Phyre^2

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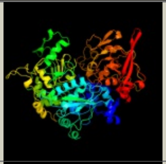
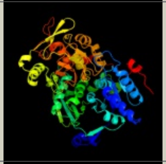
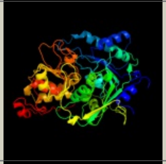
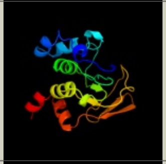
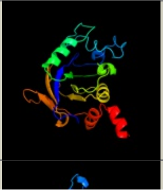
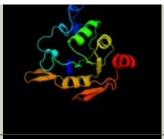
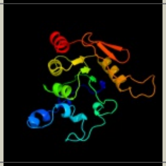
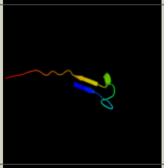
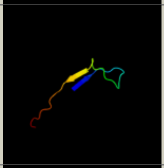
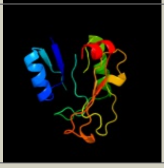
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2b3yB_	Alignment		100.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**iron-responsive element binding protein 1; **PDBTitle:** structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
2	c5acnA_	Alignment		100.0	24	**PDB header:**lyase(carbon-oxygen) **Chain:** A: **PDB Molecule:**aconitase; **PDBTitle:** structure of activated aconitase. formation of the (4fe-4s)2 cluster in the crystal
3	d2b3ya2	Alignment		100.0	23	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
4	d1acoa2	Alignment		100.0	26	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
5	d1l5ja3	Alignment		100.0	22	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
6	c1l5jB_	Alignment		100.0	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aconitate hydratase 2; **PDBTitle:** crystal structure of e. coli aconitase b.
7	d2b3ya1	Alignment		100.0	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
8	d1acoa1	Alignment		100.0	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
9	d1v7la_	Alignment		100.0	24	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
10	c2pkpA_	Alignment		100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
11	d1l5ja2	Alignment		100.0	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
						

12	c2hcuA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
13	c3q3wB_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** isopropylmalate isomerase small subunit from campylobacter jejuni.
14	c3h5jA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
15	d1g4ma1	Alignment		86.9	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
16	c1cjyB_	Alignment		85.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (cytosolic phospholipase a2); **PDBTitle:** human cytosolic phospholipase a2
17	d1cf1a1	Alignment		80.3	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
18	c2k6zA_	Alignment		64.6	21	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1943; **PDBTitle:** solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
19	d1x9la_	Alignment		54.5	16	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**DR1885-like metal-binding protein **Family:**DR1885-like metal-binding protein
20	c3dc1A_	Alignment		50.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**kynurenine/alpha-aminoadipate aminotransferase **PDBTitle:** crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
21	c2yx6C_	Alignment	not modelled	42.3	10	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein ph0822; **PDBTitle:** crystal structure of ph0822
22	c3l4gI_	Alignment	not modelled	38.0	19	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
23	d1rdua_	Alignment	not modelled	37.0	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
24	d1t3va_	Alignment	not modelled	34.5	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
25	c3bolB_	Alignment	not modelled	30.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
26	d1o13a_	Alignment	not modelled	30.5	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
27	d2r4qa1	Alignment	not modelled	30.5	21	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
28	d2q7wa1	Alignment	not modelled	30.4	8	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
29	d1yaaa_	Alignment	not modelled	29.8	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like

30	c3mo4B_	Alignment	not modelled	29.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-1,3/4-fucosidase; **PDBTitle:** the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697
31	c3gzaB_	Alignment	not modelled	25.8	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
32	c2yb1A_	Alignment	not modelled	24.9	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
33	d1t0tv_	Alignment	not modelled	24.3	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
34	c2wbrA_	Alignment	not modelled	23.6	31	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**gw182; **PDBTitle:** the rrm domain in gw182 proteins contributes to mirna-2 mediated gene silencing
35	c2wvsD_	Alignment	not modelled	23.1	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-l-fucosidase; **PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
36	d2csta_	Alignment	not modelled	22.1	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
37	d1p90a_	Alignment	not modelled	21.6	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**Nitrogenase accessory factor
38	d3bofa2	Alignment	not modelled	21.6	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
39	c3qguB_	Alignment	not modelled	20.8	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** l,l-diaminopimelate aminotransferase from chalmydomonas reinhardtii
40	d1vdha_	Alignment	not modelled	20.6	9	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
41	d1go3e1	Alignment	not modelled	20.5	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
42	c3ihjA_	Alignment	not modelled	20.5	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine aminotransferase 2; **PDBTitle:** human alanine aminotransferase 2 in complex with plp
43	d1eo1a_	Alignment	not modelled	20.2	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
44	c3cmwA_	Alignment	not modelled	19.9	19	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
45	c3a2kB_	Alignment	not modelled	19.9	8	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
46	c1pt1B_	Alignment	not modelled	19.8	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
47	d1ppya_	Alignment	not modelled	19.8	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
48	c2wfbA_	Alignment	not modelled	18.8	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein orp; **PDBTitle:** high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
49	d2ay1a_	Alignment	not modelled	18.1	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
50	c3pg8B_	Alignment	not modelled	17.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
51	d7aata_	Alignment	not modelled	16.8	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
52	c3eypB_	Alignment	not modelled	16.5	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
53	c3gitA_	Alignment	not modelled	16.4	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase/acetyl-coa synthase subunit **PDBTitle:** crystal structure of a truncated acetyl-coa synthase
54	d1lt7a_	Alignment	not modelled	16.1	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
55	c2nvgA_	Alignment	not modelled	15.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit;

						PDBTitle: soluble domain of rieske iron sulfur protein.
56	d3cdda2	Alignment	not modelled	15.5	15	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
57	c2vxhF_	Alignment	not modelled	15.3	0	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**chlorite dismutase; **PDBTitle:** the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
58	c3k7yA_	Alignment	not modelled	14.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** aspartate aminotransferase of plasmodium falciparum
59	d1x0ma1	Alignment	not modelled	14.5	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
60	d1w7la_	Alignment	not modelled	14.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
61	c2c45F_	Alignment	not modelled	13.9	11	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aspartate 1-decarboxylase precursor; **PDBTitle:** native precursor of pyruvoyl dependent aspartate2 decarboxylase
62	c3c9uB_	Alignment	not modelled	13.4	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** aathil complexed with adp and tpp
63	c2ebbA_	Alignment	not modelled	13.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
64	c3pplB_	Alignment	not modelled	12.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
65	d2r5ea1	Alignment	not modelled	12.6	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
66	c3nn4C_	Alignment	not modelled	12.5	5	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**chlorite dismutase; **PDBTitle:** structure of chlorite dismutase from candidatus nitrospira defluvii2 r173k mutant
67	c2oxlA_	Alignment	not modelled	12.3	21	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hypothetical protein ymgb; **PDBTitle:** structure and function of the e. coli protein ymgb: a protein critical2 for biofilm formation and acid resistance
68	d1l0sa_	Alignment	not modelled	12.2	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**An insect antifreeze protein **Family:**An insect antifreeze protein
69	c3m84A_	Alignment	not modelled	12.1	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole synthetase from2 francisella tularensis
70	c2jz2A_	Alignment	not modelled	12.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
71	c3muxB_	Alignment	not modelled	12.0	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative 4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
72	d2nu7b2	Alignment	not modelled	11.9	25	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
73	c3m6yA_	Alignment	not modelled	11.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
74	d1w44a_	Alignment	not modelled	11.7	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
75	c1ni5A_	Alignment	not modelled	11.4	7	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
76	c2w9mB_	Alignment	not modelled	11.3	25	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
77	c3kxyW_	Alignment	not modelled	10.7	25	**PDB header:**chaperone/transcription inhibitor **Chain:** W: **PDB Molecule:**exse; **PDBTitle:** crystal structure of the exsc-exse complex
78	c3cmuA_	Alignment	not modelled	10.7	16	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
79	d1m8na_	Alignment	not modelled	10.3	14	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**An insect antifreeze protein **Family:**An insect antifreeze protein
80	d2p5zx2	Alignment	not modelled	10.2	25	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like

81	d1ru3a_	Alignment	not modelled	10.1	23	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
82	c3eibB_	Alignment	not modelled	9.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
83	c2gp4A_	Alignment	not modelled	9.8	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
84	d1oaoc_	Alignment	not modelled	9.7	32	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
85	c3bzwA_	Alignment	not modelled	9.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative lipase; **PDBTitle:** crystal structure of a putative lipase from bacteroides2 thetaiotaomicron
86	d3bzwa1	Alignment	not modelled	9.6	12	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**BT2961-like
87	c3bkdB_	Alignment	not modelled	9.6	38	**PDB header:**viral protein, membrane protein **Chain:** B: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
88	c3bkdG_	Alignment	not modelled	9.6	38	**PDB header:**viral protein, membrane protein **Chain:** G: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
89	c3bkdD_	Alignment	not modelled	9.6	38	**PDB header:**viral protein, membrane protein **Chain:** D: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
90	c3bkdC_	Alignment	not modelled	9.6	38	**PDB header:**viral protein, membrane protein **Chain:** C: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
91	c3bkdE_	Alignment	not modelled	9.6	38	**PDB header:**viral protein, membrane protein **Chain:** E: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
92	c3bkdF_	Alignment	not modelled	9.6	38	**PDB header:**viral protein, membrane protein **Chain:** F: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
93	c3bkdA_	Alignment	not modelled	9.6	38	**PDB header:**viral protein, membrane protein **Chain:** A: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
94	c3bkdH_	Alignment	not modelled	9.6	38	**PDB header:**viral protein, membrane protein **Chain:** H: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
95	d1qlma_	Alignment	not modelled	9.4	15	**Fold:**Methenyltetrahydromethanopterin cyclohydrolase **Superfamily:**Methenyltetrahydromethanopterin cyclohydrolase **Family:**Methenyltetrahydromethanopterin cyclohydrolase
96	c2kadC_	Alignment	not modelled	9.4	38	**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
97	c2kadA_	Alignment	not modelled	9.4	38	**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
98	c2kadB_	Alignment	not modelled	9.4	38	**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
99	c2kadD_	Alignment	not modelled	9.4	38	**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