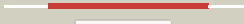

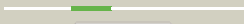
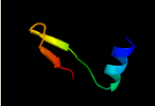
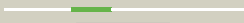


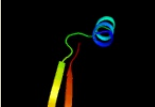

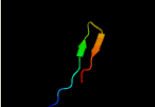

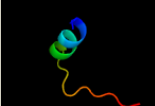





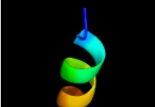






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2012 (-) _2259334_2259828
Date	Mon Aug 5 13:25:12 BST 2019
Unique Job ID	c2448e89b3173845

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2hh8a1</a>	 Alignment		99.9	17	<b>Fold:</b> YdfO-like <b>Superfamily:</b> YdfO-like <b>Family:</b> YdfO-like
2	<a href="#">c2qlxA</a>	 Alignment		58.8	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnose mutarotase; <b>PDBTitle:</b> crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
3	<a href="#">c2qlwA</a>	 Alignment		58.8	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> rhau; <b>PDBTitle:</b> crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
4	<a href="#">c6hhnA</a>	 Alignment		58.6	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnose mutarotase; <b>PDBTitle:</b> crystal structure of l-rhamnose mutarotase fa22100 from formosa2 agariphila
5	<a href="#">c6gzuA</a>	 Alignment		40.9	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved membrane protein; <b>PDBTitle:</b> structure of chlamydia abortus effector protein chladub
6	<a href="#">d1x8da1</a>	 Alignment		34.3	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> YiIL-like
7	<a href="#">c1lrjG</a>	 Alignment		32.5	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> migration inhibitory factor-related protein 14; <b>PDBTitle:</b> crystal structure of the mrp14 complexed with chaps
8	<a href="#">c1sn9D</a>	 Alignment		31.2	41	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> tetrameric beta-beta-alpha mini-protein; <b>PDBTitle:</b> an oligomeric domain-swapped beta-beta-alpha mini-protein
9	<a href="#">c1sn9C</a>	 Alignment		31.2	41	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> tetrameric beta-beta-alpha mini-protein; <b>PDBTitle:</b> an oligomeric domain-swapped beta-beta-alpha mini-protein
10	<a href="#">c1sn9A</a>	 Alignment		31.2	41	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> tetrameric beta-beta-alpha mini-protein; <b>PDBTitle:</b> an oligomeric domain-swapped beta-beta-alpha mini-protein
11	<a href="#">c1sn9B</a>	 Alignment		31.2	41	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> tetrameric beta-beta-alpha mini-protein; <b>PDBTitle:</b> an oligomeric domain-swapped beta-beta-alpha mini-protein

12	<a href="#">d1j55a_</a>	Alignment		21.0	28	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins
13	<a href="#">c3h4sE_</a>	Alignment		20.8	22	<b>PDB header:</b> motor protein/calcium binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> kcbp interacting ca2+-binding protein; <b>PDBTitle:</b> structure of the complex of a mitotic kinesin with its2 calcium binding regulator
14	<a href="#">d1m39a_</a>	Alignment		20.2	23	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
15	<a href="#">c2m0rA_</a>	Alignment		19.0	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein s100-a14; <b>PDBTitle:</b> solution structure and dynamics of human s100a14
16	<a href="#">d1k8ua_</a>	Alignment		18.8	15	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins
17	<a href="#">c1ponB_</a>	Alignment		18.5	36	<b>PDB header:</b> calcium-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> troponin c; <b>PDBTitle:</b> site iii-site iv troponin c heterodimer, nmr
18	<a href="#">c4il1A_</a>	Alignment		18.5	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> calmodulin, calcineurin subunit b type 1, serine/threonine- <b>PDBTitle:</b> crystal structure of the rat calcineurin
19	<a href="#">c4pcwD_</a>	Alignment		18.3	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> filaggrin; <b>PDBTitle:</b> crystal structure of the n-terminal domain of human profilaggrin at2 2.2 a resolution
20	<a href="#">d1xk4c1</a>	Alignment		18.2	27	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins
21	<a href="#">c2aucC_</a>	Alignment	not modelled	17.5	17	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> myosin a tail interacting protein; <b>PDBTitle:</b> structure of the plasmodium mtip-myoa complex, a key component of the2 parasite invasion motor
22	<a href="#">d1c7va_</a>	Alignment	not modelled	17.0	14	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
23	<a href="#">c4pl8H_</a>	Alignment	not modelled	16.8	38	<b>PDB header:</b> contractile protein/structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> thymosin beta-4,protein cordon-bleu,thymosin beta-4; <b>PDBTitle:</b> structure of rabbit skeletal muscle actin in complex with a hybrid2 peptide comprising thymosin beta4 and the lysine-rich region of3 cordon-bleu
24	<a href="#">c3vnnA_</a>	Alignment	not modelled	16.5	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase 4; <b>PDBTitle:</b> crystal structure of a sub-domain of the nucleotidyltransferase2 (adenylation) domain of human dna ligase iv
25	<a href="#">d3elga1</a>	Alignment	not modelled	16.3	21	<b>Fold:</b> BLIP-like <b>Superfamily:</b> BT0923-like <b>Family:</b> BT0923-like
26	<a href="#">d2imja1</a>	Alignment	not modelled	15.6	26	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PFL3262-like
27	<a href="#">c5x2eA_</a>	Alignment	not modelled	15.4	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> tegumental protein 20.8 kda; <b>PDBTitle:</b> crystal structure of calmodulin like domain of cstal3 (1-81aa)
28	<a href="#">c2x5cB_</a>	Alignment	not modelled	15.1	26	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein orf131; <b>PDBTitle:</b> crystal structure of hypothetical protein orf131 from

						pyrobaculum2 spherical virus <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> exoenzyme s synthesis regulatory protein exsa; <b>PDBTitle:</b> crystal structure of the exsa regulatory domain
29	<a href="#">c4zuaA_</a>	Alignment	not modelled	15.1	22	
30	<a href="#">c2lv7A_</a>	Alignment	not modelled	15.0	29	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-binding protein 7; <b>PDBTitle:</b> solution structure of ca2+-bound cabp7 n-terminal doman
31	<a href="#">d1ttea1</a>	Alignment	not modelled	14.8	43	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
32	<a href="#">d4icba_</a>	Alignment	not modelled	14.6	28	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calbindin D9K
33	<a href="#">c2vrgA_</a>	Alignment	not modelled	14.3	17	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> multiple coagulation factor deficiency protein 2; <b>PDBTitle:</b> structure of human mcfd2
34	<a href="#">d1r2ua_</a>	Alignment	not modelled	14.2	23	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
35	<a href="#">c3b5xB_</a>	Alignment	not modelled	14.2	11	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba; <b>PDBTitle:</b> crystal structure of msba from vibrio cholerae
36	<a href="#">c2ldyA_</a>	Alignment	not modelled	14.2	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> orf1 codes for a 40 kda product; <b>PDBTitle:</b> solution structure of the rmm-ctd domains of human line-1 orf1p
37	<a href="#">c3fs7D_</a>	Alignment	not modelled	13.8	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> parvalbumin, thymic; <b>PDBTitle:</b> crystal structure of gallus gallus beta-parvalbumin (avian thymic2 hormone)
38	<a href="#">c3jbhl_</a>	Alignment	not modelled	13.6	9	<b>PDB header:</b> contractile protein <b>Chain:</b> I: <b>PDB Molecule:</b> myosin 2 essential light chain striated muscle; <b>PDBTitle:</b> two heavy meromyosin interacting-heads motifs flexible docked into2 tarantula thick filament 3d-map allows in depth study of intra- and3 intermolecular interactions
39	<a href="#">d2pq3a1</a>	Alignment	not modelled	13.4	27	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
40	<a href="#">c1zmzA_</a>	Alignment	not modelled	13.0	9	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> centrin-2; <b>PDBTitle:</b> solution structure of the n-terminal domain (m1-s98) of2 human centrin 2
41	<a href="#">d1xk4a1</a>	Alignment	not modelled	13.0	15	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins
42	<a href="#">c6b12B_</a>	Alignment	not modelled	12.9	41	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> tni2; <b>PDBTitle:</b> structure of tne2 in complex with tni2
43	<a href="#">c3l23A_</a>	Alignment	not modelled	12.8	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
44	<a href="#">d1wrka1</a>	Alignment	not modelled	12.8	19	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
45	<a href="#">d2obha1</a>	Alignment	not modelled	12.5	23	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
46	<a href="#">c2kluA_</a>	Alignment	not modelled	12.3	35	<b>PDB header:</b> immune system, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd4; <b>PDBTitle:</b> nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
47	<a href="#">d1m45a_</a>	Alignment	not modelled	12.2	24	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
48	<a href="#">d1wlza1</a>	Alignment	not modelled	12.1	14	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
49	<a href="#">c5tbyC_</a>	Alignment	not modelled	12.1	17	<b>PDB header:</b> contractile protein <b>Chain:</b> C: <b>PDB Molecule:</b> myosin light chain 3; <b>PDBTitle:</b> human beta cardiac heavy meromyosin interacting-heads motif obtained2 by homology modeling (using swiss-model) of human sequence from3 aphonopelma homology model (pdb-3jhb), rigidly fitted to human beta-4 cardiac negatively stained thick filament 3d-reconstruction (emd-5 2240)
50	<a href="#">d1fw4a_</a>	Alignment	not modelled	12.1	18	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
51	<a href="#">c6ozdB_</a>	Alignment	not modelled	12.0	18	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of putative exported protein (bpss2145) from2 burkholderia pseudomallei k96243
52	<a href="#">c1ozsA_</a>	Alignment	not modelled	12.0	16	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin c, slow skeletal and cardiac muscles; <b>PDBTitle:</b> c-domain of human cardiac troponin c in complex with the2 inhibitory region of human cardiac troponin i
53	<a href="#">c2kvaA_</a>	Alignment	not modelled	11.9	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein s100-a5;

53	<a href="#">c2k9aA_</a>	Alignment	not modelled	11.9	19	<b>PDBTitle:</b> solution structure and dynamics of s100a5 in the apo and2 ca2+ -bound states
54	<a href="#">c2rgiA_</a>	Alignment	not modelled	11.8	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein s100-a2; <b>PDBTitle:</b> crystal structure of ca2+-free s100a2 at 1.6 a resolution
55	<a href="#">c3lcpC_</a>	Alignment	not modelled	11.7	18	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> multiple coagulation factor deficiency protein 2; <b>PDBTitle:</b> crystal structure of the carbohydrate recognition domain of lman1 in2 complex with mcf2
56	<a href="#">c2m28A_</a>	Alignment	not modelled	11.6	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-binding protein 4; <b>PDBTitle:</b> nmr structure of ca2+ bound cabp4 c-domain
57	<a href="#">d1yuta1</a>	Alignment	not modelled	11.4	16	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins
58	<a href="#">c1wizD_</a>	Alignment	not modelled	11.3	14	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> cap-binding protein complex interacting protein <b>PDBTitle:</b> crystal structure of djbp fragment which was obtained by2 limited proteolysis
59	<a href="#">c2m1uA_</a>	Alignment	not modelled	11.3	25	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin light chain mlcb; <b>PDBTitle:</b> solution structure of the small dictyostelium discoideium myosin light2 chain mlcb provides insights into iq-motif recognition of class i3 myosin myo1b
60	<a href="#">d3d37a1</a>	Alignment	not modelled	11.2	17	<b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
61	<a href="#">c2kn2A_</a>	Alignment	not modelled	11.2	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calmodulin; <b>PDBTitle:</b> solution structure of the c-terminal domain of soybean calmodulin2 isoform 4 fused with the calmodulin-binding domain of ntmkp1
62	<a href="#">d1e8aa_</a>	Alignment	not modelled	11.2	28	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins
63	<a href="#">d1dtla_</a>	Alignment	not modelled	10.8	18	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
64	<a href="#">d1n0yb_</a>	Alignment	not modelled	10.8	15	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
65	<a href="#">c3obeB_</a>	Alignment	not modelled	10.7	33	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
66	<a href="#">c5mkkB_</a>	Alignment	not modelled	10.6	18	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> multidrug resistance abc transporter atp-binding and <b>PDBTitle:</b> crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
67	<a href="#">d1pvaa_</a>	Alignment	not modelled	10.6	26	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Parvalbumin
68	<a href="#">c2k2aA_</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin c; <b>PDBTitle:</b> solution structure of the apo c terminal domain of lethocerus troponin2 c isoform f1
69	<a href="#">c2pmyB_</a>	Alignment	not modelled	10.5	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ras and ef-hand domain-containing protein; <b>PDBTitle:</b> ef-hand domain of human rasef
70	<a href="#">c2derA_</a>	Alignment	not modelled	10.1	22	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna-specific 2-thiouridylyase mnma; <b>PDBTitle:</b> cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
71	<a href="#">c2qdrA_</a>	Alignment	not modelled	10.1	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative dioxygenase (npun_f5605) from nostoc2 punctiforme pcc 73102 at 2.60 a resolution
72	<a href="#">c2k7bA_</a>	Alignment	not modelled	9.9	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-binding protein 1; <b>PDBTitle:</b> nmr structure of mg2+-bound cabp1 n-domain
73	<a href="#">d1ksoa_</a>	Alignment	not modelled	9.9	12	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins
74	<a href="#">d5pala_</a>	Alignment	not modelled	9.8	33	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Parvalbumin
75	<a href="#">c2m97A_</a>	Alignment	not modelled	9.8	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> optimized ratiometric calcium sensor; <b>PDBTitle:</b> optimized ratiometric calcium sensors for functional in vivo imaging2 of neurons and t-lymphocytes
76	<a href="#">c1eg4A_</a>	Alignment	not modelled	9.7	15	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> dystrophin; <b>PDBTitle:</b> structure of a dystrophin ww domain fragment in complex2 with a beta-dystroglycan peptide
77	<a href="#">c6ccia_</a>	Alignment	not modelled	9.7	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein eskimo 1; <b>PDBTitle:</b> the crystal structure of xoat1
78	<a href="#">c2l0vB_</a>	Alignment	not modelled	9.6	29	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein s100-a16;

					<b>PDBTitle:</b> solution structure of calcium(ii) bound s100a16
79	<a href="#">d1jc2a_</a>	Alignment	not modelled	9.6	19 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
80	<a href="#">c1jc2A_</a>	Alignment	not modelled	9.6	19 <b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> troponin c, skeletal muscle; <b>PDBTitle:</b> complex of the c-domain of troponin c with residues 1-40 of2 troponin i
81	<a href="#">c5ve9B_</a>	Alignment	not modelled	9.5	33 <b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> microtubule-actin cross-linking factor 1, isoforms 1/2/3/5; <b>PDBTitle:</b> structure of hacf7 ef1-ef2-gar domains
82	<a href="#">c2m29A_</a>	Alignment	not modelled	9.5	18 <b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> calcium-binding protein 4; <b>PDBTitle:</b> nmr structure of ca2+ bound cabp4 n-domain
83	<a href="#">c4fq5B_</a>	Alignment	not modelled	9.5	21 <b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> maleate cis-trans isomerase; <b>PDBTitle:</b> crystal structure of the maleate isomerase iso(c200a) from pseudomonas2 putida s16 with maleate
84	<a href="#">c2amiA_</a>	Alignment	not modelled	9.4	16 <b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> caltractin; <b>PDBTitle:</b> solution structure of the calcium-loaded n-terminal sensor domain of2 centrin
85	<a href="#">d1f53a_</a>	Alignment	not modelled	9.4	19 <b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Killer toxin-like protein SKLP
86	<a href="#">d1k9ua_</a>	Alignment	not modelled	9.3	15 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Polcalcin
87	<a href="#">d1topa_</a>	Alignment	not modelled	9.2	23 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
88	<a href="#">c2vtgA_</a>	Alignment	not modelled	9.2	14 <b>PDB header:</b> metal-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> ionized calcium-binding adapter molecule 2; <b>PDBTitle:</b> crystal structure of human iba2, trigonal crystal form
89	<a href="#">c2e75C_</a>	Alignment	not modelled	9.2	55 <b>PDB header:</b> photosynthesis <b>Chain:</b> C; <b>PDB Molecule:</b> apocytochrome f; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
90	<a href="#">c2ggmA_</a>	Alignment	not modelled	9.2	23 <b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> centrin-2; <b>PDBTitle:</b> human centrin 2 xeroderma pigmentosum group c protein2 complex
91	<a href="#">d1qx2a_</a>	Alignment	not modelled	9.1	20 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calbindin D9K
92	<a href="#">d1ggza_</a>	Alignment	not modelled	9.1	23 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
93	<a href="#">c3ox6C_</a>	Alignment	not modelled	9.1	18 <b>PDB header:</b> calcium binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> calcium-binding protein 1; <b>PDBTitle:</b> crystal structure of the calcium sensor calcium-binding protein 12 (cabp1)
94	<a href="#">d3e46a1</a>	Alignment	not modelled	9.1	60 <b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
95	<a href="#">d2f3ga_</a>	Alignment	not modelled	9.0	22 <b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
96	<a href="#">d1tiza_</a>	Alignment	not modelled	8.8	18 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
97	<a href="#">d1oqpa_</a>	Alignment	not modelled	8.7	7 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
98	<a href="#">d1br1b_</a>	Alignment	not modelled	8.6	18 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
99	<a href="#">d1qlka_</a>	Alignment	not modelled	8.6	28 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins