

Supplementary Table S1. Sequence similarity between OsLsi2 and two other Si transporters from rat (*Rattus norvegicus*) and the diatom *Phaeodactylum tricornutum*. Two other bacterial transporters with predicted structural similarity with OsLsi2 but no reported Si-transport function are also included (SLC13A5 from the bacterium *Vibrio cholera* and arsB from the bacterium *Escherichia coli*; see text for details; see also Supplementary Fig. S1).

Protein	Species	# Residues	% identity in X residues overlap (relative to OsLsi2)*	Score*	Gap frequency*
OsLsi2	Rice (<i>O. sativa</i>)	472			
SLC34A2	Rat (<i>R. norvegicus</i>)	695	40% in 20	34.0	0%
PtSIT1	Diatom (<i>P. tricornutum</i>)	512	23.5% in 34	36.0	0%
NaCT (SLC13A5)	<i>V. cholera</i>	449	23.4% in 184	86.0	3.3%
arsB	<i>E. coli</i>	429	20.6% in 218	90.0	2.8%

*According to the Expasy SIM Alignment Tool (<https://web.expasy.org/sim/>).

Supplementary Table S2. Lsi2 secondary structure predictions based on the SOSUI algorithm (https://harrier.nagahama-i-bio.ac.jp/sosui/sosui_submit.html).

Protein	Species	Total length (aa)	Average hydrophobicity	Predicted # TM domains	TM6-7 gap (aa)**
OsLsi2	Rice (<i>Oryza sativa</i>)	472	0.71	11	71
ZmLsi2	Maize (<i>Zea mays</i>)	472	0.79	11	71
HvLsi2	Barley (<i>Hordeum vulgare</i>)	474	0.71	11	74
TaLsi2*	Wheat (<i>Triticum aestivum</i>)	474	0.71	11	74
Monocots (avg ± stdev)		473 ± 1.16	0.73 ± 0.04		72.5 ± 1.73
CmLsi2	Pumpkin (<i>Curcubita moschata</i>)	529	0.46	11	139
CsLsi2	Cucumber (<i>Cucumis sativus</i>)	547	0.38	11	157
GmLsi2*	Soybean (<i>Glycine max</i>)	536	0.56	11	146
AtLsi2*	Arabidopsis (<i>Arabidopsis thaliana</i>)	502	0.47	11	115
Dicots (avg ± stdev)		528.5 ± 19.16	0.47 ± 0.07		139.25 ± 17.78

* not functionally verified to date; ** number of amino acid residues spanning transmembrane domains 6 and 7; aa, number of amino-acid residues; TM, transmembrane.