

Supplementary Figure 1

	(...)	
mSlc4a10	RISAIESLFGASMTGIAYSLFGGQPLTIL GSTGP VLVFEKILFKFCKEYGLSYLSLRASI	597
rSlc4a8	RISAIESLFGASMTGIAYSLFAGQPLTIL GSTGP VLVFEKILFKFCKDYALSYSLRACI	566
mSlc4a8	RISAIESLFGASMTGIAYSLFAGQPLTIL GSTGP VLVFEKILFKFCKDYALSYSLRALI	564
	*****.*****:*.***** *	
mSlc4a10	GLWTATLCIILVATDASSLVCYITRFTEEA FASLICI IFIYEALEKLFELSETYPINMHN	657
rSlc4a8	GLWTAFLCIVLVATDASSLVCYITRFTEEA FASLICI IFIYEAIEKLIHLAETYP IHMS	626
mSlc4a8	GLWTAFLCIVLVATDASSLVCYITRFTEEA FASLICI IFIYEAIEKLIHLAETYP IHMS	624
	***** **:*****:***:.*:*****:*. *	
	(...)	
mSlc4a10	AIGIPSPKLQVPSVFKPTRDDRGWFVTPLGPNPWWTIIAAIIPALLCTIL I IFMD ₈₃₁ QQIT ₈₃₅ AV	837
rSlc4a8	LIGVPSPKLQVPSVFKPTRDDRGWFISPIGPNPWWTVIAAIIPALLCTIL I IFMD ₈₀₀ QQIT ₈₀₄ AV	806
mSlc4a8	LIGVPSPKLQVPNVFKPTRDDRGWFINPIGPNPWWTVIAAIIPALLCTIL I IFMD ₇₉₈ QQIT ₈₀₂ AV	804
	:*.....*:.*:***:***** **** **	
mSlc4a10	IINRKEHKLKKGCGYHLDLLMVAVMLGVCSIMGLPW FVAAT ₈₇₈ VLSITHVNSLKLESECSAP	897
rSlc4a8	IINRKEHKLKKGCGYHLDLLVVAIMLGVC SLMGLPW FVAAT ₈₄₇ VLSITHVNSLKLESECSAP	866
mSlc4a8	IINRKEHKLKKGCGYHLDLLMVAVMLGVCSIMGLPW FVAAT ₈₄₅ VLSITHVNSLKLESECSAP	864
	*****:*.*****:***** *****	
mSlc4a10	GEQPKFLGIREQRTGLMIFILMGSSVFMTSILKFIPMPVLYGVFLYMGASSLKGIQLFD	957
rSlc4a8	GEQPKFLGIREQRTGLMIFVLMGCSVFMTAVLKFIPMPVLYGVFLYMGVSSLQGIQFFD	926
mSlc4a8	GEQPKFLGIREQRTGLMIFVLMGCSVFMTAVLKFIPMPVLYGVFLYMGVSSLQGIQFFD	924
	*****:***.*****:*****.***:***:*	
mSlc4a10	RIKLFWMPAKHQPDFIYLRHVPLRKVHLFTVIQMSCLGLLWIIKVSRAAIV F PMMVLALV	1017
rSlc4a8	RLKLFGMPAKHQPDFIYLRHVPLRKVHLFTLVQLTCLVLLWVIKASPA AIV F PMMVLALV	986
mSlc4a8	RLKLFGMPAKHQPDFIYLRHVPLRKVHLFTLVQLTCLVLLWVIKASPA AIV F PMMVLALV	984
	*.*** *****.***.*** ***** *	

Figure S1. Fragments of the multiple sequence alignment of Slc4a8 from *Mus musculus* (mSlc4a8), *Rattus norvegicus* (rSlc4a8) and Slc4a10 from *Mus musculus* (mSlc4a10). Sequences were retrieved from the UniProtKB database; accession codes are Q8JZR6 for mSlc4a8, F1LUB7 for rSlc4a8 and Q5DTL9 for mSlc4a10. Residues from the S1 site are highlighted in bold and those coordinating Na⁺ (D800, T804, and T847) in rat Slc4a8 structure (PDB: 7rtm) are underlined. We defined the S1 site by residues within 8.0 Å from K⁺ and CO₃²⁻ ions in the rSlc4a8 structure.

Supplementary Figure 2

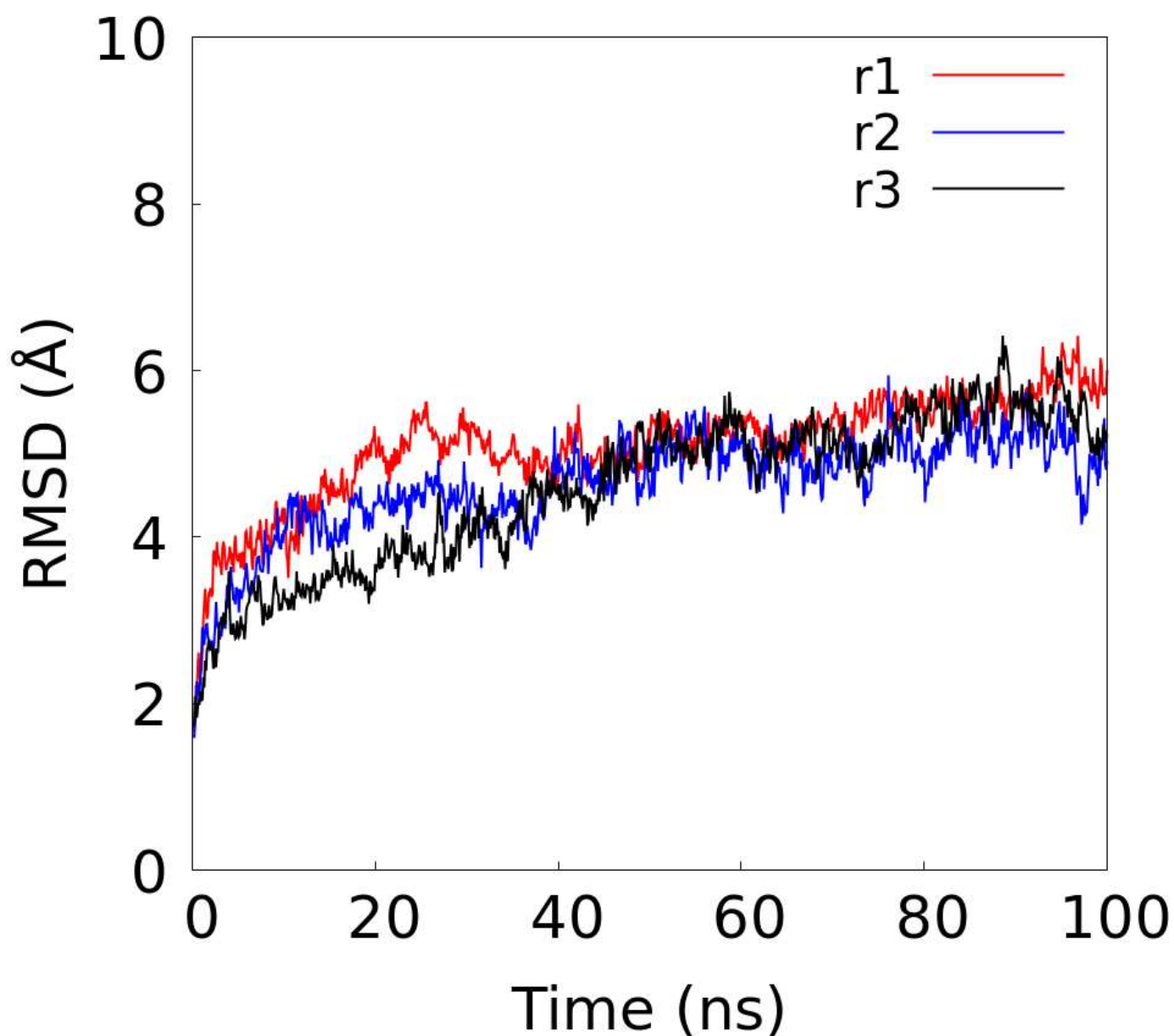


Figure S2. Root mean square deviation (RMSD) of backbone atoms during 100 ns for the three MD simulations (referred as r1, r2, and r3). RMSD was computed with reference to the first frame of each MD.