Phyre2

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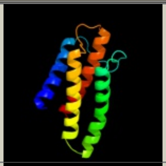
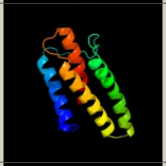
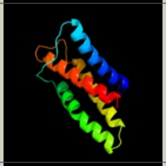
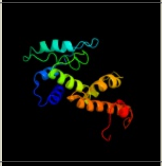
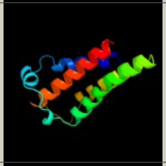
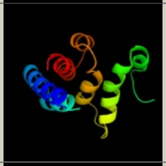
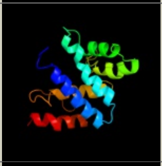
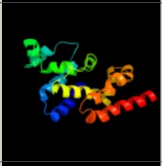
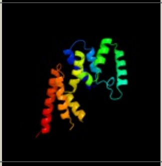
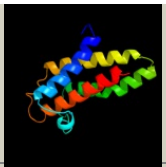
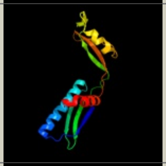
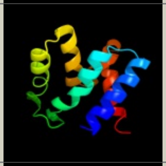
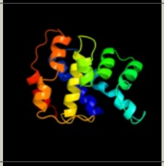
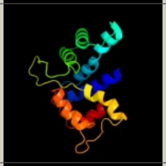
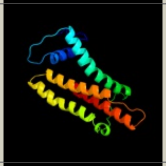
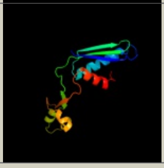
Description	P00961
Date	Wed Jan 25 15:20:10 GMT 2012
Unique Job ID	46276fdd3490e129

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1f7ua1	Alignment		99.4	20	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
2	c1f7uA_	Alignment		98.4	20	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg
3	c2zufA_	Alignment		98.0	17	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
4	c1iq0A_	Alignment		97.9	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** thermus thermophilus arginyl-trna synthetase
5	c3gw7A_	Alignment		97.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein yedj; **PDBTitle:** crystal structure of a metal-dependent phosphohydrolase2 with conserved hd domain (yedj) from escherichia coli in3 complex with nickel ions. northeast structural genomics4 consortium target er63
6	d1iq0a1	Alignment		97.6	19	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
7	c2o08B_	Alignment		97.5	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bh1327 protein; **PDBTitle:** crystal structure of a putative hd superfamily hydrolase (bh1327) from2 bacillus halodurans at 1.90 a resolution
8	d2pq7a1	Alignment		97.3	20	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
9	d2pjqa1	Alignment		97.3	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
10	d2qgsa1	Alignment		97.2	14	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
11	c3ccgA_	Alignment		97.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd superfamily hydrolase; **PDBTitle:** crystal structure of predicted hd superfamily hydrolase involved in2 nad metabolism (np_347894.1) from clostridium acetobutylicum at 1.503 a resolution

12	c3fnrA_	Alignment		97.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of putative arginyl t-rna synthetase from2 campylobacter jejuni;
13	c2ogiA_	Alignment		96.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein sag1661; **PDBTitle:** crystal structure of a putative metal dependent phosphohydrolase2 (sag1661) from streptococcus agalactiae serogroup v at 1.85 a3 resolution
14	d1r89a3	Alignment		96.7	12	**Fold:**Ferredoxin-like **Superfamily:**PAP/Archaeal CCA-adding enzyme, C-terminal domain **Family:**Archaeal tRNA CCA-adding enzyme
15	d3djba1	Alignment		96.3	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
16	c3hc1A_	Alignment		95.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized hdod domain protein; **PDBTitle:** crystal structure of hdod domain protein with unknown function2 (np_953345.1) from geobacter sulfurreducens at 1.90 a resolution
17	c3m1tA_	Alignment		95.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of putative phosphohydrolase (yp_929327.1) from2 shewanella amazonensis sb2b at 1.62 a resolution
18	c2x1lC_	Alignment		95.6	16	**PDB header:**ligase **Chain:** C: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of mycobacterium smegmatis methionyl-trna2 synthetase in complex with methionine and adenosine
19	d3dtoa1	Alignment		95.6	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
20	c1sz1A_	Alignment		94.4	13	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna nucleotidyltransferase; **PDBTitle:** mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
21	c3kflA_	Alignment	not modelled	94.3	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
22	d3b57a1	Alignment	not modelled	94.2	13	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
23	c1pfuA_	Alignment	not modelled	93.6	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate
24	c2ct8A_	Alignment	not modelled	92.3	18	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 anologue
25	c1rqgA_	Alignment	not modelled	91.2	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from pyrococcus abyssi
26	c1woyA_	Alignment	not modelled	88.8	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
27	c2ztgA_	Alignment	not modelled	87.8	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase lacking the c-terminal dimerization domain in3 complex with ala-sa
28	d1ynba1	Alignment	not modelled	87.6	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain

29	c2cqzA_	Alignment	not modelled	85.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**177aa long hypothetical protein; **PDBTitle:** crystal structure of ph0347 protein from pyrococcus horikoshii ot3
30	c3i7aA_	Alignment	not modelled	82.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent phosphohydrolase; **PDBTitle:** crystal structure of putative metal-dependent phosphohydrolase2 (yp_926882.1) from shewanella amazonensis sb2b at 2.06 a resolution
31	d1pfva1	Alignment	not modelled	79.0	12	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
32	c2zzfA_	Alignment	not modelled	73.5	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of alanyl-trna synthetase without2 oligomerization domain
33	d2paqa1	Alignment	not modelled	72.1	9	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
34	d1rqga1	Alignment	not modelled	67.7	11	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
35	d1vqra_	Alignment	not modelled	67.4	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**modified HD domain
36	c3d5lA_	Alignment	not modelled	63.9	5	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of regulatory protein recx
37	d1xx7a_	Alignment	not modelled	63.0	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
38	d1riqa1	Alignment	not modelled	54.4	15	**Fold:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Superfamily:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Family:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
39	c3mzoA_	Alignment	not modelled	51.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lin2634 protein; **PDBTitle:** crystal structure of a hd-domain phosphohydrolase (lin2634) from2 listeria innocua at 1.98 a resolution
40	c3sp1B_	Alignment	not modelled	48.2	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** crystal structure of cysteinyl-trna synthetase (cyss) from borrelia2 burgdorferi
41	c1yfsB_	Alignment	not modelled	45.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
42	c2k89A_	Alignment	not modelled	38.4	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phospholipase a-2-activating protein; **PDBTitle:** solution structure of a novel ubiquitin-binding domain from2 human plaa (pfuc, gly76-pro77 cis isomer)
43	c1sb7A_	Alignment	not modelled	38.4	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase d; **PDBTitle:** crystal structure of the e.coli pseudouridine synthase trud
44	c1z2zB_	Alignment	not modelled	38.0	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**probable trna pseudouridine synthase d; **PDBTitle:** crystal structure of the putative trna pseudouridine2 synthase d (trud) from methanosarcina mazei, northeast3 structural genomics target mar1
45	c2gfnA_	Alignment	not modelled	37.9	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator pksa related protein; **PDBTitle:** crystal structure of hth-type transcriptional regulator pksa related2 protein from rhodococcus sp. rha1
46	d1pkxa1	Alignment	not modelled	36.7	27	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
47	c3kh1B_	Alignment	not modelled	36.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**predicted metal-dependent phosphohydrolase; **PDBTitle:** crystal structure of predicted metal-dependent2 phosphohydrolase (zp_00055740.2) from magnetospirillum3 magnetotacticum ms-1 at 1.37 a resolution
48	d2d5ba1	Alignment	not modelled	35.5	17	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
49	c1hynQ_	Alignment	not modelled	34.0	15	**PDB header:**membrane protein **Chain:** Q: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein
50	c3l3fX_	Alignment	not modelled	33.5	19	**PDB header:**protein binding **Chain:** X: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of a pfu-pul domain pair of saccharomyces cerevisiae2 doa1/ufd3
						PDB header:transcription **Chain:** A: **PDB Molecule:**mmoq response regulator;

51	c3ljvA_	Alignment	not modelled	33.3	21	**PDBTitle:** crystal structure of mmoq response regulator (fragment 29-302) from2 methylococcus capsulatus str. bath, northeast structural genomics3 consortium target mcr175m
52	c3dfgA_	Alignment	not modelled	31.0	11	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx: a potent inhibitor protein of2 reca from xanthomonas campestris
53	d2gfna1	Alignment	not modelled	30.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
54	c3hxxA_	Alignment	not modelled	28.8	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
55	c1ileA_	Alignment	not modelled	27.3	10	**PDB header:**aminoacyl-trna synthetase **Chain:** A: **PDB Molecule:**isoleucyl-trna synthetase; **PDBTitle:** isoleucyl-trna synthetase
56	c3pstA_	Alignment	not modelled	26.4	19	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of pul and pfu(mutate) domain
57	c3b81A_	Alignment	not modelled	25.4	4	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, acrr family; **PDBTitle:** crystal structure of predicted dna-binding transcriptional regulator2 of tetr/acrr family (np_350189.1) from clostridium acetobutylicum at3 2.10 a resolution
58	c2zihC_	Alignment	not modelled	23.9	16	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**vacuolar protein sorting-associated protein 74; **PDBTitle:** crystal structure of yeast vps74
59	c2o59B_	Alignment	not modelled	23.9	16	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase 3; **PDBTitle:** structure of e. coli topoisomerase iii in complex with an 8-2 base single stranded oligonucleotide. frozen in glycerol3 ph 8.0
60	d1szwa_	Alignment	not modelled	23.4	13	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**tRNA pseudouridine synthase TruD
61	c2ziiA_	Alignment	not modelled	23.2	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 74; **PDBTitle:** crystal structure of yeast vps74-n-term truncation variant
62	d1hynp_	Alignment	not modelled	22.9	17	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**Anion transport protein, cytoplasmic domain
63	d2guma1	Alignment	not modelled	22.5	10	**Fold:**Viral glycoprotein ectodomain-like **Superfamily:**Viral glycoprotein ectodomain-like **Family:**Glycoprotein B-like
64	c3kpbA_	Alignment	not modelled	22.2	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj0100; **PDBTitle:** crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
65	c3orgB_	Alignment	not modelled	21.0	31	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cmclc; **PDBTitle:** crystal structure of a eukaryotic clc transporter
66	c2qv5A_	Alignment	not modelled	20.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
67	c3nw8B_	Alignment	not modelled	20.4	10	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**envelope glycoprotein b; **PDBTitle:** glycoprotein b from herpes simplex virus type 1, y179s mutant, high-ph
68	c3e3vA_	Alignment	not modelled	19.9	21	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx from lactobacillus salivarius
69	d1i7da_	Alignment	not modelled	19.4	19	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
70	d2j0sc1	Alignment	not modelled	19.1	63	**Fold:**Mago nashi protein **Superfamily:**Mago nashi protein **Family:**Mago nashi protein
71	c1nyjC_	Alignment	not modelled	18.7	26	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
72	c1nyjD_	Alignment	not modelled	18.7	26	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
73	c2kqtC_	Alignment	not modelled	18.7	26	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
74	c2kqtA_	Alignment	not modelled	18.7	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
75	c2kqtB_	Alignment	not modelled	18.7	26	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
						PDB header:viral protein

76	c1nyjB_	Alignment	not modelled	18.7	26	**Chain:** B: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
77	c1mp6A_	Alignment	not modelled	18.7	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**matrix protein m2; **PDBTitle:** structure of the transmembrane region of the m2 protein h+2 channel by solid state nmr spectroscopy
78	c2kqtD_	Alignment	not modelled	18.7	26	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
79	c1nyjA_	Alignment	not modelled	18.7	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
80	c3ooxA_	Alignment	not modelled	18.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 2og-fe(ii) oxygenase family protein; **PDBTitle:** crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution
81	c2ph7B_	Alignment	not modelled	18.0	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein af_2093; **PDBTitle:** crystal structure of af2093 from archaeoglobus fulgidus
82	c3memA_	Alignment	not modelled	17.5	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative signal transduction protein; **PDBTitle:** crystal structure of a putative signal transduction protein2 (maqu_0641) from marinobacter aquaeolei vt8 at 2.25 a resolution
83	c2gajA_	Alignment	not modelled	17.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
84	c2kadA_	Alignment	not modelled	15.3	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
85	c2kadD_	Alignment	not modelled	15.3	26	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
86	c2kadC_	Alignment	not modelled	15.3	26	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
87	c2kadB_	Alignment	not modelled	15.3	26	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
88	d2gycw1	Alignment	not modelled	14.2	14	**Fold:**Long alpha-hairpin **Superfamily:**Ribosomal protein L29 (L29p) **Family:**Ribosomal protein L29 (L29p)
89	c2jmxA_	Alignment	not modelled	14.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase o subunit, mitochondrial; **PDBTitle:** oscp-nt (1-120) in complex with n-terminal (1-25) alpha2 subunit from f1-atpase
90	d1x9na2	Alignment	not modelled	13.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
91	c2zkrv_	Alignment	not modelled	13.7	20	**PDB header:**ribosomal protein/rna **Chain:** V: **PDB Molecule:**rna expansion segment es9 part2; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
92	d1gw5b_	Alignment	not modelled	13.5	16	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Clathrin adaptor core protein
93	c3kaeC_	Alignment	not modelled	13.3	28	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**possible protein of nuclear scaffold; **PDBTitle:** cdc27 n-terminus
94	c3c9jD_	Alignment	not modelled	12.8	21	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
95	c3c9jA_	Alignment	not modelled	12.8	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
96	c3c9jB_	Alignment	not modelled	12.8	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
97	c3c9jC_	Alignment	not modelled	12.8	21	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
98	c2g9tT_	Alignment	not modelled	12.6	54	**PDB header:**viral protein **Chain:** T: **PDB Molecule:** **PDBTitle:** crystal structure of the sars coronavirus nsp10 at 2.1a
						Fold: RuvA C-terminal domain-like

99	d1wgla_	Alignment	not modelled	12.4	11	**Superfamily:**UBA-like **Family:**CUE domain