

Supplementary materials

<i>Sa</i> NRT1.1	1	MAHNITSMDMEIGKD	I	VCDAWDYKGRPA	A	RSKTGGWQ	SAAMILGGEACERL	TTLG	IAVNLVTYLT	TGVMHLGNAASANTVTNFMGT	85	
<i>Sf</i> NRT1.1	1	MAHNITSMDMEIGKD	T	VCDAWDYKGRPAD	R	SKTGGWQ	SAAMILGGEACERL	TTLG	IAVNLVTYLT	TGVMHLGNAASANTVTNFMGT	85	
<i>Sg</i> NRT1.1	1	MAHNITSMDMEIGKD	T	VCDAWDYKGRPAD	R	SKTGGWK	SAAMILGGEACERL	TTLG	IAVNLVTYLT	TGVMHLGNAASANTVTNFMGT	85	
<i>Sa</i> NRT1.1	86	SFMLCLLGGF	I	ADTFLGRYLT	I	AIFATIQALG	VTVLT	I	STIIPSLRPPK	CEEGSDSCIPASDTQLGVLYLALYLTALGTGGVKAS	170	
<i>Sf</i> NRT1.1	86	SFMLCLLGGF	I	ADTFLGRYLT	I	AIFATIQALG	VTVLT	I	STIIPSLRPPK	CEEGSDSCIPASDTQLGVLYLALYLTALGTGGVKAS	170	
<i>Sg</i> NRT1.1	86	SFMLCLLGGF	I	ADTFLGRYLT	I	AIFATIQALG	VTVLT	I	STIIPSLRPPK	CV	EEGSDSCIPASDTQLGVLYLALYLTALGTGGVKAS	170
<i>Sa</i> NRT1.1	171	VSGFGTDQFDES	N	KD	EKLHMIKFFNW	FFFF	I	SLGSLAAVT	ILVYIQDNMGRQWGYG	I	CACAIMLALVIFLCGTRRYRFKKLVGSP	255
<i>Sf</i> NRT1.1	171	VSGFGTDQFDES	N	K	EKLHMIKFFNW	FFFF	I	SLGSLAAVT	ILVYIQDNMGRQWGYG	I	CACAIMLALVIFLCGTRRYRFKKLVGSP	255
<i>Sg</i> NRT1.1	171	VSGFGTDQFDES	N	K	EKLHMIKFFNW	FFFF	I	SLGSLAAVT	ILVYIQDNMGRQWGYG	I	CACAIMLALVIFLCGTRRYRFKKLVGSP	255
<i>Sa</i> NRT1.1	256	LTQIAAVFVAAWRKRHMELPSDSSLLFN	I	DDLADGGKHKKQKLPHSKQYRFLDRAAI	KDPQMPSVVT	KVNIWYLP	T	STDVEEVKL			340	
<i>Sf</i> NRT1.1	256	LTQIAAVFVAAWRKRHMELPSDSSLLFN	I	DDLADGGKHKKQKLPHSKQYRFLDRAAI	KDPQMPSVVT	KVNIWYLP	T	STDVEEVKL			340	
<i>Sg</i> NRT1.1	256	LTQIAAVFVAAWRKRHMELPSDSSLLFN	I	DDLADGGKHKKQKLPHSKQYRFLDRAAI	KDPQMPSVVT	KVNIWYLP	T	STDVEEVKL			340	
<i>Sa</i> NRT1.1	341	VLRMLPIWATTII	F	WTIYAQMSTFSVSQATTMDRH	I	GSSFR	I	PAASLTVFFVGSILITVPIYDRVVP	I	AS	KLLHNPPQGLTPLQR	425
<i>Sf</i> NRT1.1	341	VLRMLPIWATTII	F	WTIYAQMSTFSVSQATTMDRH	I	GSSFR	I	PAASLTVFFVGSILITVPIYDRVVP	I	AS	RLLHNPPQGLTPLQR	425
<i>Sg</i> NRT1.1	341	VLRMLPIWATTII	F	WTIYAQMSTFSVSQATTMDRS	I	GSSFQ	I	PAASLTVFFVGSILITVPIYDRVVP	I	AS	KILLHNPPQGLTPLQR	425
<i>Sa</i> NRT1.1	426	IAVGLVFSII	SMVSAALVEIRRLKVAQ	D	AGLVNKP	FQVVPLSVFWLVPQFFFVGAGEAFTYIGQLDFFLRECPKGMKTMSTGLFL					510	
<i>Sf</i> NRT1.1	426	IAVGLVFSII	SMVSAALVEIRRLKVAQ	D	AGLVNKP	FQVVPLSVFWLVPQFFFVGAGEAFTYIGQLDFFLRECPKGMKTMSTGLFL					510	
<i>Sg</i> NRT1.1	426	IAVGLVFSII	SMVSAALVEIRRLKVAQ	E	AGLVNKP	FQVVPLSVFWLVPQFFFVGAGEAFTYIGQLDFFLRECPKGMKTMSTGLFL					510	
<i>Sa</i> NRT1.1	511	TTLSLGFFVSSVLVS	AVHKITGDKHPW	IADNLNRGR	LDYFYWLLAGLSVLNFLVYLLFAKWYVYKEKRLA	E	EGYIVEEEDDGPAC				595	
<i>Sf</i> NRT1.1	511	TTLSLGFFVSSVLVS	AVHKITGDKHPW	IADNLNRGR	LDYFYWLLAGLSVLNFLVYLLFAKWYVYKEKRLA	D	EGYIVEEEDDGPAC				595	
<i>Sg</i> NRT1.1	511	TTLSLGFFVSSVLVS	AVHKITGDKHPW	IADNLNRGR	LDYFYWLLAGLSVLNFLVYLLFAKWYVYKEKRLA	E	EGYIVEEEDDGPAC				595	
<i>Sa</i> NRT1.1	596	H									596	
<i>Sf</i> NRT1.1	596	H									596	
<i>Sg</i> NRT1.1	596	H									596	

Figure S1. Alignment of the proteins from *Suaeda*, *Sa*NRT1.1, *Sf*NRT1.1 and *Sg*NRT1.1. The protein sequences of *Sf*NRT1.1 and *Sg*NRT1.1 were obtained by translation of the contigs in the *S. fruticosa* and *S. glauca* transcriptomes.

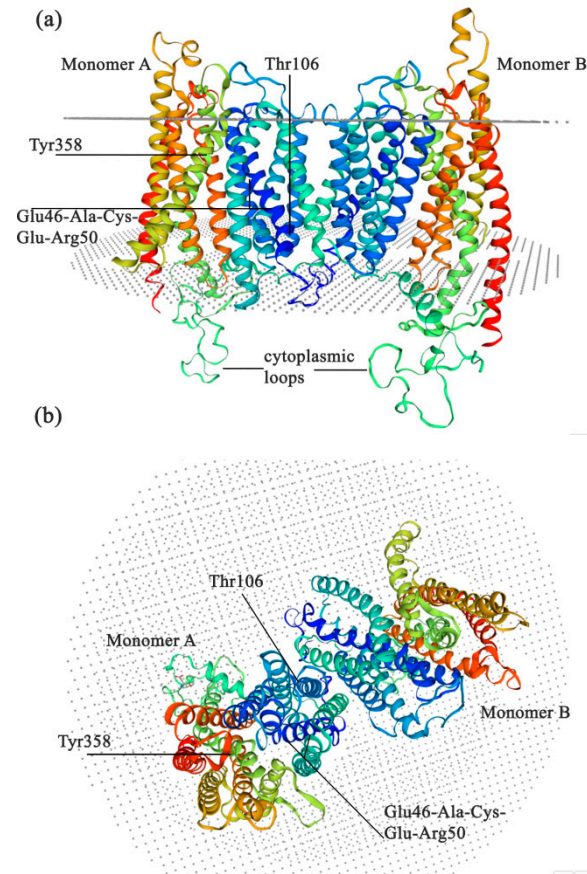


Figure S2. SaNPF6.3 model predicted by Swiss-Model software (<https://swissmodel.expasy.org/> (accessed on 20 September 2023)). The key motifs (ExxER, EACER), amino acid residues (Thr106, Tyr358) and cytoplasmic loops are marked; (a) side view and (b) top view.

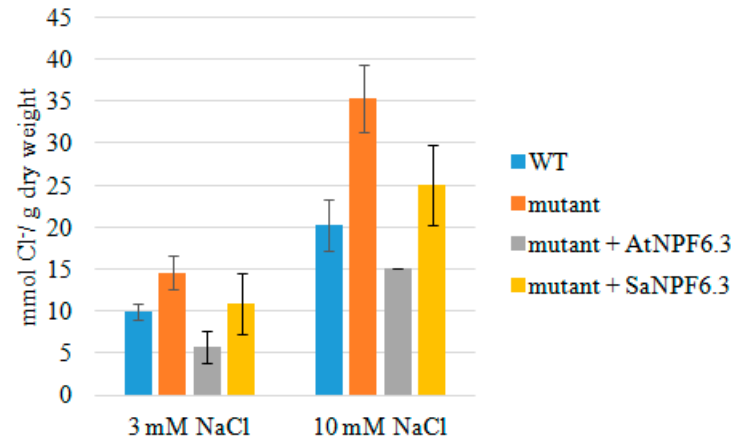


Figure S3. Chloride absorption from the liquid minimal SD media containing NaCl (3 or 10 mM) and NaNO₃ (1 mM) by the yeast strains; the initial wet weight of the yeast suspension was 10 mg/ml. Controls: wild type DL-1 strain and the mutant *Δynt1* strain, transformed with vectors pCHLX and pCCUR2, and the mutant *Δynt1* strain transformed with pCHLX-*AtNPF6.3* and pCCUR2. The yeast cells grew in the liquid media for 18 hours at 37°C; absorption of chloride by the cells was determined by measuring chloride concentration decline in incubation media using Cl⁻-selective electrode (Niko-Analit, Moscow, Russia).

Table S1. List of the primers used in the research.

Primer name	Nucleotide sequences (5'-3')	Primer designation
SaNPF6.3_f	GACAGACCAATTCGACGAGA	Amplification of the cDNA central part of the SaNPF6.3 gene; Amplification of 5'- and 3'- fragments of SaNPF6.3 cDNA (1st round of PCR)
SaNPF6.3_r	CTAATAAGTAGTGTACGGTTGTCA	
SaNPF6.3_F1	CCTAGTCGAAATCAGGCG	Amplification of 5'- and 3'- fragments of SaNPF6.3 cDNA (2nd round of PCR);
SaNPF6.3_5'RACE_R1	GATGTTGGCAAGTACCAGATGTTG	
SaNPF6.3_R1	CTCCCACGAAGAAGAATTGAG	RT-qPCR with SaNPF6.3_F1 primer
ZeoYNTRfl_F	GGCTTTAATTTGCAATCGGCCGAACACGTGGTCAAGATCTGTTTTTCCC	Amplification of the right flanking sequence of the YNT1 locus to
pBlueYNTRfl_R	GGCTTTAATTTGCAATCGGCCGAACACGTGGTCAAGATCTGTTTTTCCC	

		obtain a deletion mutant $\Delta ynt1$
pBlueYNTLfl_F	CTGCAGGAATTCGATCGGAGGTTCATGGATCAGGC	Amplification of the left flanking sequence of the YNT1 locus to obtain a deletion mutant $\Delta ynt1$
YNTLflZeo_R	TGGTGTGTGGGGCGGCCGAACAAGAAGAGGCGGAAAAGCAAACC	
ZeoCas1	GTTCGGCCGCCCCACACACCATAGCTTCAAA	Zeocin resistance gene amplification
ZeoCas2	GTTCGGCCGATTGCAAATTAAAGCCTTCGAG	
SaNPF6.3_Gib_F	ATGGCTCATAATATTACTAGTATGGATATGGAAATTGG	SaNPF6.3 full-length coding sequence amplification from cDNA
SaNPF6.3_Gib_R	TTAGTGACATGCTGGCCCGT	
AtNPF6.3_Gib_F	ATGTCTCTTCCTGAACTAAATCTGATG	AtNPF6.3 full-length coding sequence amplification from cDNA
AtNPF6.3_Gib_R	TCAATGACCCATTGGAATACTCGGC	
pYNR1_F	GGTCGACGGTATCGATAAGCTTATGGGGCTCCATATATCGTATGAC	amplification of the YNR1 nitrate reductase promoter
pYNR1_R	CCATACTAGTAATATTATGAGCCATTACAACCTATCCAAAGTTCGTGAGGA	
tYNR1_F	CGGGCCAGCATGTCACTAACCTAAGCGAAATCGAAATCAAACT	amplification of the nitrate reductase terminator
tYNR1_R	CCCGGGCTGCAGGAATTAATTCAGTATTTCAGAATCATGACCCC	

		YNR1
SaNPF6.3_1074_F	GCACAAATGAGTACTTTCTCCGTG	Introduction of Tyr358His amino acid substitution
SaNPF6.3_Tyr358His_R	ATGGATTGTCCAGAAAATAATAGTGGTG	
SaNPF6.3_318_F	ATTGCTATCTTTGCAACAATCCAAGC	Introduction of the amino acid substitution Thr106Asp or Thr106Ala
SaNPF6.3_Thr106Asp_R	ATCTAGATACCTTCCAAGGAAGGTGTCAG	
SaNPF6.3_Thr106Ala_R	AGCTAGATACCTTCCAAGGAAGGTGTC	
pYNR1_GFP_F	CACGAACTTTGGATAGTTGTAATGAGCAAGGGCGAGGAACTG	mGFP amplification
TEV_GFP_R	TGAAAATATAAATTTTCCCCGGGCTTGTACAGCTCGTCCATGC	
TEV_SaNPF6.3_F	CCCGGGGAAAATTTATATTTTCAAGGTCAATTTATGGCTCATAATATTACTAGTATGGATAT	SaNPF6.3 full-length coding sequence amplification from pCHLX-GFP-SaNPF6.3 cDNA
SaNPF6.3_Gib_R	TTAGTGACATGCTGGCCCGT	
pYNR1_R3	TACAACTATCCAAAGTTCGTGAGGA	Amplification of a linear form of pCHLX-pYNR1-tYNR1
DL-1_Chr2_HpURA3_F	GAGGTGAAGTCGTTGACGCA	PCR screening
Hp_DL-1_Chr1_R	TTGGTACCACCGCACTTCTC	PCR screening
AtNPF6.3_388R	ATCTTGGTGGTCGAAGTCCC	sequencing
AtNPF6.3_934F	ATCAGGAAGCGGGAGTTACC	
AtNPF6.3_1106R	GTCTCGGATTGTGCGACTGA	
pYNR1_R2	CATCAGATTTAGTTTCAGGAAGAGACATTACAACCTATCCAAAGTTCGTGAGGA	Amplification of

tYNR1_F2	GCCGAGTATTCCAATGGGTCATTGACCTAAGCGAAATCGAAATCAAAACT	the nitrate reductase promoter and terminator
SaNPF6.3_1632R	GCGGTTCAAGTTGTCAGCAA	sequencing
SaNPF6.3_391R	GCAGGCTCGGGATTATGGTAG	
SaeEF1alfa_F1	TGAGATGTGTGGCAATCC	RT-qPCR
SaeEF1alfa_R1	GTTGCTTCTGACTCCAAGAAT	
SaPP2A_RT_F1	GAGCTTTTTCGTATCGGCGG	
SaPP2A_RT_R1	CCAGCAGCGTAACAGTCTCT	

Table S2. List of the *A. thaliana* NPF genes and the corresponding proteins.

Gene	Araport ID (TAIR)	UniProtKB ID
<i>AtNPF1.1</i>	AT3G16180	Q8LPL2
<i>AtNPF1.2</i>	AT1G52190	Q9M817
<i>AtNPF1.3</i>	AT5G11570	Q9LYD5
<i>AtNPF2.1</i>	AT3G45720	Q9M171
<i>AtNPF2.2</i>	AT3G45690	Q9M174
<i>AtNPF2.3</i>	AT3G45680	Q9M175
<i>AtNPF2.4</i>	AT3G45700	Q9M173
<i>AtNPF2.5</i>	AT3G45710	Q9M172
<i>AtNPF2.6</i>	AT3G45660	Q9M1E1
<i>AtNPF2.7</i>	AT3G45650	Q9M1E2
<i>AtNPF2.8</i>	AT5G28470	Q3E8X3
<i>AtNPF2.9</i>	AT1G18880	Q9MV7
<i>AtNPF2.10</i>	AT3G47960	Q944G5
<i>AtNPF2.11</i>	AT5G62680	Q9LV10
<i>AtNPF2.12</i>	AT1G27080	Q9LFX9
<i>AtNPF2.13</i>	AT1G69870	Q8RX77
<i>AtNPF2.14</i>	AT1G69860	Q9CAR9
<i>AtNPF3.1</i>	AT1G68570	Q9SX20
<i>AtNPF4.1</i>	AT3G25260	Q9LSF0
<i>AtNPF4.2</i>	AT3G25280	Q9LSE8
<i>AtNPF4.3</i>	AT1G59740	Q93VV5
<i>AtNPF4.4</i>	AT1G33440	Q56XQ6
<i>AtNPF4.5</i>	AT1G27040	Q8VYE4
<i>AtNPF4.6</i>	AT1G69850	Q8H157
<i>AtNPF4.7</i>	AT5G62730	Q9FM20
<i>AtNPF5.1</i>	AT2G40460	Q8VZR7
<i>AtNPF5.2</i>	AT5G46050	Q9FNL7
<i>AtNPF5.3</i>	AT5G46040	Q9FNL8
<i>AtNPF5.4</i>	AT3G54450	Q9M1I2
<i>AtNPF5.6</i>	AT2G37900	P0CI03
<i>AtNPF5.7</i>	AT3G53960	Q9M331
<i>AtNPF5.8</i>	AT5G14940	Q9LFR1
<i>AtNPF5.9</i>	AT3G01350	Q9SRI2
<i>AtNPF5.10</i>	AT1G22540	Q0WP01
<i>AtNPF5.11</i>	AT1G72130	Q8RX67
<i>AtNPF5.12</i>	AT1G72140	Q9C7U1
<i>AtNPF5.13</i>	AT1G72125	Q0WSZ6
<i>AtNPF5.14</i>	AT1G72120	Q8VZE2
<i>AtNPF5.15</i>	AT1G22570	Q9SK99
<i>AtNPF5.16</i>	AT1G22550	Q9SK96
<i>AtNPF6.1</i>	AT5G13400	Q9LYR6
<i>AtNPF6.2</i>	AT2G26690	Q9SZY4
<i>AtNPF6.3</i>	AT1G12110	Q05085
<i>AtNPF6.4</i>	AT3G21670	Q9LVE0
<i>AtNPF7.1</i>	AT5G19640	Q3E9B5
<i>AtNPF7.2</i>	AT4G21680	Q8GXN2
<i>AtNPF7.3</i>	AT1G32450	Q9LQL2
<i>AtNPF8.1</i>	AT3G54140	Q9M390
<i>AtNPF8.2</i>	AT5G01180	Q9LFB8
<i>AtNPF8.3</i>	AT2G02040	P46032
<i>AtNPF8.4</i>	AT2G02020	Q84WG0
<i>AtNPF8.5</i>	AT1G62200	Q93Z20

Table S3. List of several gene sequences homologous to sequence *AtNPF6.3*, key motifs and amino acid residues of the corresponding proteins.

Species	Protein name	Glu-x-x-Glu-Arg motif (ExxER)	Thr(T)	Lys (K)	His(H)/ Tyr(Y)	Glu (E)	Pro (P)	Gene ID (GenBank)
<i>Arabidopsis thaliana</i>	AtNPF6.3	41–45 Glu-Ala-Val-Glu-Arg (EAVER)	101	164	His 356	476	492	NP_563899.1
<i>Suaeda altissima</i>	SaNPF6.3	46–50 Glu-Ala-Cys-Glu-Arg (EACER)	106	168	Tyr 358	482	498	OQ330855
<i>Thellungiella halophila</i>	ThNPF6.3	38–42 Glu-Val-Val-Glu-Arg (EVVER)	98	159	Tyr 346	463	479	BAJ33792.1
<i>Salicornia bigelovii</i>	SbNPF6.3	54–58 Glu-Ala-Cys-Glu-Arg (EACER)	114	176	Tyr 366	490	506	Sbi_g26995.t1*
<i>Medicago truncatula</i>	MtNPF6.3	41–45 Glu-Ala-Cys-Glu-Arg (EACER)	101	164	Tyr 356	480	496	XP_003608752.1
	MtNPF6.8 (NRT1.3)	44–48 Glu-Leu-Ala-Glu-Arg (ELAER)	104	169	Tyr 350	465	481	GU966590.1
<i>Zea mays</i>	ZmNPF6.4 (NRT1.1A)	46–50 Glu-Leu-Asn-Glu-Arg (ELNER)	106	172	Tyr 370	493	509	BT053880.1
	ZmNPF6.6 (NRT1.1B)	44–48 Glu-Leu-Phe-Glu-Arg (ELFER)	104	169	His 362	479	495	XM_008660202.3
	ZmNRT1.1C	44–48 Glu-Leu-Phe-Glu-Arg (ELFER)	104	166	His 356	472	488	XM_008660209.3
	ZmNRT1.1D	49–53 Glu-Leu-Asn-Glu-Arg (ELNER)	109	176	Tyr 368	484	500	XM_008651564.2
<i>Oryza sativa</i>	OsNPF6.3(NRT1.1A)	47–51 Glu-Leu-Asn-Glu-Arg (ELNER)	107	169	Tyr 366	488	504	XP_015650127.1
	OsNPF6.5(NRT1.1B)	44–48 Glu-Leu-Phe-Glu-Arg (ELFER)	104	169	His 362	479	495	XP_015614015.1
	OsNPF6.4(NRT1.1C)	58–62 Glu-Leu-Asn-Glu-Arg	118	180	Tyr 369	482	498	XP_015632236.1

		(ELNER)						
<i>Sorghum bicolor</i>	SbNRT1.1A	46–50 Glu-Leu-Asn-Glu-Arg (ELNER)	106	170	Tyr 364	486	502	XM_002443834.2
	SbNRT1.1B	44–48 Glu-Leu-Phe-Glu-Arg (ELFER)	104	169	His 359	478	494	XM_002464914.2
	SbNRT1.1C	53–57 Glu-Leu-Asn-Glu-Arg (ELNER)	113	177	Tyr 374	490	506	XM_002468647.2
<i>Populus trichocarpa</i> (black cottonwood)	PtNPF6.3	40–44 Glu-Ala-Met-Glu-Arg (EAMER)	100	161	Tyr 347	471	487	XM_002303476.4
<i>Brachypodium distachyon</i> (purple false brome)	BdNRT1.1A	44–48 Glu-Leu-Asn-Glu-Arg (ELNER)	104	168	Tyr 363	484	500	XP_003573480.1
	BdNRT1.1B	48–52 Glu-Leu-Phe-Glu-Arg (ELFER)	108	173	His 365	481	497	XP_003574312.1
	BdNRT1.1C	52–56 Glu-Leu-Phe-Glu-Arg (ELFER)	112	177	His 367	483	499	XP_003572060.1
	BdNRT1.1D	64–68 Glu-Leu-Asn-Glu-Arg (ELNER)	124	189	Tyr 381	494	510	XP_003562233.3
<i>Brassica napus</i> (rapeseed)	BnNPF6.3	40–44 Glu-Ala-Val-Glu-Arg (EAVER)	100	163	His 355	475	491	XP_013698339.2
<i>Brassica rapa</i> (Chinese cabbage)	BrNPF6.3	40–44 Glu-Ala-Val-Glu-Arg (EAVER)	100	163	His 355	475	491	XP_009110669.1
<i>Capsicum annuum</i> (pepper)	CaNPF6.3	42–46 Glu-Ala-Val-Glu-Arg (EAVER)	102	164	Tyr 354	478	494	KAF3635032.1
<i>Citrus</i>	CcNPF6.3	41–45 Glu-Ala-Cys-Glu-Arg	101	164	Tyr 356	479	495	XP_006440344.1

<i>clementina</i>		(EACER)						
<i>Glycine max</i> (soybean)	GmNPF6.3	41–45 Glu-Val-Met-Glu-Arg (EVMER)	101	164	His 347	471	487	XM_003517379.5
<i>Lactuca sativa</i> (lettuce)	LsNPF6.3	41–45 Glu-Ala-Cys-Glu-Arg (EACER)	101	164	Tyr 359	483	499	XP_023738876.1
<i>Nicotiana tabacum</i> (tobacco)	NtNPF6.3	42–46 Glu-Ala-Val-Glu-Arg (EAVER)	102	165	Tyr 359	482	498	XP_016452049.1
<i>Prunus persica</i> (peach)	PpNPF6.3	44–48 Glu-Ala-Cys-Glu-Arg (EACER)	104	167	Tyr 359	483	499	BAC81420.1
<i>Solanum lycopersicum</i> (tomato)	SINPF6.3	42–46 Glu-Ala-Val-Glu-Arg (EAVER)	102	164	Tyr 354	478	494	XP_004244572.1
<i>Solanum tuberosum</i> (potato)	StNPF6.3	42–46 Glu-Ala-Val-Glu-Arg (EAVER)	101	164	Tyr 354	478	494	XP_006358355.1
<i>Vitis vinifera</i> (grape)	VvNPF6.3	93–97 Glu-Ala-Cys-Glu-Arg (EACER)	153	216	Tyr 408	532	548	WJZ82426.1

Note: *amino acid sequence of SbNPF6.3 found in the *Salicornia* database (<https://www.salicorniadb.org/Home.html> (accessed on 20 September 2023)).