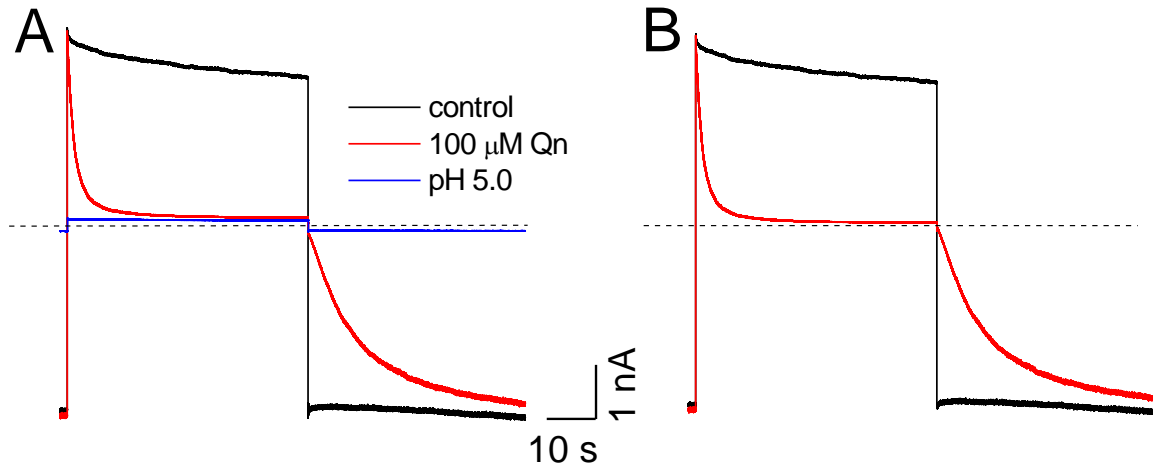
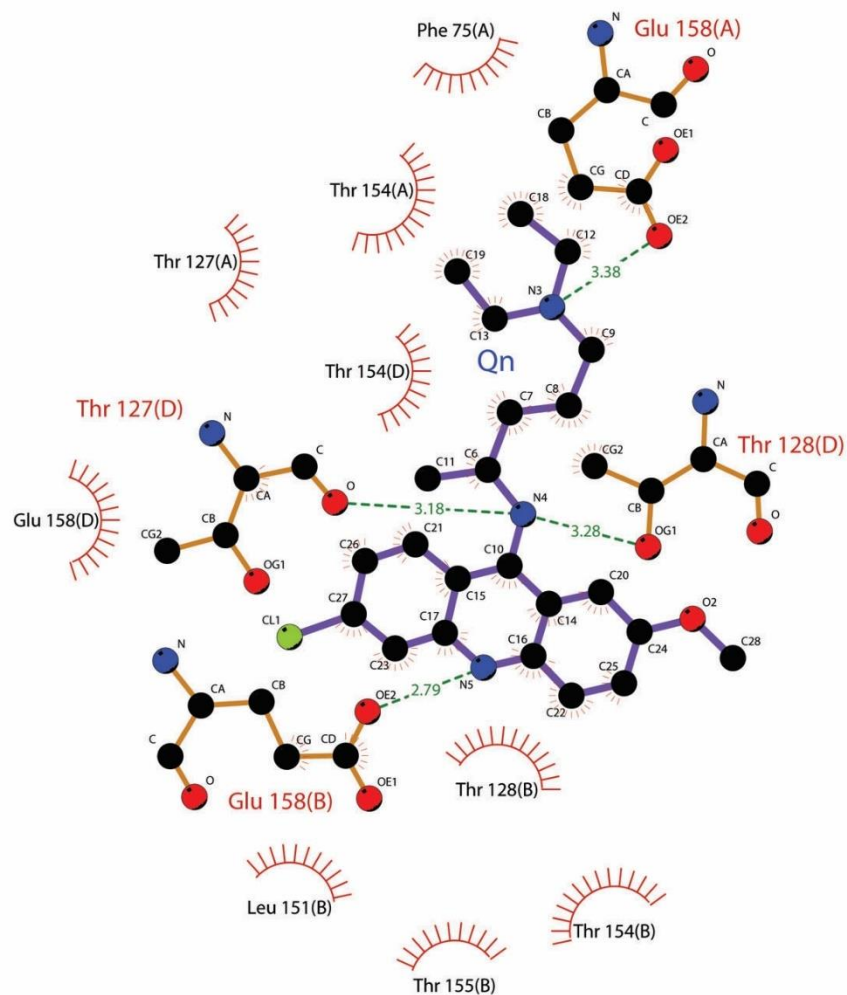


**Table S1.** Intermolecular hydrogen-bonds and hydrophobic contacts between quinacrine and Kir4.1 channels.

Quinacrine		Kir4.1		
		<i>Hydrogen-bonds</i>		
Donor	Atom	Acceptor	Atom	Distance (Å)
Qn	N3	GLU158 (A)	OE2	3.38
Qn	N4	THR128 (D)	OG1	3.28
Qn	N4	THR127 (D)	O	3.18
Qn	N5	GLU158 (B)	OE2	2.79
		<i>Hydrophobic contacts</i>		
Donor	Atom	Acceptor	Atom	Distance (Å)
Qn	C7	GLU158 (D)	CD	3.60
Qn	C6	GLU158 (D)	CD	3.29
Qn	C21	GLU158 (D)	CD	3.57
Qn	C15	GLU158 (D)	CD	3.72
Qn	C8	THR154 (D)	CG2	3.74
Qn	C7	THR154 (D)	CG2	3.83
Qn	C8	THR128 (D)	CG2	3.52
Qn	C7	THR128 (D)	CG2	3.77
Qn	C26	THR127 (D)	CA	3.83
Qn	C21	THR127 (D)	CA	3.72
Qn	C25	GLU158 (B)	CD	3.61
Qn	C22	GLU158 (B)	CD	3.93
Qn	C16	GLU158 (B)	CD	3.35
Qn	C22	GLU158 (B)	CG	3.84
Qn	C23	THR155 (B)	CB	3.66
Qn	C23	THR154 (B)	CG2	3.57
Qn	C22	THR154 (B)	CG2	3.38
Qn	C17	THR154 (B)	CG2	3.47
Qn	C16	THR154 (B)	CG2	3.33
Qn	C27	LEU151 (B)	CD2	3.82
Qn	C23	LEU151 (B)	CD1	3.51
Qn	C27	LEU151 (B)	CG	3.77
Qn	C23	LEU151 (B)	CG	3.75
Qn	C20	THR128 (B)	CG2	3.82
Qn	C14	THR128 (B)	CG2	3.68
Qn	C10	THR128 (B)	CG2	3.79
Qn	C18	GLU158 (A)	CD	3.62
Qn	C12	GLU158 (A)	CD	3.77
Qn	C9	GLU158 (A)	CD	3.83
Qn	C19	GLU158 (A)	CG	3.72
Qn	C18	GLU158 (A)	CG	3.86
Qn	C19	THR154 (A)	CG2	3.69
Qn	C13	THR154 (A)	CG2	3.80
Qn	C18	THR154 (A)	CG2	3.89
Qn	C13	THR127 (A)	C	3.83
Qn	C18	PHE75 (A)	CE1	3.75



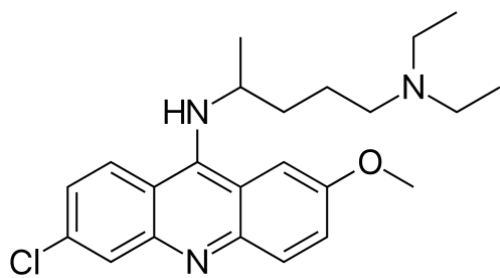
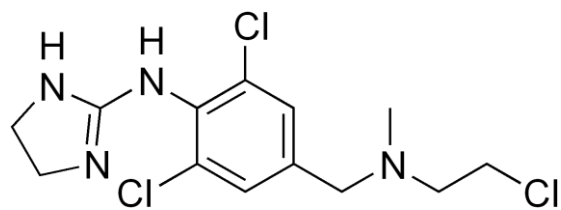
**Fig. S1.** Subtraction of endogenous/leak currents. (A) Uncorrected (raw) Kir4.1 current traces in control (black), 100  $\mu$ M Qn (red) and pH 5.0 (blue) conditions. (B) Kir4.1 currents in control (black) and 100  $\mu$ M Qn (red) conditions after the subtraction of endogenous/leak currents (blue trace en A).



### Key

- |                              |   |
|------------------------------|---|
| Ligand bond                  | His 53 Non-ligand residues involved in hydrophobic contact(s) |
| Non-ligand bond              | Corresponding atoms involved in hydrophobic contact(s)        |
| Hydrogen bond and its length |   |

**Fig. S2.** Schematic depiction of the main interactions of Kir4.1 and quinacrine (Qn). This image was generated with LIGPLOT program. A distance between donor and acceptor of less than 3.5 Å is considered as a hydrogen-bond, and a 4.1 Å distance between two hydrophobic atoms is considered a hydrophobic interaction.

**A****B**

**Fig. S3.** Structures of quinacrine (A) and chloroethylclonidine (B).