

Supplementary Figure S1

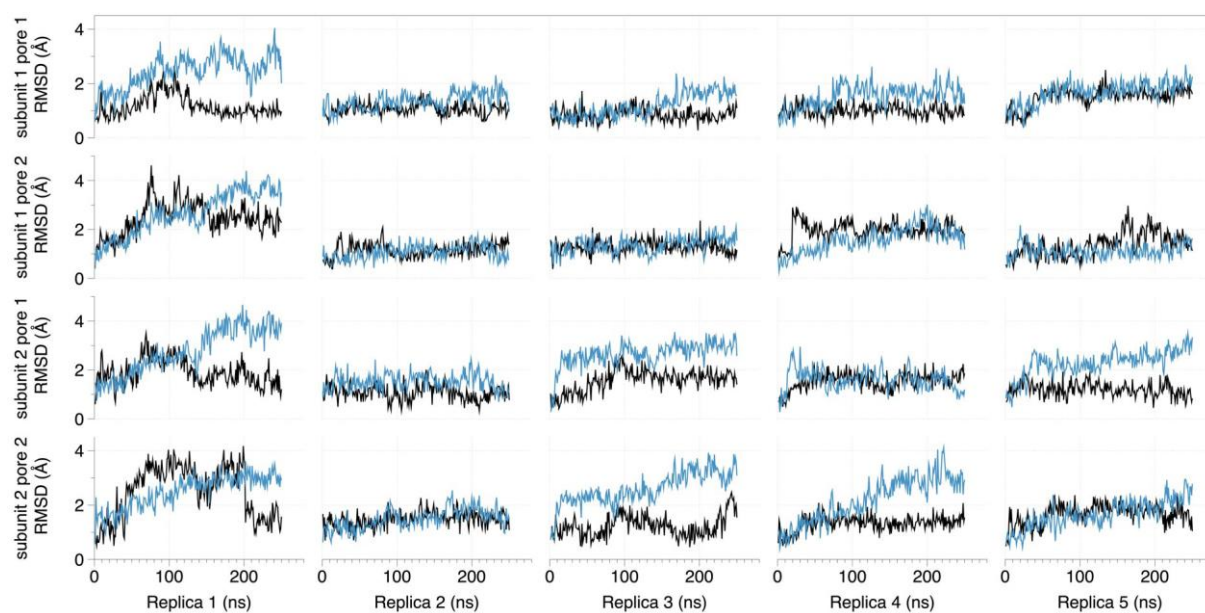


Figure S1. Structural stability of the selectivity filter. Analysis of root-mean-square deviation (RMSD) of the backbone of residues forming the selectivity filter of AtTPC1 in the presence of 0.15 M KCl (black) and 0.15 M NaCl (blue).

Supplementary Figure S2

	AtTPC1-D269		AtTPC1-E637	
Medicago_truncatula_Medtr2g090380.1	NLILAVVYDSFKSELV	[...]	GNWHEELMESYKDLT	Angiosperm TPC1
Arabidopsis_thaliana_AT4G03560.1	NLILAVVYDSFKQLA	[...]	GNWQVWMEISYKDLT	
Vitis_vinifera_GSVIVT01020549001	NLILAVYDSFKNOLA	[...]	NNWQVWMSQSYKDLT	
Chenopodium_quinoa_LOC110703516	NLILAVVYDSFKSELA	[...]	GNWQAWMQTYWDLT	
Chenopodium_quinoa_LOC110685197	NLILAVVYDSFKSELA	[...]	GNWQAWMQTYWDLT	
Populus_trichocarpa_Potri.013G131100.2	NLILAVVYDSFKDLV	[...]	GNWHEWMSQSYKDLT	
Nicotiana_tabacum_Nitab4.5-0000512g0020.1	NLILAVVYDSFKSELV	[...]	GNWQVWMSQSYKELT	
Aquilegia_coerulea_Aqcoe4G103300.1	NLILAVVYDSFKQLV	[...]	GNWQVWMEISYKELT	
Spirodela_polyrhiza_Spipo14G0028300	NLILAVVYDSFKQLA	[...]	GNWQVWMEISYRDLT	
Oryza_sativa_LOC_Os01g48680.1	NLILAVYDSFKQLA	[...]	GNWQAWMEISYRDLT	
Salvinia_cucullata_Sacu-v1.1-s0093.g019069	NLILAVVYDSFKDLA	[...]	GNWQVWLESEFVILT	Fern TPC1
Blechnum_spicant_scaffold-VITX-2006239	NLILAVVYDSFKQLA	[...]	GNWQVWLESYVTLT	
Thuidium_delicatulum_scaffold-EEMJ-2039009	NLILAVVYDSFKQLA	[...]	GNWHVWMDGFLEVT	Bryophyte TPC1a
Physcomitrella_patens_Pp3c15-12230V3.1	NLILSVVYDSFKQLA	[...]	GNWHIWMDSYQEVLT	
Sphagnum_fallax_Sphfalx04G006400.1	NLILAVVYDSFKQLA	[...]	GNWQVWMDGYAQLT	
Takakia_lepidozioides_scaffold-SKQD-2009335	NLILAVVYDSFKQLA	[...]	SNWHVWMDGYAELT	
Physcomitrella_patens_Pp3c1-6272V3.1	NLILAVVYDSFKQLA	[...]	GSWQVWMDSYVVLTL	
Physcomitrella_patens_Pp3c1-6270V3.1	NLILAVVYDSFKQLA	[...]	GSWQVWMDSYVVLTL	
Thuidium_delicatulum_scaffold-EEMJ-2007306	NLILAVVYDSFKQLA	[...]	GNWQSWMDSEFVILT	
Marchantia_polymorpha_Mapoly0002s0274.1	NLILAVVYDSFKQLA	[...]	GNWQVWMDSTYGILS	
Nothoceros_vincentianus_scaffold-TCBC-2005470	NLILAVVYDSFKQLA	[...]	GNWQVWMEISYAHLT	
Klebsormidium_nitens_kfl100312-0080-v1.1	NLILAVLEDSFKQLG	[...]	ADWQDWMDSGYAILG	Klebsormidium TPC1
Klebsormidium_nitens_kfl100110-0290-v1.1	NLILAVLEDSFKQLG	[...]	ASWQDWMDSGYAVLS	
Klebsormidium_nitens_kfl100097-0180-v1.1	SLILAVVYNGYKDLT	[...]	TLVSDWQSIASNTY	
Klebsormidium_nitens_kfl100001-0210-v1.1	SLILAVVYNGYKDLT	[...]	SLFVSWLTIAGRIT	
Klebsormidium_nitens_kfl100012-0290-v1.1	NLILAVLEAFKEQVV	[...]	SSWLTQDAFVRAT	Chara TPC1
Chara_australis_CL6562.Contig1-All.p1	SLILSVVERGYQRLA	[...]	RDWIVFAKGYVAAT	
Marchantia_polymorpha_Mapoly0050s0061.1	HLILFALTYNNYKVOLA	[...]	NNWYVIMDYGIVAAS	Bryophyte TPC1b
Marchantia_polymorpha_Mapoly0062s0036.1	NVAFAVIYTNEKROMA	[...]	GNWYIIMEGYSAAT	
Physcomitrella_patens_Pp3c3-16950V3.1	NLIVFTVYYSNYKAQMV	[...]	NNWYVIMDAYAVAT	
Takakia_lepidozioides_scaffold-SKQD-2009261	NLVFSVYYSNYKAQIA	[...]	NNWYVIMDAYAAAT	
Sphagnum_fallax_Sphfalx16G086000.1	NLAFMVYYSNYKVEIA	[...]	NNWYVIMDAYAFVT	
Sphagnum_fallax_Sphfalx19G080400.1	NLAFVYYSNYKAQIA	[...]	NNWYVIMDAYAIVT	
Sphagnum_fallax_Sphfalx03G070700.1	NLAFSVYYSNYKAQMA	[...]	NKMYVIMDAYAAVT	
Buxbaumia_aphylla_scaffold-HRWG-2017281	NLAFSVYYSNYKAQMA	[...]	NKMYVIMDAYAAVT	
Physcomitrella_patens_Pp3c19-18680V3.1	NLAFSLIYYSNYKAQMA	[...]	NKMYVIMDAYAAVT	
Thuidium_delicatulum_scaffold-EEMJ-2039845	NLAFSVYYSNYKAQMA	[...]	NKMYVIMDAYAAVT	
Physcomitrella_patens_Pp3c18-10190V3.1	NLAFSVYYSNYKAQMA	[...]	NKMYVIMDAYAAVT	
Physcomitrella_patens_Pp3c21-11410V3.1	NLAFSVYYSNYKAQMA	[...]	NKMYVIMDAYAAVT	
Takakia_lepidozioides_scaffold-SKQD-2080274	NLVFSVYYSNYKAQMA	[...]	NKMYVIMDAYAVAT	
Sphagnum_fallax_Sphfalx16G017900.1	SLAFSVYYSNYKSQMV	[...]	NKMYVIMDAYAAAT	
Buxbaumia_aphylla_scaffold-HRWG-2013254	NLAFSVYYSNYKAQMA	[...]	NKMYVIMDGYAAAA	
Physcomitrella_patens_Pp3c14-20770V3.1	NLAFSVYYSNYKAQMA	[...]	NKMYVIMDGYAAAT	
Physcomitrella_patens_Pp3c1-28370V3.1	NLAFSVYYSNYKAQMA	[...]	NKMYVIMDGYAAAT	
Physcomitrella_patens_Pp3c2-10230V3.1	NLAFSVYYSNYKAQMA	[...]	NKMYVIMDGYAAAT	

Figure S2. Sequence comparison of TPC1s from different species. Shown are the regions around AtTPC1-D269 and AtTPC1-E637. Sequence data are from [9].

Supplementary Figure S3

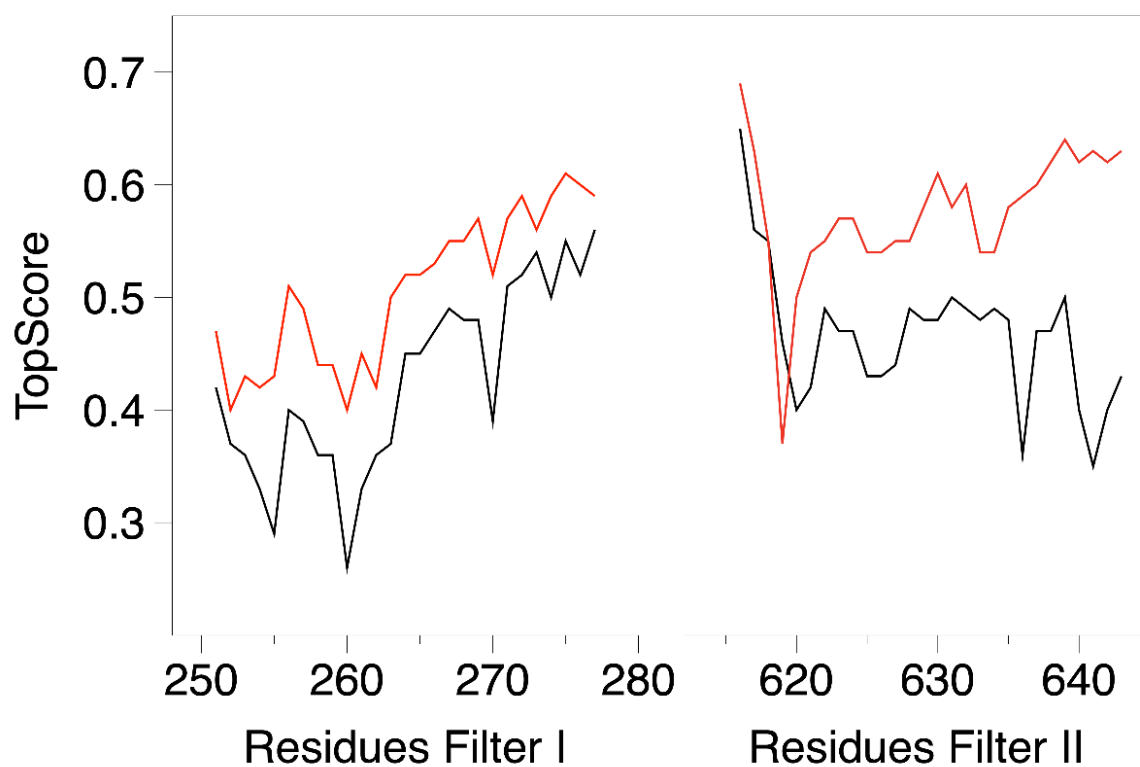


Figure S3. Per-residue TopScore of the filter regions in the AtTPC1 crystal structure of the closed configuration (black) and in the model of the open configuration (red). TopScore [55] provides a meta quality assessment of the protein structure at the global and per-residue level by estimating the error in a scale from 0 to 1. There is only a moderate increase in the estimated error between the crystal closed configuration and the modelled open configuration. The largest differences are observed for the selectivity filter residues in the second domain of AtTPC1. These residues are located in the vicinity of the IIS6 helix, which is the helix responsible for channel opening.