SA0943)-like <b>Family:</b> MW0975(SA0943)-like
96	<a href="#">c3qh9A_</a>	Alignment	not modelled	61.2	19	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> liprin-beta-2; <b>PDBTitle:</b> human liprin-beta2 coiled-coil
97	<a href="#">c3n4xB_</a>	Alignment	not modelled	60.8	18	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> monopolin complex subunit csm1; <b>PDBTitle:</b> structure of csm1 full-length
98	<a href="#">c1gaxB_</a>	Alignment	not modelled	60.5	3	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> valyl-trna synthetase; <b>PDBTitle:</b> crystal structure of thermus thermophilus valyl-trna2 synthetase complexed with trna(val) and valyl-adenylate3 analogue
99	<a href="#">c1gk4A_</a>	Alignment	not modelled	59.2	11	<b>PDB header:</b> vimentin <b>Chain:</b> A: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> human vimentin coil 2b fragment (cys2)
100	<a href="#">c3okqA_</a>	Alignment	not modelled	57.9	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> bud site selection protein 6; <b>PDBTitle:</b> crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
101	<a href="#">c3lllA_</a>	Alignment	not modelled	55.9	12	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c and casein kinase substrate in neurons <b>PDBTitle:</b> crystal structure of mouse pacsin2 f-bar domain
102	<a href="#">c2odvA_</a>	Alignment	not modelled	55.2	15	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> plectin 1; <b>PDBTitle:</b> crystal structure of a fragment of the plakin domain of plectin, cys2 to ala mutant.
103	<a href="#">d1fxka_</a>	Alignment	not modelled	54.4	17	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Prefoldin <b>Family:</b> Prefoldin
						<b>PDB header:</b> contractile protein

104	<a href="#">c1j1eB_</a>	Alignment	not modelled	53.8	17	<b>Chain:</b> B; <b>PDB Molecule:</b> troponin t; <b>PDBTitle:</b> crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
105	<a href="#">c1yv0T_</a>	Alignment	not modelled	52.9	15	<b>PDB header:</b> contractile protein <b>Chain:</b> T; <b>PDB Molecule:</b> troponin t, fast skeletal muscle isoforms; <b>PDBTitle:</b> crystal structure of skeletal muscle troponin in the ca2+-2 free state
106	<a href="#">c2p03A_</a>	Alignment	not modelled	51.8	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-2-macroglobulin receptor-associated <b>PDBTitle:</b> the structure of receptor-associated protein(rap)
107	<a href="#">c3ipdB_</a>	Alignment	not modelled	51.6	11	<b>PDB header:</b> exocytosis <b>Chain:</b> B; <b>PDB Molecule:</b> syntaxin-1a; <b>PDBTitle:</b> helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
108	<a href="#">c3d5cX_</a>	Alignment	not modelled	49.9	20	<b>PDB header:</b> ribosome <b>Chain:</b> X; <b>PDB Molecule:</b> peptide chain release factor 1; <b>PDBTitle:</b> structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
109	<a href="#">c1lwuH_</a>	Alignment	not modelled	49.3	7	<b>PDB header:</b> blood clotting <b>Chain:</b> H; <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of fragment d from lamprey fibrinogen complexed with2 the peptide gly-his-arg-pro-amide
110	<a href="#">c3m3wA_</a>	Alignment	not modelled	48.3	13	<b>PDB header:</b> endocytosis <b>Chain:</b> A; <b>PDB Molecule:</b> protein kinase c and casein kinase ii substrate protein 3; <b>PDBTitle:</b> crystal structure of mouse pacsin3 bar domain mutant
111	<a href="#">c2ve7A_</a>	Alignment	not modelled	48.1	12	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> kinetochore protein hec1, kinetochore protein spc25; <b>PDBTitle:</b> crystal structure of a bonsai version of the human ndc802 complex
112	<a href="#">d1j1ja_</a>	Alignment	not modelled	47.5	8	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Translin <b>Family:</b> Translin
113	<a href="#">d1k4ta1</a>	Alignment	not modelled	47.3	17	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Eukaryotic DNA topoisomerase I, dispensable insert domain <b>Family:</b> Eukaryotic DNA topoisomerase I, dispensable insert domain
114	<a href="#">c3sfvB_</a>	Alignment	not modelled	47.3	19	<b>PDB header:</b> protein transport/protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> lida protein, substrate of the dot/icm system; <b>PDBTitle:</b> crystal structure of the gdp-bound rab1a s25n mutant in complex with2 the coiled-coil domain of lida from legionella pneumophila
115	<a href="#">c3vbbB_</a>	Alignment	not modelled	47.1	18	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> seryl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase from human at 2.9 angstroms
116	<a href="#">c3dpgE_</a>	Alignment	not modelled	46.2	11	<b>PDB header:</b> chaperone, peptide binding protein <b>Chain:</b> E; <b>PDB Molecule:</b> chaperone protein dnak; <b>PDBTitle:</b> crystal structure of the substrate binding domain of e.2 coli dnak in complex with a long pyrrococin-derived3 inhibitor peptide (form b)
117	<a href="#">c2d4yA_</a>	Alignment	not modelled	45.6	14	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> flagellar hook-associated protein 1; <b>PDBTitle:</b> crystal structure of a 49k fragment of hap1 (flgk)
118	<a href="#">c3g67A_</a>	Alignment	not modelled	45.3	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of a soluble chemoreceptor from thermotoga2 maritima
119	<a href="#">c1ekuA_</a>	Alignment	not modelled	44.6	12	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> interferon gamma; <b>PDBTitle:</b> crystal structure of a biologically active single chain2 mutant of human ifn-gamma
120	<a href="#">c3cvfA_</a>	Alignment	not modelled	44.3	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> homer protein homolog 3; <b>PDBTitle:</b> crystal structure of the carboxy terminus of homer3