Phyre2

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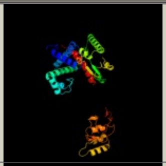
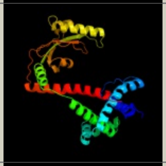
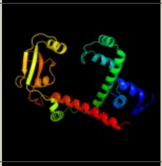
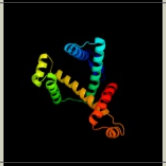
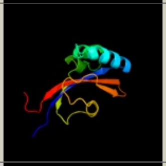
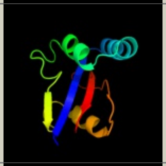
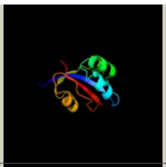
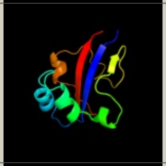
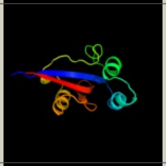
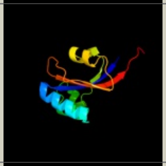
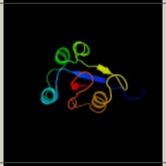
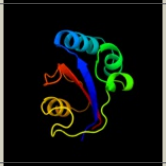
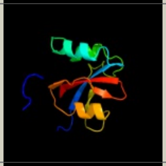
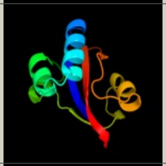
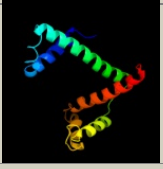
Description	P0ADY1
Date	Thu Jan 5 11:22:05 GMT 2012
Unique Job ID	ae0950031df61d5c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1m5yB_	Alignment		100.0	22	**PDB header:**isomerase, cell cycle **Chain:** B: **PDB Molecule:**survival protein sura; **PDBTitle:** crystallographic structure of sura, a molecular chaperone2 that facilitates outer membrane porin folding
2	c3nrkA_	Alignment		100.0	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**lic12922; **PDBTitle:** the crystal structure of the leptospiral hypothetical protein lic12922
3	c2pv3B_	Alignment		100.0	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**chaperone sura; **PDBTitle:** crystallographic structure of sura fragment lacking the second2 peptidyl-prolyl isomerase domain complexed with peptide nftlkfwdifrk
4	c3rgcB_	Alignment		100.0	16	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**possible periplasmic protein; **PDBTitle:** the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally related sura-like chaperones in the human pathogen3 campylobacter jejuni
5	c3rfwA_	Alignment		100.0	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cell-binding factor 2; **PDBTitle:** the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally-related sura-like chaperones in the human pathogen3 campylobacter jejuni
6	d1m5ya1	Alignment		99.9	24	**Fold:**Triger factor/SurA peptide-binding domain-like **Superfamily:**Triger factor/SurA peptide-binding domain-like **Family:**Porin chaperone SurA, peptide-binding domain
7	c2kgjA_	Alignment		99.8	96	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase d; **PDBTitle:** solution structure of parvulin domain of ppid from e.coli
8	c2rqsA_	Alignment		99.8	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**parvulin-like peptidyl-prolyl isomerase; **PDBTitle:** 3d structure of pin from the psychrophilic archeon cenarcheaum2 symbiosum (cspin)
9	d1pina2	Alignment		99.8	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
10	d1jnsa_	Alignment		99.8	22	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
11	c1yw5A_	Alignment		99.8	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl prolyl cis/trans isomerase; **PDBTitle:** peptidyl-prolyl isomerase ess1 from candida albicans

12	c2jzvA_	Alignment		99.8	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** solution structure of s. aureus prsa-ppiase
13	d1eq3a_	Alignment		99.8	20	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
14	d1m5ya3	Alignment		99.8	31	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
15	c3gpkA_	Alignment		99.8	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ppic-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution.
16	d1j6ya_	Alignment		99.8	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
17	c1zk6A_	Alignment		99.8	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** nmr solution structure of b. subtilis prsa ppiase
18	c1f8aB_	Alignment		99.8	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase nima- **PDBTitle:** structural basis for the phosphoserine-proline recognition2 by group iv ww domains
19	d2pv2a1	Alignment		99.7	38	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
20	c3gtyX_	Alignment		97.2	15	**PDB header:**chaperone/ribosomal protein **Chain:** X: **PDB Molecule:**trigger factor; **PDBTitle:** promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
21	c2nsaA_	Alignment	not modelled	97.1	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** structures of and interactions between domains of trigger factor from2 themotoga maritim
22	c1w26B_	Alignment	not modelled	96.9	17	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
23	d1w26a1	Alignment	not modelled	96.6	17	**Fold:**Triger factor/SurA peptide-binding domain-like **Superfamily:**Triger factor/SurA peptide-binding domain-like **Family:**TF C-terminus
24	c1t11A_	Alignment	not modelled	94.8	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor
25	d1t11a1	Alignment	not modelled	94.2	21	**Fold:**Triger factor/SurA peptide-binding domain-like **Superfamily:**Triger factor/SurA peptide-binding domain-like **Family:**TF C-terminus
26	c2fcdA_	Alignment	not modelled	35.0	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**myosin light chain 1; **PDBTitle:** solution structure of n-lobe myosin light chain from2 saccharomices cerevisiae
27	d1wdcb_	Alignment	not modelled	25.9	14	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
28	c2dguA_	Alignment	not modelled	20.7	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein q; **PDBTitle:** solution structure of the rna binding domain in2 heterogeneous nuclear ribonucleoprotein q

29	c2osqA_	Alignment	not modelled	18.0	6	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nucleolar protein 3; **PDBTitle:** nmr structure of rrm-1 of yeast npl3 protein
30	c3fkkA_	Alignment	not modelled	15.7	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
31	c2phcB_	Alignment	not modelled	14.9	36	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
32	c3mmlD_	Alignment	not modelled	14.4	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
33	c2dgtA_	Alignment	not modelled	12.6	6	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-binding protein 30; **PDBTitle:** solution structure of the second rna binding domain in rna-2 binding protein 30
34	c2zp2B_	Alignment	not modelled	12.5	18	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
35	d1wrka1	Alignment	not modelled	12.1	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
36	c3ipdB_	Alignment	not modelled	11.5	21	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
37	c1slmA_	Alignment	not modelled	11.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
38	d2phcb1	Alignment	not modelled	11.1	36	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
39	d1u14a_	Alignment	not modelled	10.9	15	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
40	d1j7ga_	Alignment	not modelled	10.6	6	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
41	d1sknp_	Alignment	not modelled	10.4	21	**Fold:**A DNA-binding domain in eukaryotic transcription factors **Superfamily:**A DNA-binding domain in eukaryotic transcription factors **Family:**A DNA-binding domain in eukaryotic transcription factors
42	d1ggwa_	Alignment	not modelled	10.1	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
43	d1zata2	Alignment	not modelled	10.0	18	**Fold:**L,D-transpeptidase pre-catalytic domain-like **Superfamily:**L,D-transpeptidase pre-catalytic domain-like **Family:**L,D-transpeptidase pre-catalytic domain-like
44	c2dnqA_	Alignment	not modelled	9.7	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-binding protein 4b; **PDBTitle:** solution structure of rna binding domain 1 in rna-binding2 protein 30
45	c2dnpA_	Alignment	not modelled	9.3	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna-binding protein 14; **PDBTitle:** solution structure of rna binding domain 2 in rna-binding2 protein 14
46	c2jvoA_	Alignment	not modelled	8.6	6	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nucleolar protein 3; **PDBTitle:** segmental isotope labeling of npl3
47	c2ekwC_	Alignment	not modelled	8.5	15	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**myosin catalytic light chain lc-1, mantle muscle; **PDBTitle:** the crystal structure of squid myosin s1 in the presence of2 so4 2-
48	d1qv0a_	Alignment	not modelled	8.4	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
49	d1oqpa_	Alignment	not modelled	8.3	20	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
50	d2cxaa1	Alignment	not modelled	8.1	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**LFTR-like
51	c2cxaA_	Alignment	not modelled	8.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucyl/phenylalanyl-trna-protein transferase; **PDBTitle:** crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
52	d1wi6a1	Alignment	not modelled	8.1	6	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
53	c2kz2A_	Alignment	not modelled	8.0	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calmodulin; **PDBTitle:** calmodulin, c-terminal domain, f92e mutant
54	c2oy6B_	Alignment	not modelled	7.8	19	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin regulatory light chain lc-2; **PDBTitle:** crystal structure of squid mg.adp myosin s1
55	c2d58A_	Alignment	not modelled	7.7	12	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**allograft inflammatory factor 1;

						PDBTitle: human microglia-specific protein iba1
56	d2e74h1	Alignment	not modelled	7.7	11	**Fold:**Single transmembrane helix **Superfamily:**PetN subunit of the cytochrome b6f complex **Family:**PetN subunit of the cytochrome b6f complex
57	c1vf5H_	Alignment	not modelled	7.5	13	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**protein pet n; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
58	c1vf5U_	Alignment	not modelled	7.5	13	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**protein pet n; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
59	c2d2cU_	Alignment	not modelled	7.5	13	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**cytochrome b6-f complex subunit viii; **PDBTitle:** crystal structure of cytochrome b6f complex with dbmib from2 m. laminosus
60	c2d2cH_	Alignment	not modelled	7.5	13	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit viii; **PDBTitle:** crystal structure of cytochrome b6f complex with dbmib from2 m. laminosus
61	d1fw4a_	Alignment	not modelled	7.5	20	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
62	c2a4jA_	Alignment	not modelled	7.5	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**centrin 2; **PDBTitle:** solution structure of the c-terminal domain (t94-y172) of2 the human centrin 2 in complex with a 17 residues peptide3 (p1-xpc) from xeroderma pigmentosum group c protein
63	c3eb2A_	Alignment	not modelled	7.5	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
64	c3sibA_	Alignment	not modelled	7.5	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ure3-bp sequence specific dna binding protein; **PDBTitle:** crystal structure of ure3-binding protein, wild-type
65	c2e76H_	Alignment	not modelled	7.3	11	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
66	c2e75H_	Alignment	not modelled	7.3	11	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
67	c2e74H_	Alignment	not modelled	7.3	11	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**cytochrome b6-f complex subunit 8; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
68	d1c07a_	Alignment	not modelled	7.2	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
69	d2hg7a1	Alignment	not modelled	7.0	16	**Fold:**gpW/XkdW-like **Superfamily:**XkdW-like **Family:**XkdW-like
70	c2hg7A_	Alignment	not modelled	7.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage-like element pbsx protein xkdw; **PDBTitle:** solution nmr structure of phage-like element pbsx protein2 xkdw, northeast structural genomics consortium target sr355
71	c3oepA_	Alignment	not modelled	6.9	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0988; **PDBTitle:** crystal structure of ttha0988 in space group p43212
72	d1lkja_	Alignment	not modelled	6.9	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
73	d1wg1a_	Alignment	not modelled	6.9	6	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
74	d1ap4a_	Alignment	not modelled	6.8	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
75	c2kz5A_	Alignment	not modelled	6.8	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor nf-e2 45 kda subunit; **PDBTitle:** solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
76	c1djyB_	Alignment	not modelled	6.7	10	**PDB header:**lipid degradation **Chain:** B: **PDB Molecule:**phosphoinositide-specific phospholipase c, **PDBTitle:** phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate
77	c2kgrA_	Alignment	not modelled	6.7	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** solution structure of protein itsn1 from homo sapiens.2 northeast structural genomics consortium target hr5524a
78	c1jc2A_	Alignment	not modelled	6.7	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, skeletal muscle; **PDBTitle:** complex of the c-domain of troponin c with residues 1-40 of2 troponin i
79	d1jc2a_	Alignment	not modelled	6.7	14	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
80	c2amiA_	Alignment	not modelled	6.6	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**caltractin; **PDBTitle:** solution structure of the calcium-loaded n-terminal sensor2 domain of centrin

81	c1wsuA_	Alignment	not modelled	6.6	11	**PDB header:**translation/rna **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** c-terminal domain of elongation factor selb complexed with2 secis rna
82	c3aqpB_	Alignment	not modelled	6.5	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
83	d1whya_	Alignment	not modelled	6.5	16	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
84	d1wdcc_	Alignment	not modelled	6.4	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
85	d1whza_	Alignment	not modelled	6.4	21	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like
86	d1stza1	Alignment	not modelled	6.3	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
87	c2voyB_	Alignment	not modelled	6.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
88	c2k7bA_	Alignment	not modelled	6.2	9	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcium-binding protein 1; **PDBTitle:** nmr structure of mg2+-bound cabp1 n-domain
89	c2xnqA_	Alignment	not modelled	6.1	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nuclear polyadenylated rna-binding protein 3; **PDBTitle:** structural insights into cis element recognition of non-2 polyadenylated rnas by the nab3-rrm
90	c2k29A_	Alignment	not modelled	6.1	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
91	d1kf6c_	Alignment	not modelled	6.1	11	**Fold:**Heme-binding four-helical bundle **Superfamily:**Fumarate reductase respiratory complex transmembrane subunits **Family:**Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
92	c2ytcA_	Alignment	not modelled	6.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor rbm22; **PDBTitle:** solution structure of rna binding domain in pre-mrna-2 splicing factor rbm22
93	d1whxa_	Alignment	not modelled	6.0	16	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
94	c2k1lB_	Alignment	not modelled	6.0	24	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
95	c2k1kB_	Alignment	not modelled	6.0	24	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
96	c2k1kA_	Alignment	not modelled	6.0	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
97	c2k1lA_	Alignment	not modelled	6.0	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
98	c3hkzY_	Alignment	not modelled	6.0	10	**PDB header:**transferase **Chain:** Y: **PDB Molecule:**dna-directed rna polymerase subunit 13; **PDBTitle:** the x-ray crystal structure of rna polymerase from archaea
99	c2ktgA_	Alignment	not modelled	6.0	17	**PDB header:**ca-binding protein **Chain:** A: **PDB Molecule:**calmodulin, putative; **PDBTitle:** calmodulin like protein from entamoeba histolytica: solution structure2 and calcium binding properties of a partially folded protein