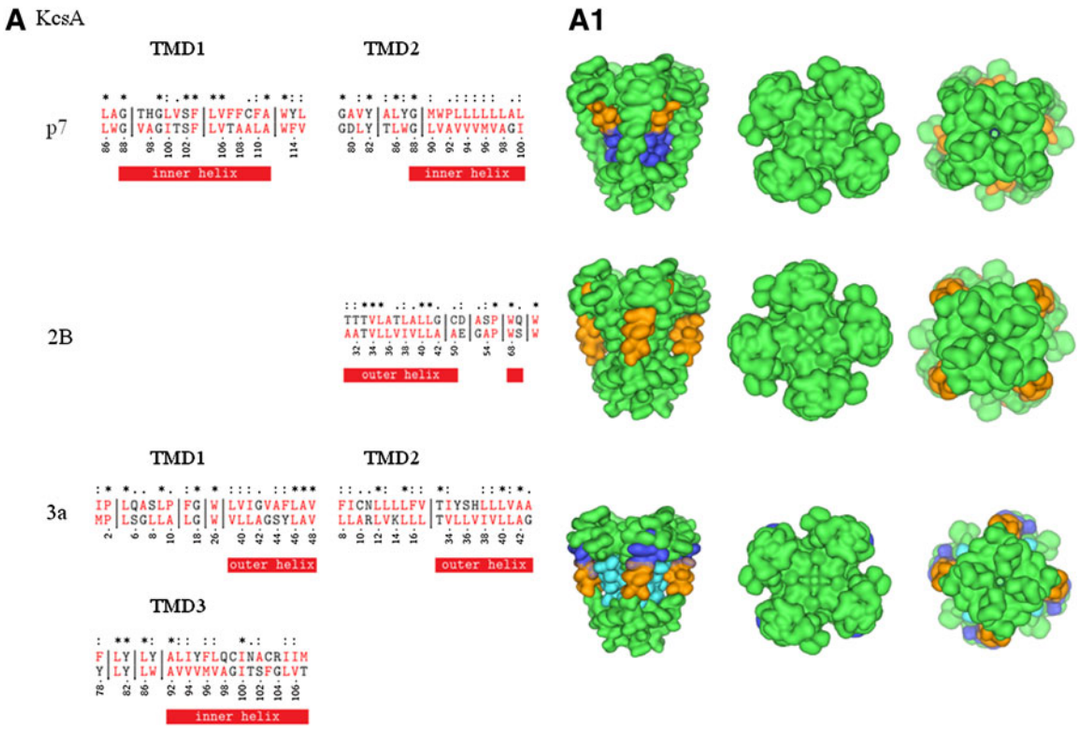
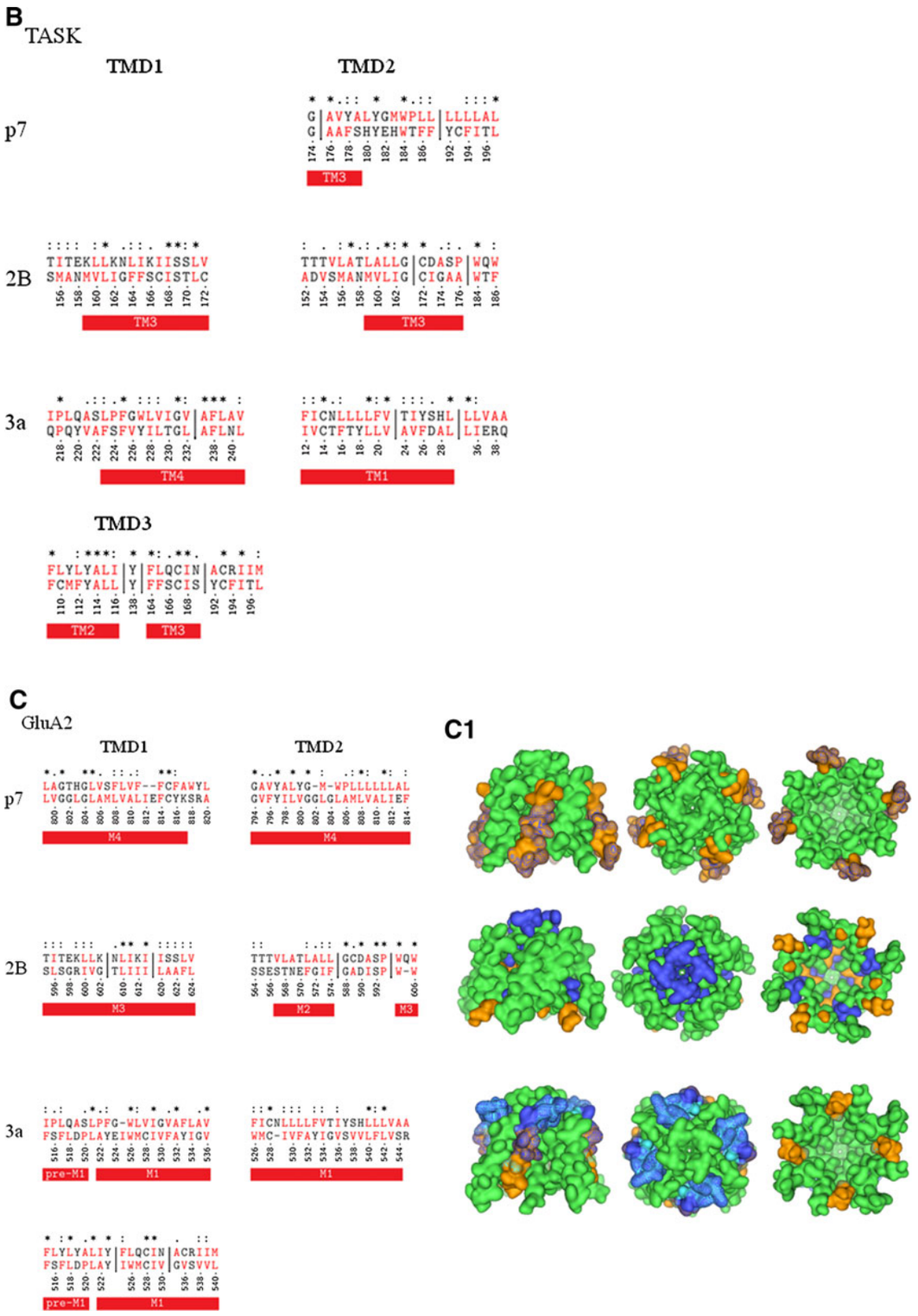
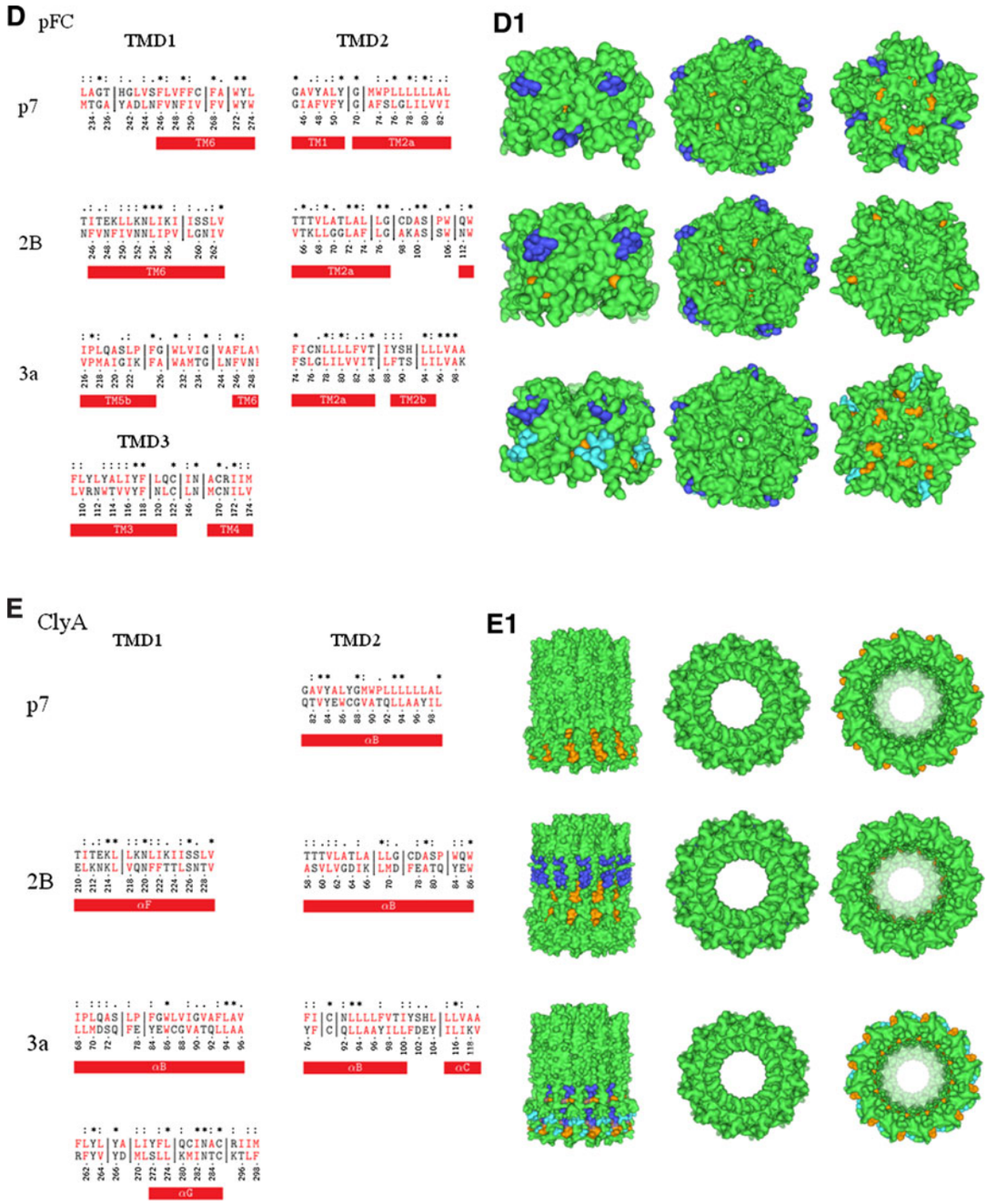
Supplementary Material



SUPPLEMENTARY FIG. S1. Sequence alignment of p7 (HCV), 2B (Polio virus), and 3a (SARS-CoV) with K^+ channel from *Streptomyces lividans* (KcsA, 1BL8) (**A**) with mapping of the aligned sequence onto the crystal structure **(A1)**; acid-sensitive potassium channel protein (TASK, UniProtKB/Swiss-Prot O14649) (**B**), α-amino-3-hydroxy-5-methyl-4-isoxazole propionic acid (AMPA)-sensitive, homotetrameric rat glutamate A2 receptor (GluA2, 3KG2) (**C**), with mapping of the aligned sequence onto the crystal structure **(C1)**; pentameric formate channel (pFC, 3KLY) (**D**) with mapping of the aligned sequence onto the crystal structure **(D1)**; and Cytolysin A (ClyA, 2WCD) (**E**) with mapping of the aligned sequence onto the crystal structure **(E1)**. The symbols are defined as follows: ''*'' = identical residues; '':'' = conserved substitution; and ''.'' = semi-conserved substitution. Vertical lines indicate gaps. Hydrophobic residues are shown in red. The red bars indicate helical TMDs of the proteins, the green bars indicate β-sheet, and yellow indicates turn structures. The helices of the toxin and the nonviral channels are named according to their respective notation in the literature. The color code for mapping is as follows: alignments according to viral TMD1s are shown in blue, those according to TMD2s in orange, and those according to TMD3 of 3a in cyan.



SUPPLEMENTARY FIG. S1. (Continued).



SUPPLEMENTARY FIG. S1. (Continued).

Supplementary Table S1A. Similarity of $2B_{1-18}$ with Respective Toxin and Nonviral Channel Proteins: GluA2, TASK, ClyA, α-hemolysin, KcsA, MscL, nAChR, pLGIC (ELIC), 3A, Vpu, BST-2, and pFC

	Aa of TMD1	*	:	.	-	*Gaps*	*Aa in gaps*	*Aromatic aa*
MscL; TMD1 [2OAR] nAChR; [2BG9]	11	3	4	3	1	-	-	F
A/D: M3	13	5	5	1	2	-	-	-
B:M1	9	5	2	1	1	-	-	-
C:M1	15	3	6	2	4	-	-	-
E: M1	6	5	1	-	-	-	-	-
TASK; TM3	14	4	4	2	4	-	-	F
GluA2; M2 [3KG2]	18	3	11	1	3	-	-	F
pFC; TM6 [3KLY]	17	4	8	3	2	1	1	F
ClyA; αF [2WCD]	18	5	7	3	3	1	2	F

Entry Code in the protein data bank (www.rcbs.org) is given in brackets. Identical aromatic amino acids are listed. The helices of the toxin and the nonviral channel proteins are named according to their respective sequence number in the literature.

''Aa'' = amino acids; ''*'' = identical residues; '':'' = conserved substitution; ''.'' = semi-conserved substitution; ''TMD'' = transmembrane domain.

Supplementary Table S1B. Similarity of $2B_{27-46}$ with Respective Toxin and Nonviral Channel Proteins

	Aa of TMD2	*	:	.	-	*Gaps*	*Aa in gaps*	*Aromatic aa*
MscL; TMD1 [2OAR]	9	2	4	1	2	-	-	-
pLGIC; α1 [2VL0]	4	3	-	1	-	2	16	W
KcsA; outer/pore helix [1BL8]	13/2	5/1	3/-	4/1	1/-	1/-	7/-	-/W
TASK; TM3	10	3	3	3	1	1	8	-
GluA2; M2/M3 [3KG2]	8/2	-/2	3/-	1/-	4/-	-/-	-/-	F/W
pFC; TM2a/TM3 [3KLY]	12/2	6/1	2/1	3/-	1/-	1/-	1/-	F/W
ClyA; αB [2WCD]	20	3	10	3	4	3	2/4/2	F,W

SUPPLEMENTARY TABLE S2A. SIMILARITY OF $3A_{35-55}$ WITH RESPECTIVE TOXIN AND NONVIRAL CHANNEL PROTEINS: GLUA2, TASK, CLYA, α-HEMOLYSIN, KCSA, MSCL, NACHR, PLGIC (ELIC), 3A, VPU, BST-2, AND PFC

	Aa of TMD1	*	:	.	-	*Gaps*	*Aa in gaps*	*Aromatic aa*
MscL; TMD2 [2OAR]	20	6	5	4	5	-	-	F
nAChR; [2BG9]								
A/D: M1	18	5	5	5	3	1	3	F,Y
pLGIC; α4 [2VL0]	21	6	7	3	5	1	3	F
KcsA; outer helix [1BL8]	10	3	5	1	1	-	-	-
TASK; TM4	15	5	6	1	3	1	4	F,Y
GluA2; preM1/M1 [3KG2]	6/14	-/4	2/2	2/3	2/5	-/1	-/1	F/F,Y,W
pFC; TM5b/TM6 [3KLY]	9/4	2/1	3/1	1/1	3/1	1/-	1/-	F/F
ClyA; αB [2WCD]	21	3	8	4	6	2	3/5	F,Y,W

Entry Code in the protein data bank (www.rcbs.org) is given in brackets. Identical aromatic amino acids are listed. The helices of the toxin and the nonviral channel proteins are named according to their respective sequence number in the literature.

''Aa'' = amino acids; ''*'' = identical residues; '':'' = conserved substitution; ''.'' = semi-conserved substitution; ''TMD'' = transmembrane domain.

Supplementary Table S2B. Similarity of $3A_{79-99}$ with Respective Toxin and Nonviral Channel Proteins

	Aa of TMD2	*	:	.	-	*Gaps*	*Aa in gaps*	*Aromatic aa*
MscL; TMD2 [2OAR]	11	2	4	1	4	-	-	F
nAChR; [2BG9]								
A/D: M4	21	3	13	-	5	2	4/1	F
B:M1/M2	12/7	5/4	4/1	1/1	2/1	2/-	(6/2)/-	F,Y/F
E: M1/M2/M3	2/9/10	1/4/2	1/3/5	-/1/-	-/1/3	-/1/-	-/9/-	F/F/F
pLGIC; α2/α3 [2VL0]	5/15	1/3	2/8	1/1	1/3	-/1	-/3	Y/F
KcsA; outer helix [1BL8]	11	3	4	1	3	-	-	-
TASK; TM1	16	4	7	2	3	1	2	F
GluA2; M1 [3KG2]	19	3	9	-	7	1	1	F,Y,W
pFC; TM2a/TM2b [3KLY]	11/5	4/1	3/3	2/-	2/1	-/-	-/-	F/F
ClyA; αB/αC [2WCD]	12/5	3/1	5/2	-/1	4/1	2/-	13/-	Y,F/-

Supplementary Table S2C. Similarity of $3A_{105-125}$ with Respective Toxin and Nonviral Channel Proteins

	Aa of TMD3	*	:	.	-	*Gaps*	*Aa in gaps*	*Aromatic aa*
MscL; TMD2 [2OAR]	12	4	3	-	5	-	-	F,Y
nAChR; [2BG9]								
A/D: M1	12	3	3	1	5	1	1	F
B: MA/M4	2/18	-/5	1/6	-/1	1/6	-/1	-/1	W/F
C: M1	13	4	3	3	3	-	-	Y
E: M2/M3/M4	6/5/9	4/2/4	1/2/3	-/1/1	1/-/1	-/-/-	-/-/-	F/F/F
pLGIC; α1/α2 [2VL0]	8/8	2/1	4/5	-/1	2/2	1/1	11/5	F,W/F
KcsA; inner helix [1BL8]	16	2	7	1	6	-	-	-
TASK; TM2/TM3	8/6	4/3	2/1	-/2	2/-	-/-	-/-	F,Y/F
GluA2; pre-M1/M1 [3KG2]	6/14	2/3	1/3	1/1	2/7	-/1	-/1	F/Y
pFC; TM3/TM4 [3KLY]	13/6	3/2	6/2	-/1	4/1	1/-	1/-	W,F/-
ClyA; αG [2WCD]	9	4	3	-	2	-	5	-