Phyre2

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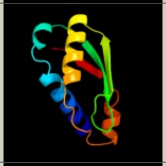
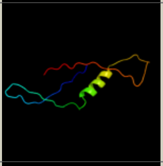
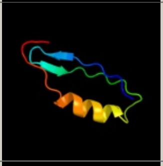
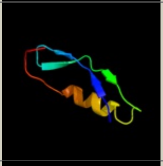
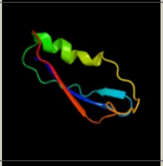
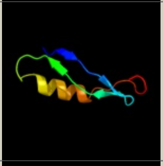
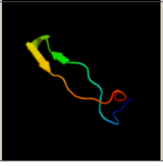
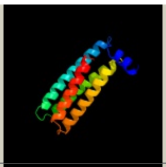
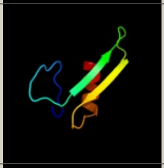
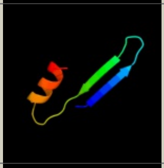
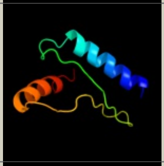
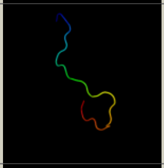
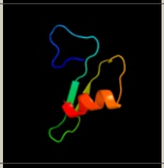
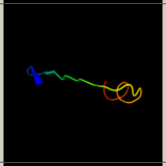
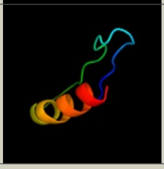
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1tolA_	Alignment		100.0	95	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (fusion protein consisting of minor coat **PDBTitle:** fusion of n-terminal domain of the minor coat protein from2 gene iii in phage m13, and c-terminal domain of e. coli3 protein-tola
2	d1tola2	Alignment		99.9	100	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TolA
3	c2x9aB_	Alignment		99.9	100	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**membrane spanning protein, required for outer membrane **PDBTitle:** crystal structure of g3p from phage if1 in complex with its2 coreceptor, the c-terminal domain of tola
4	d1lr0a_	Alignment		99.8	16	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TolA
5	d1ihra_	Alignment		97.7	9	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
6	c2grxC_	Alignment		97.2	15	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**protein tonb; **PDBTitle:** crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
7	c1xx3A_	Alignment		97.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tonb protein; **PDBTitle:** solution structure of escherichia coli tonb-ctd
8	d2gskb1	Alignment		96.9	9	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
9	c2k9kA_	Alignment		96.7	20	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**tonb2; **PDBTitle:** molecular characterization of the tonb2 protein from vibrio2 anguillarum
10	d1u07a_	Alignment		96.6	9	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
11	c2dzkA_	Alignment		54.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubx domain-containing protein 2; **PDBTitle:** structure of the ubx domain in mouse ubx domain-containing2 protein 2

12	c1y4cA_	Alignment		50.4	17	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
13	c2kxjA_	Alignment		47.2	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubx domain-containing protein 4; **PDBTitle:** solution structure of ubx domain of human ubxd2 protein
14	d2ba0g2	Alignment		41.0	16	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
15	d1r4xa2	Alignment		38.4	16	**Fold:**Subdomain of clathrin and coatomer appendage domain **Superfamily:**Subdomain of clathrin and coatomer appendage domain **Family:**Coatomer appendage domain
16	d2e7ga1	Alignment		35.4	11	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
17	c2ytxA_	Alignment		35.3	36	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**cold shock domain-containing protein e1; **PDBTitle:** solution structure of the second cold-shock domain of the human2 kiaa0885 protein (unr protein)
18	d2nn6c2	Alignment		35.1	19	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
19	c2zfdB_	Alignment		33.6	11	**PDB header:**signaling protein/transferase **Chain:** B: **PDB Molecule:**putative uncharacterized protein t20l15_90; **PDBTitle:** the crystal structure of plant specific calcium binding protein atcbl22 in complex with the regulatory domain of atcipk14
20	c1ybxA_	Alignment		32.0	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum
21	d1wj4a_	Alignment	not modelled	31.8	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
22	c2kzfA_	Alignment	not modelled	31.0	11	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**ribosome-binding factor a; **PDBTitle:** solution nmr structure of the thermotoga maritima protein tm0855 a2 putative ribosome binding factor a
23	c1r4xA_	Alignment	not modelled	29.0	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer gamma subunit; **PDBTitle:** crystal structure analys of the gamma-copi appendage domain
24	d2nn6e2	Alignment	not modelled	28.3	10	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
25	c2vbcA_	Alignment	not modelled	27.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dengue 4 ns3 full-length protein; **PDBTitle:** crystal structure of the ns3 protease-helicase from dengue2 virus
26	c1pzdA_	Alignment	not modelled	25.4	13	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**coatomer gamma subunit; **PDBTitle:** structural identification of a conserved appendage domain2 in the carboxyl-terminus of the copi gamma-subunit.
27	c3mfbA_	Alignment	not modelled	21.8	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the s-type pyocin domain of eca16692 protein from erwinia carotovora, northeast structural3 genomics consortium target ewr82c
28	c2dnrA_	Alignment	not modelled	20.0	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**synaptojanin-1; **PDBTitle:** solution structure of rna binding domain in synaptojanin 1

29	c2zv4O_	Alignment	not modelled	19.7	10	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
30	c3htyC_	Alignment	not modelled	19.2	15	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein bt_0869; **PDBTitle:** crystal structure of hypothetical protein bt_0869 from bacteroides2 thetaiotaomicron vpi-5482 (np_809782.1) at 1.95 a resolution
31	c3mlpE_	Alignment	not modelled	18.8	11	**PDB header:**transcription/dna **Chain:** E: **PDB Molecule:**transcription factor coe1; **PDBTitle:** early b-cell factor 1 (ebf1) bound to dna
32	c1dxzA_	Alignment	not modelled	18.6	26	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**acetylcholine receptor protein, alpha chain; **PDBTitle:** m2 transmembrane segment of alpha-subunit of nicotinic2 acetylcholine receptor from torpedo californica, nmr, 203 structures
33	d1jbia_	Alignment	not modelled	18.4	12	**Fold:**LCCL domain **Superfamily:**LCCL domain **Family:**LCCL domain
34	c2i1jA_	Alignment	not modelled	17.4	17	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin from spodoptera frugiperda at 2.1 angstroms resolution
35	d2dyja1	Alignment	not modelled	16.5	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
36	c3ol0C_	Alignment	not modelled	16.3	17	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
37	d2nn6a2	Alignment	not modelled	15.4	25	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
38	c2kncB_	Alignment	not modelled	15.1	11	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
39	d2cjoa_	Alignment	not modelled	15.0	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
40	d1wg1a_	Alignment	not modelled	14.0	33	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
41	d1kkga_	Alignment	not modelled	14.0	12	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
42	d1j8ba_	Alignment	not modelled	13.4	10	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
43	d2je6a2	Alignment	not modelled	12.8	20	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
44	d1s48a_	Alignment	not modelled	11.7	22	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
45	c2rmzA_	Alignment	not modelled	11.4	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-3; **PDBTitle:** bicelle-embedded integrin beta3 transmembrane segment
46	d1kyfa2	Alignment	not modelled	11.3	12	**Fold:**Subdomain of clathrin and coatomer appendage domain **Superfamily:**Subdomain of clathrin and coatomer appendage domain **Family:**Clathrin adaptor appendage, alpha and beta chain-specific domain
47	c3pn1A_	Alignment	not modelled	11.2	20	**PDB header:**ligase/ligase inhibitor **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
48	d2ux9a1	Alignment	not modelled	11.1	23	**Fold:**Dodecin subunit-like **Superfamily:**Dodecin-like **Family:**Dodecin-like
49	c1sfeA_	Alignment	not modelled	10.9	21	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**ada o6-methylguanine-dna methyltransferase; **PDBTitle:** ada o6-methylguanine-dna methyltransferase from escherichia coli
50	c1x65A_	Alignment	not modelled	10.7	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**unr protein; **PDBTitle:** solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein)
51	d2k8ea1	Alignment	not modelled	10.4	14	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
52	d1x6oa2	Alignment	not modelled	10.2	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
53	d1nkza_	Alignment	not modelled	9.7	15	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
						PDB header:hydrolase

54	c3ecyA_	Alignment	not modelled	9.6	19	**Chain:** A: **PDB Molecule:**cg4584-pa, isoform a (bcdna.ld08534); **PDBTitle:** crystal structural analysis of drosophila melanogaster dutpase
55	d1sfea1	Alignment	not modelled	9.6	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain **Family:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain
56	d2cr5a1	Alignment	not modelled	9.5	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
57	d1tl2a_	Alignment	not modelled	9.5	14	**Fold:**5-bladed beta-propeller **Superfamily:**Tachylectin-2 **Family:**Tachylectin-2
58	c3ajbB_	Alignment	not modelled	9.1	42	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**peroxisomal biogenesis factor 19; **PDBTitle:** crystal structure of human pex3p in complex with n-terminal pex19p2 peptide
59	d1h8ca_	Alignment	not modelled	9.0	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
60	c1cu1B_	Alignment	not modelled	9.0	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (protease/helicase ns3); **PDBTitle:** crystal structure of an enzyme complex from hepatitis c2 virus
61	d1pa4a_	Alignment	not modelled	9.0	10	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
62	c1ky6A_	Alignment	not modelled	8.9	12	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**alpha-adaptin c; **PDBTitle:** ap-2 clathrin adaptor alpha-appendage in complex with epsin2 dpw peptide
63	d1puga_	Alignment	not modelled	8.9	3	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
64	d1v9pa3	Alignment	not modelled	8.8	15	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
65	d1ccwb_	Alignment	not modelled	8.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Glutamate mutase, large subunit
66	c3onrI_	Alignment	not modelled	8.7	20	**PDB header:**metal binding protein **Chain:** I: **PDB Molecule:**protein transport protein sece2; **PDBTitle:** crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
67	d1n1ba1	Alignment	not modelled	8.6	23	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpenoid cyclase N-terminal domain
68	c2zsjB_	Alignment	not modelled	8.6	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**threonine synthase; **PDBTitle:** crystal structure of threonine synthase from aquifex aeolicus vf5
69	d1i42a_	Alignment	not modelled	8.5	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
70	c2k59B_	Alignment	not modelled	8.5	33	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**neuronal acetylcholine receptor subunit beta-2; **PDBTitle:** nmr structures of the second transmembrane domain of the2 neuronal acetylcholine receptor beta 2 subunit
71	d3bzka5	Alignment	not modelled	8.5	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
72	d1ta8a_	Alignment	not modelled	8.3	22	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
73	c3p2oB_	Alignment	not modelled	8.3	11	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
74	c2jpxA_	Alignment	not modelled	8.2	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** a18h vpu tm structure in lipid bilayers
75	c2l7qA_	Alignment	not modelled	8.2	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of conjugate transposon protein bvu_1572(27-2 141) from bacteroides vulgatus, northeast structural genomics3 consortium target bvr155
76	c1zbtA_	Alignment	not modelled	8.0	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** crystal structure of peptide chain release factor 1 (rf-1) (smu.1085)2 from streptococcus mutans at 2.34 a resolution
77	c1s1hJ_	Alignment	not modelled	8.0	13	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**40s ribosomal protein s20; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
78	c2kncA_	Alignment	not modelled	8.0	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex

79	d1ijda_	Alignment	not modelled	7.9	15	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
80	c2ihr1_	Alignment	not modelled	7.9	12	**PDB header:**translation **Chain:** 1: **PDB Molecule:**peptide chain release factor 2; **PDBTitle:** rf2 of thermus thermophilus
81	d1j3wa_	Alignment	not modelled	7.9	22	**Fold:**Profilin-like **Superfamily:**Roadblock/LC7 domain **Family:**Roadblock/LC7 domain
82	c3p2oA_	Alignment	not modelled	7.8	11	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
83	c3muxB_	Alignment	not modelled	7.6	21	**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
84	d1oysa1	Alignment	not modelled	7.6	15	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
85	c2l3bA_	Alignment	not modelled	7.5	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of the bt_0084 lipoprotein from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr376
86	c3oqtP_	Alignment	not modelled	7.4	16	**PDB header:**flavoprotein **Chain:** P: **PDB Molecule:**rv1498a protein; **PDBTitle:** crystal structure of rv1498a protein from mycobacterium tuberculosis
87	c2y69R_	Alignment	not modelled	7.3	33	**PDB header:**electron transport **Chain:** R: **PDB Molecule:**cytochrome c oxidase subunit 5a; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
88	d1v54e_	Alignment	not modelled	7.3	33	**Fold:**alpha-alpha superhelix **Superfamily:**Cytochrome c oxidase subunit E **Family:**Cytochrome c oxidase subunit E
89	c1a4iB_	Alignment	not modelled	7.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
90	d1vk8a_	Alignment	not modelled	7.1	18	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
91	d1dxwa_	Alignment	not modelled	7.1	31	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
92	d1b04a_	Alignment	not modelled	7.1	15	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
93	c1a11A_	Alignment	not modelled	7.0	30	**PDB header:**acetylcholine receptor **Chain:** A: **PDB Molecule:**acetylcholine receptor m2; **PDBTitle:** nmr structure of membrane spanning segment 2 of the2 acetylcholine receptor in dpc micelles, 10 structures
94	c1yq3C_	Alignment	not modelled	7.0	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate dehydrogenase cytochrome b, large subunit; **PDBTitle:** avian respiratory complex ii with oxaloacetate and ubiquinone
95	c1eq8B_	Alignment	not modelled	7.0	30	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**acetylcholine receptor protein; **PDBTitle:** three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
96	c1eq8D_	Alignment	not modelled	7.0	30	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**acetylcholine receptor protein; **PDBTitle:** three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
97	c1eq8C_	Alignment	not modelled	7.0	30	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**acetylcholine receptor protein; **PDBTitle:** three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
98	c1eq8E_	Alignment	not modelled	7.0	30	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**acetylcholine receptor protein; **PDBTitle:** three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
99	c1eq8A_	Alignment	not modelled	7.0	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**acetylcholine receptor protein; **PDBTitle:** three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment