

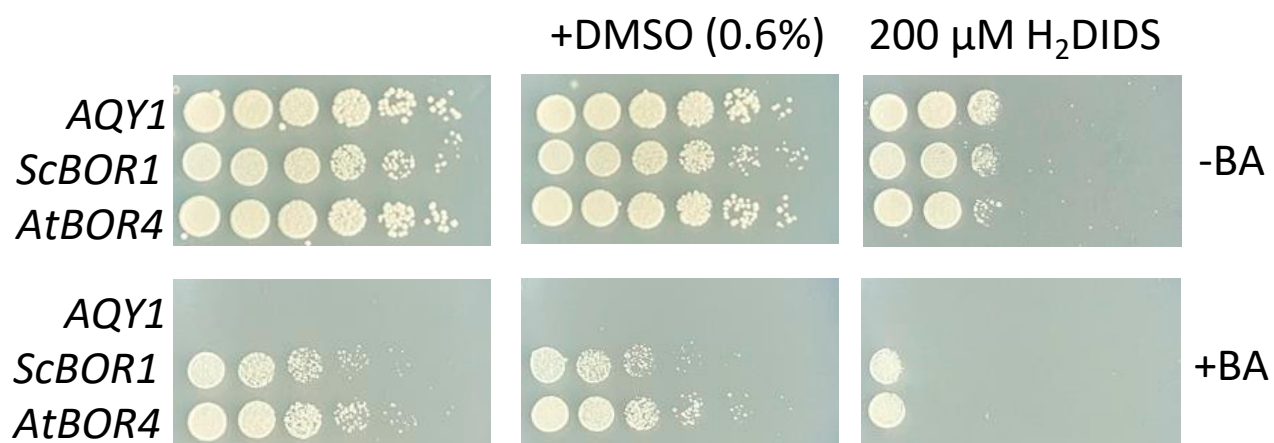
**A**

		Helix H1	
HsSLC4A1	-----GLVRD	IRRRYPYYLS	395
AtBOR1	-----MEETFV--PFEGIKNDLKGRLMCYKQ		24
SmBorlp	MLKDSTGVTISRGFASRECTQPSEETNDEPNTESSVVDSRNDDEESHEKLSRRRLPKLGMGIWLDLDKDRIPYYKS		75
ScBorlp	MSNESTRVTVSRGCTASDECAQALERTNDELDRRESSVSESRSDEESHEKLSRRRFPTLGIGIWLDLDKDRIPYYKS		75
	TM1	TM2	
HsSLC4A1	DITDAFSP--QVLAAVIFIYFAALSPAIFGGLLGEKTRNQMGVSELLISTAVQGILFALLGAQPLLVVGFSGPL		468
AtBOR1	DWTGGFKAGFRILAPTTYIFFASAIPVISFGEQLERSTDGVLTAVQTLASTAICGMIHSII GGQPLLI LGVAEPT		99
SmBorlp	DWVDAFNY--RVIPSTVDTYFN NLLPAIAFAQDMFDRTDNSYG VNEVL LSSAMAGIVFGVL AGQPLCIVGVTGPI		148
ScBorlp	DWVDAFNY--RVIPSIVDTYFN NLLPAIAFAQDMFDRTDNSYG VNEVL LSSAMAGIVFGVL GGQPLCIVGVTGPI		14
	N96	G135	
	TM3	TM4	TM5
HsSLC4A1	LVFEEAFFSFCETNG----LEYIVGRVWIGFWLILLVLVVAFEGSFLVRFI SRYTQEIFS FLISLI FIYETFSK		539
AtBOR1	VIMYTFMFNFAKARPELGRDLFLAWSGWVCVWTALMLFVLAICGACSIINRFTRVAGELFGLLIAMLFMQQAIKG		174
SmBorlp	SIFNYTVYEIIKPLN----TSYFGFMFWICLWSMIFHLLLAFTNVVCLLQYVTTFFPCDIFGLFINVVYIQKGIQI		219
ScBorlp	SIFNYTVYEIIKPLN----TSYFGFMFWICMWSMIFHLVLAFNAVCLLQYVTTFFPCDIFGLFINVVYIQKGIQI		219
		Y212	
	TM6		
HsSLC4A1	LIIKFQDHPLQKTYNNVLMVPKPGQPLPNTALLSLVLMAGTFFFAMMLRKFKNSSYFPGKLRRVIGDFGVPISI		614
AtBOR1	LVDEFRIPERENQK-LKEF---LPSWRF-ANGMFALVLSFGLLLTG LRSRKARSWRYGTGWLRS LIADYGVP LMV		244
SmBorlp	LTRQFHNTSGEKSV-----QDG FASVVVALVM TAFGLFFKSFHHY PLFTHKIRT FISDY STALS V		279
ScBorlp	LTRQFSAKSGEKSV-----QDG FASVVVALVM TAFGLFFKLFHY YPLFSHRIRTFISDY STALS V		279
	TM7	TM8	
HsSLC4A1	LIMVLVDEFFIQ---DITYTQKLSVPDGFKVSNS SARGWVIHPLGL-----RSEFP IWM MFASAL PALLVF ILIFL		680
AtBOR1	LVWTVGSYI-----PAGDV PKGI PRRLF SPNP WSPGAYGNW TVVKEM LDVIPY I IGAF IPASMI AVLYYF		315
SmBorlp	LFWSSFTHFGGYLNDVKFKKLPITK-----SFFPTS KFNRP QNTWLAYE---PIPV KDVFIAL PF GII LTILFYF		346
ScBorlp	LFWSSFTHFGGYLHDVKFKKLPITK-----AFFPTS KVNRP QNTWLAYE---PIPV KDVFIAL PF GI FLTILFYF		346
	TM9	TM10	
HsSLC4A1	ESQITT LIVSKPERKMVGSGFHL D LLLV VMGGVAALFGMPWL SATTV RSVTHAN-----		736
AtBOR1	DHSV ASQLAQ QKEFNLRKPSSYHY D LLLGFLTMCGL LGVPPS NGVIP QSPMHTKSLATLKYQLLRNL VATAR		385
SmBorlp	DHN VSSLMAQRHQYKLRKPSSFH Y DFALL GLTTCISGV LGIPAP NGLIP QAPLHTETLLVRDS-----		409
ScBorlp	DHN VSSLMAQRHQYK LKKPSSFH Y DFALL GLTTCISGV LGIPAP NGLIP QAPLHTETLLVRDS-----		409
	D347	D371	N391 Q396A
HsSLC4A1	-----ALTVM GKASTPG-----AAAQ IQEV		756
AtBOR1	RSIKTNASLGQLYDNMQEAYHHMQTPLVYQQPQGLKELKESTIQATTFTG NLNAPVDET LF DIEKE IDDLLPVEV		460
SmBorlp	-----NQ NVRC		416
ScBorlp	-----NQKVISC		416
	TM11	TM12	
HsSLC4A1	KEQR ISGLLVAVLVGLSIL--MEPILSRIP LAVLFGIFLYM GVTSLSGIQLFDRILL LFKPPKYHPDVP-----		823
AtBOR1	KEQ RVSN LLQSTMVGGCVA--AMPILK MIPTSV LWGYFAFMAIESLP GNQFW ERILL FTAPS RR FKVLEDYHAT		533
SmBorlp	VEQ RL TNT FQGLMILGTMT RPLL VCLGEIP QAVLSGLFF IMINGL M TNV I IHRIV L FSDPKRR DN NSPL---		487
ScBorlp	VEQ RF TNT FQGLMILGTMT RPLL VCLGEIP QAVLSGLFF IMINGL M TNS IIQRLV L FSDPNRR DN TSPL---		487
	R420 T422	G458	
	TM13	TM14	
HsSLC4A1	YVKRVKTWRMHL---FTGIQII CLAVL WVVKSTPASLALPFVLILT VPLRRVLLPLIFRNVELQC LDADD AKAT		894
AtBOR1	FVETVPFKTIAMFTLFQT TYLLICFGLTWIPI---AGVMFPLMIMFLIPVRQYLLPRFFKGAHLQDLDA AEYEEA		605
SmBorlp	--AKISK RSMVIF---LCFSLAGFTGEFAITNTIAAIGFPLVLLLSVIVS-FSFTYIFP SEELKVLD NNVAQR F		555
ScBorlp	--MKVSKKS MLIF---LSFSLTG FAGEFAITNTIAAIGFPLVLLLSVLVS-FSFAYIFP TEELKILD TNVAQKF		555
HsSLC4A1	FDE-----EEG-----RDEYDEVAMPV-	911	
AtBOR1	PALPFN LA AETEIGSTTSYPGDLEILDEVMTRS RGEFR HTSSPKV	650	
SmBorlp	TLKNLLLL ENI-----RDAKFSDRHKF-----	576	
ScBorlp	TIKNLLLL ENI-----RDAKFCDKHED-----	576	

**B**

	ScBor1p	SmBor1p	AtBOR1	HsSLC4A1
ScBor1p	100.00%	88.89%	27.79%	24.69%
SmBor1p	88.89%	100.00%	27.98%	24.69%
AtBOR1	27.79%	27.98%	100.00%	28.24%
HsSLC4A1	24.69%	24.69%	28.24%	100.00%

**Figure S1.** Alignment of borate transporters with human SLC4A1. **(A)** Alignment was performed in UniProt using the full-length sequences for ScBor1p, SmBor1p, AtBOR1, and the membrane domain sequence for human SLC4A1. Marked in red are residues investigated in this study, with *S. cerevisiae* numbering below. Helix H1 and all 14 transmembrane helices are indicated above their respective sequences. In blue are regions which when deleted result in lost function. **(B)** UniProt output for the percent identity matrix for the four sequences.



**Figure S2.** Sensitivity to H<sub>2</sub>DIDS. Plasmids encoding the specified gene were tested against H<sub>2</sub>DIDS in 0.6% DMSO or just 0.6% DMSO in the presence or absence of 20mM boric acid and plated on CSM-His selective media. Plates were incubated at 30°C and imaged after 5 days.