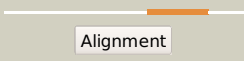
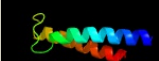
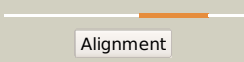

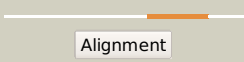

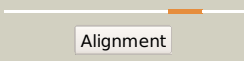

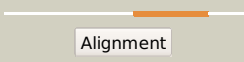

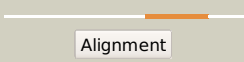

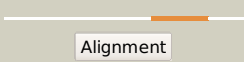

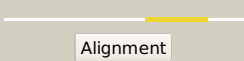

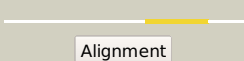

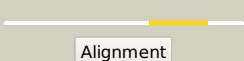

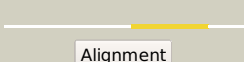
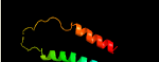



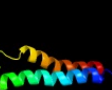






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1233c_(-)_1376236_1376832
Date	Wed Jul 31 22:05:32 BST 2019
Unique Job ID	11d1c217ce9ff9df

Detailed template information

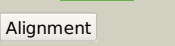

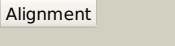
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4p79A_</a>	 Alignment		88.7	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> claudin-15; <b>PDBTitle:</b> crystal structure of mouse claudin-15
2	<a href="#">c5wivA_</a>	 Alignment		85.6	11	<b>PDB header:</b> signaling protein/antagonist <b>Chain:</b> A: <b>PDB Molecule:</b> d(4) dopamine receptor, soluble cytochrome b562 chimera; <b>PDBTitle:</b> structure of the sodium-bound human d4 dopamine receptor in complex2 with nemonapride
3	<a href="#">c4x5mB_</a>	 Alignment		82.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of semisweet in the inward-open conformation
4	<a href="#">c2m67A_</a>	 Alignment		82.3	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> full-length mercury transporter protein merf in lipid bilayer2 membranes
5	<a href="#">c3v2yA_</a>	 Alignment		82.2	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sphingosine 1-phosphate receptor 1, lysozyme chimera <b>PDBTitle:</b> crystal structure of a lipid g protein-coupled receptor at 2.80a
6	<a href="#">c6me5A_</a>	 Alignment		80.9	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of melatonin receptor type 1a and glga <b>PDBTitle:</b> xfel crystal structure of human melatonin receptor mt1 in complex with2 agomelatine
7	<a href="#">c4grvA_</a>	 Alignment		80.5	20	<b>PDB header:</b> signaling protein/agonist <b>Chain:</b> A: <b>PDB Molecule:</b> neurotensin receptor type 1, lysozyme chimera; <b>PDBTitle:</b> the crystal structure of the neurotensin receptor nts1 in complex with2 neurotensin (8-13)
8	<a href="#">c5ztyA_</a>	 Alignment		78.8	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> g protein coupled receptor,t4 lysozyme,g protein coupled <b>PDBTitle:</b> crystal structure of human g protein coupled receptor
9	<a href="#">c5qliA_</a>	 Alignment		77.6	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> endothelin receptor subtype-b; <b>PDBTitle:</b> human endothelin receptor type-b in the ligand-free form
10	<a href="#">c6m9tA_</a>	 Alignment		77.2	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> prostaglandin e2 receptor ep3 subtype, endolysin chimera; <b>PDBTitle:</b> crystal structure of ep3 receptor bound to misoprostol-fa
11	<a href="#">c2yevB_</a>	 Alignment		75.7	8	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase subunit 2; <b>PDBTitle:</b> structure of caa3-type cytochrome oxidase

12	<a href="#">c5zlgA</a>	Alignment		75.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome b reductase 1; <b>PDBTitle:</b> human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
13	<a href="#">c4rngE</a>	Alignment		74.7	11	<b>PDB header:</b> sugar binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> mtn3/saliva family; <b>PDBTitle:</b> crystal structure of a bacterial homologue of sweet transporters
14	<a href="#">c6g7oA</a>	Alignment		74.5	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline ceramidase 3,soluble cytochrome b562; <b>PDBTitle:</b> crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution
15	<a href="#">c3rzeA</a>	Alignment		74.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histamine h1 receptor, lysozyme chimera; <b>PDBTitle:</b> structure of the human histamine h1 receptor in complex with doxepin
16	<a href="#">c4k5yA</a>	Alignment		74.5	10	<b>PDB header:</b> membrane protein, receptor <b>Chain:</b> A: <b>PDB Molecule:</b> corticotropin-releasing factor receptor 1, t4-lysozyme <b>PDBTitle:</b> crystal structure of human corticotropin-releasing factor receptor 12 (crf1r) in complex with the antagonist cp-376395
17	<a href="#">c6e59A</a>	Alignment		73.8	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> substance-p receptor, glga glycogen synthase, substance-p <b>PDBTitle:</b> crystal structure of the human nk1 tachykinin receptor
18	<a href="#">c4jkvA</a>	Alignment		73.2	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562, smoothed homolog; <b>PDBTitle:</b> structure of the human smoothed 7tm receptor in complex with an2 antitumor agent
19	<a href="#">c5gasN</a>	Alignment		73.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> N: <b>PDB Molecule:</b> archaeal/vacuolar-type h+-atpase subunit i; <b>PDBTitle:</b> thermus thermophilus v/a-atpase, conformation 2
20	<a href="#">c6o3cA</a>	Alignment		71.7	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> smoothed homolog; <b>PDBTitle:</b> crystal structure of active smoothed bound to sag21k, cholesterol,2 and nbsmo8
21	<a href="#">c5zbhA</a>	Alignment	not modelled	71.7	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> neuropeptide y receptor type 1,t4 lysozyme,neuropeptide y <b>PDBTitle:</b> the crystal structure of human neuropeptide y y1 receptor with bms-2 193885
22	<a href="#">c4rnbA</a>	Alignment	not modelled	71.6	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> orexin receptor type 2, glga glycogen synthase; <b>PDBTitle:</b> crystal structure of the human ox2 orexin receptor bound to the2 insomnia drug suvorexant
23	<a href="#">c2lj2A</a>	Alignment	not modelled	71.4	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> integral membrane core domain of the mercury transporter merf in lipid2 bilayer membranes
24	<a href="#">c5xpdA</a>	Alignment	not modelled	71.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar transporter; <b>PDBTitle:</b> sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
25	<a href="#">c5b2gG</a>	Alignment	not modelled	70.4	23	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> endolysin,claudin-4; <b>PDBTitle:</b> crystal structure of human claudin-4 in complex with c-terminal2 fragment of clostridium perfringens enterotoxin
26	<a href="#">c4rfsS</a>	Alignment	not modelled	69.3	16	<b>PDB header:</b> hydrolase, transport protein <b>Chain:</b> S: <b>PDB Molecule:</b> substrate binding prtein s; <b>PDBTitle:</b> structure of a pantothenate energy coupling factor transporter
27	<a href="#">c5z62M</a>	Alignment	not modelled	69.0	14	<b>PDB header:</b> electron transport <b>Chain:</b> M: <b>PDB Molecule:</b> cytochrome c oxidase subunit 8a, mitochondrial; <b>PDBTitle:</b> structure of human cytochrome c oxidase
28	<a href="#">c2jwaA</a>	Alignment	not modelled	68.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2;

						<b>PDBTitle:</b> erbb2 transmembrane segment dimer spatial structure
29	<a href="#">c2ks1A</a>	Alignment	not modelled	68.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
30	<a href="#">c4zwlA</a>	Alignment	not modelled	68.3	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of human rhodopsin, mouse s-arrestin, and <b>PDBTitle:</b> crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser
31	<a href="#">c3kp9A</a>	Alignment	not modelled	66.2	18	<b>PDB header:</b> blood coagulation,oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> vkorc1/thioredoxin domain protein; <b>PDBTitle:</b> structure of a bacterial homolog of vitamin k epoxide reductase
32	<a href="#">c4zwlC</a>	Alignment	not modelled	66.1	11	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> chimera protein of human rhodopsin, mouse s-arrestin, and <b>PDBTitle:</b> crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser
33	<a href="#">c5x33A</a>	Alignment	not modelled	66.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ltb4 receptor,lysozyme,ltb4 receptor; <b>PDBTitle:</b> leukotriene b4 receptor blt1 in complex with biii260
34	<a href="#">c4u16A</a>	Alignment	not modelled	65.1	22	<b>PDB header:</b> membrane protein/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> muscarinic acetylcholine receptor m3,lysozyme,muscarinic <b>PDBTitle:</b> m3-mt4l receptor bound to nms
35	<a href="#">c3jbrE</a>	Alignment	not modelled	64.5	17	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> voltage-dependent calcium channel gamma-1 subunit; <b>PDBTitle:</b> cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
36	<a href="#">c2rifA</a>	Alignment	not modelled	64.5	35	<b>PDB header:</b> proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> proton channel m2 from influenza a in complex with2 inhibitor rimantadine
37	<a href="#">c3uonA</a>	Alignment	not modelled	64.4	20	<b>PDB header:</b> signaling protein/antagonist <b>Chain:</b> A: <b>PDB Molecule:</b> human m2 muscarinic acetylcholine, receptor t4 lysozyme <b>PDBTitle:</b> structure of the human m2 muscarinic acetylcholine receptor bound to2 an antagonist
38	<a href="#">c5tjvA</a>	Alignment	not modelled	62.4	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cannabinoid receptor 1,glga glycogen synthase,cannabinoid <b>PDBTitle:</b> high-resolution crystal structure of the human cb1 cannabinoid2 receptor
39	<a href="#">c2l35B</a>	Alignment	not modelled	62.2	32	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> structure of the dap12-nkg2c transmembrane heterotrimer
40	<a href="#">c6bkkH</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to amantadine
41	<a href="#">c6bmzN</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> N: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
42	<a href="#">c1nyjD</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> matrix protein m2; <b>PDBTitle:</b> the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
43	<a href="#">c6bmzG</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
44	<a href="#">c6bkkG</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to amantadine
45	<a href="#">c5jooA</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> xfel structure of influenza a m2 wild type tm domain at low ph in the2 lipidic cubic phase at room temperature
46	<a href="#">c5um1A</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> xfel structure of influenza a m2 wild type tm domain at intermediate2 ph in the lipidic cubic phase at room temperature
47	<a href="#">c2kqtB</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
48	<a href="#">c1nyjB</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> matrix protein m2; <b>PDBTitle:</b> the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
49	<a href="#">c4qkcA</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> influenza m2 monomer; <b>PDBTitle:</b> influenza a m2 wild type tm domain at low ph in the lipidic cubic2 phase under cryo diffraction conditions
50	<a href="#">c5ttcA</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> xfel structure of influenza a m2 wild type tm domain at high ph in the2 lipidic cubic phase at room temperature
51	<a href="#">c2kqtD</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
52	<a href="#">c6bkkE</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> matrix protein 2;

52	<a href="#">c00k1_</a>	Alignment	not modelled	62.2	39	<b>PDBTitle:</b> influenza a m2 transmembrane domain bound to amantadine <b>PDB header:</b> viral protein
53	<a href="#">c1nyjC_</a>	Alignment	not modelled	62.2	39	<b>Chain:</b> C; <b>PDB Molecule:</b> matrix protein m2; <b>PDBTitle:</b> the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
54	<a href="#">c6bkkE_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> E; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to amantadine
55	<a href="#">c2kqtC_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
56	<a href="#">c6bkkC_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to amantadine
57	<a href="#">c4qkmA_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> influenza m2 monomer; <b>PDBTitle:</b> influenza a m2 wild type tm domain at low ph in the lipidic cubic2 phase under room temperature diffraction conditions
58	<a href="#">c6bkkB_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to amantadine
59	<a href="#">c6bocA_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine in the2 inward(open) conformation
60	<a href="#">c6bocD_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine in the2 inward(open) conformation
61	<a href="#">c6bocC_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine in the2 inward(open) conformation
62	<a href="#">c6bkkA_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to amantadine
63	<a href="#">c2kqtA_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> m2 protein; <b>PDBTitle:</b> solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
64	<a href="#">c4qk7A_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> influenza m2 monomer; <b>PDBTitle:</b> influenza a m2 wild type tm domain at high ph in the lipidic cubic2 phase under cryo diffraction conditions
65	<a href="#">c4qk1A_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> influenza m2 monomer, tm domain (22-46); <b>PDBTitle:</b> influenza a m2 wild type tm domain at high ph in the lipidic cubic2 phase under room temperature diffraction conditions
66	<a href="#">c1mp6A_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> matrix protein m2; <b>PDBTitle:</b> structure of the transmembrane region of the m2 protein h+2 channel by solid state nmr spectroscopy
67	<a href="#">c1nyjA_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> matrix protein m2; <b>PDBTitle:</b> the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
68	<a href="#">c6bkkD_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to amantadine
69	<a href="#">c6bocB_</a>	Alignment	not modelled	62.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine in the2 inward(open) conformation
70	<a href="#">c2y69Z_</a>	Alignment	not modelled	62.2	11	<b>PDB header:</b> electron transport <b>Chain:</b> Z; <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 8h; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
71	<a href="#">c2bl2F_</a>	Alignment	not modelled	61.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> v-type sodium atp synthase subunit k; <b>PDBTitle:</b> the membrane rotor of the v-type atpase from enterococcus2 hirae
72	<a href="#">c6bmzM_</a>	Alignment	not modelled	61.8	39	<b>PDB header:</b> membrane protein <b>Chain:</b> M; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
73	<a href="#">c6bmzE_</a>	Alignment	not modelled	61.8	39	<b>PDB header:</b> membrane protein <b>Chain:</b> E; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
74	<a href="#">c6bmzL_</a>	Alignment	not modelled	61.8	39	<b>PDB header:</b> membrane protein <b>Chain:</b> L; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
75	<a href="#">c6bmzH_</a>	Alignment	not modelled	61.8	39	<b>PDB header:</b> membrane protein <b>Chain:</b> H; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
76	<a href="#">c6bkIE_</a>	Alignment	not modelled	61.8	39	<b>PDB header:</b> membrane protein <b>Chain:</b> E; <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine
77	<a href="#">c6bmzA_</a>	Alignment	not modelled	61.8	39	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> matrix protein 2;

77	<a href="#">c6bmzA_</a>	Alignment	not modelled	61.8	39	<b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor <b>PDB header:</b> membrane protein
78	<a href="#">c6bklA_</a>	Alignment	not modelled	61.8	39	<b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine
79	<a href="#">c6bmzO_</a>	Alignment	not modelled	61.8	39	<b>PDB header:</b> membrane protein <b>Chain:</b> O: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
80	<a href="#">c6bmzP_</a>	Alignment	not modelled	61.8	39	<b>PDB header:</b> membrane protein <b>Chain:</b> P: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
81	<a href="#">c6bmzC_</a>	Alignment	not modelled	61.8	39	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
82	<a href="#">c6bmzK_</a>	Alignment	not modelled	61.8	39	<b>PDB header:</b> membrane protein <b>Chain:</b> K: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
83	<a href="#">c6bmzI_</a>	Alignment	not modelled	61.8	39	<b>PDB header:</b> membrane protein <b>Chain:</b> I: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
84	<a href="#">c6bklG_</a>	Alignment	not modelled	61.4	39	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine
85	<a href="#">c6bmzJ_</a>	Alignment	not modelled	61.4	39	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
86	<a href="#">c6bklD_</a>	Alignment	not modelled	61.4	39	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine
87	<a href="#">c6bmzD_</a>	Alignment	not modelled	61.4	39	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
88	<a href="#">c6bklB_</a>	Alignment	not modelled	61.4	39	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine
89	<a href="#">c6bklF_</a>	Alignment	not modelled	61.4	39	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine
90	<a href="#">c6bmzF_</a>	Alignment	not modelled	61.4	39	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
91	<a href="#">c6bmzB_</a>	Alignment	not modelled	61.4	39	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to a spiroadamantane2 inhibitor
92	<a href="#">c6bklC_</a>	Alignment	not modelled	61.4	39	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine
93	<a href="#">c6bklH_</a>	Alignment	not modelled	61.4	39	<b>PDB header:</b> membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain bound to rimantadine
94	<a href="#">c4wo1A_</a>	Alignment	not modelled	61.4	32	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
95	<a href="#">c2l34B_</a>	Alignment	not modelled	61.4	32	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> structure of the dap12 transmembrane homodimer
96	<a href="#">c2l34A_</a>	Alignment	not modelled	61.4	32	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> structure of the dap12 transmembrane homodimer
97	<a href="#">c4wo1A_</a>	Alignment	not modelled	61.3	32	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
98	<a href="#">c4wo1B_</a>	Alignment	not modelled	61.3	32	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
99	<a href="#">c4wo1D_</a>	Alignment	not modelled	61.3	32	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
100	<a href="#">c4wo1C_</a>	Alignment	not modelled	61.3	32	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
101	<a href="#">c5sv0C_</a>	Alignment	not modelled	60.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> biopolymer transport protein exbb; <b>PDBTitle:</b> structure of the exbb/exbd complex from e. coli at ph 7.0

102	<a href="#">c5ws4A_</a>	 Alignment	not modelled	59.8	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of tripartite-type abc transporter macb from <i>2 acinetobacter baumannii</i>
103	<a href="#">c4wolC_</a>	 Alignment	not modelled	59.6	32	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
104	<a href="#">c4wolB_</a>	 Alignment	not modelled	59.6	32	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
105	<a href="#">c5xijA_</a>	 Alignment	not modelled	59.5	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multi drug efflux transporter; <b>PDBTitle:</b> crystal structure of a mate family protein
106	<a href="#">c4or2A_</a>	 Alignment	not modelled	59.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562, metabotropic glutamate receptor 1; <b>PDBTitle:</b> human class c g protein-coupled metabotropic glutamate receptor 1 in2 complex with a negative allosteric modulator
107	<a href="#">c6mjhE_</a>	 Alignment	not modelled	58.6	39	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> the s31n mutant of the influenza a m2 proton channel in two distinct2 conformational states
108	<a href="#">c6mjhC_</a>	 Alignment	not modelled	58.6	39	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> the s31n mutant of the influenza a m2 proton channel in two distinct2 conformational states
109	<a href="#">c5c02A_</a>	 Alignment	not modelled	58.6	39	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> influenza a m2 transmembrane domain drug-resistant s31n mutant at ph2 8.0
110	<a href="#">c6mjhD_</a>	 Alignment	not modelled	58.6	39	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> the s31n mutant of the influenza a m2 proton channel in two distinct2 conformational states
111	<a href="#">c6mjhG_</a>	 Alignment	not modelled	58.6	39	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> the s31n mutant of the influenza a m2 proton channel in two distinct2 conformational states
112	<a href="#">c6mjhF_</a>	 Alignment	not modelled	58.6	39	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> the s31n mutant of the influenza a m2 proton channel in two distinct2 conformational states
113	<a href="#">c6mjhB_</a>	 Alignment	not modelled	58.6	39	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> the s31n mutant of the influenza a m2 proton channel in two distinct2 conformational states
114	<a href="#">c6mjhA_</a>	 Alignment	not modelled	58.6	39	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> the s31n mutant of the influenza a m2 proton channel in two distinct2 conformational states
115	<a href="#">c6mjhH_</a>	 Alignment	not modelled	58.6	39	<b>PDB header:</b> membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> matrix protein 2; <b>PDBTitle:</b> the s31n mutant of the influenza a m2 proton channel in two distinct2 conformational states
116	<a href="#">c5xu1M_</a>	 Alignment	not modelled	58.6	13	<b>PDB header:</b> transport protein <b>Chain:</b> M: <b>PDB Molecule:</b> abc transporter permeae; <b>PDBTitle:</b> structure of a non-canonical abc transporter from <i>streptococcus2 pneumoniae</i> r6
117	<a href="#">c6akfC_</a>	 Alignment	not modelled	58.4	21	<b>PDB header:</b> membrane protein/toxin <b>Chain:</b> C: <b>PDB Molecule:</b> claudin-3; <b>PDBTitle:</b> crystal structure of mouse claudin-3 p134a mutant in complex with c-2 terminal fragment of <i>clostridium perfringens</i> enterotoxin
118	<a href="#">c4nl6C_</a>	 Alignment	not modelled	57.5	21	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> survival motor neuron protein; <b>PDBTitle:</b> structure of the full-length form of the protein smn found in healthy2 patients
119	<a href="#">c6c14A_</a>	 Alignment	not modelled	57.2	13	<b>PDB header:</b> membrane protein, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> protocadherin-15; <b>PDBTitle:</b> cryoem structure of mouse pcdh15-1ec-lhfpl5 complex
120	<a href="#">c5o9hA_</a>	 Alignment	not modelled	56.8	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> c5a anaphylatoxin chemotactic receptor 1; <b>PDBTitle:</b> crystal structure of thermostabilised human c5a anaphylatoxin2 chemotactic receptor 1 (c5ar) in complex with ndt9513727