



Phosphoregulation of the intracellular termini of $K^+ - Cl^-$ cotransporter 2 (KCC2) enables flexible control of its activity

Received for publication, June 7, 2018, and in revised form, September 1, 2018. Published, Papers in Press, September 10, 2018, DOI 10.1074/jbc.RA118.004349

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Edited by Mike Shipston

The pivotal role of $K^+ - Cl^-$ cotransporter 2 (KCC2) in inhibitory neurotransmission and severe human diseases fosters interest in understanding posttranslational regulatory mechanisms such as (de)phosphorylation. Here, the regulatory role of the five *bona fide* phosphosites Ser³¹, Thr³⁴, Ser⁹³², Thr⁹⁹⁹, and Thr¹⁰⁰⁸ was investigated by the use of alanine and aspartate mutants. TI^+ -based flux analyses in HEK-293 cells demonstrated increased transport activity for S932D (mimicking phosphorylation) and T1008A (mimicking dephosphorylation), albeit to a different extent. Increased activity was due to changes in intrinsic activity, as it was not caused by increased cell-surface abundance. Substitutions of Ser³¹, Thr³⁴, or Thr⁹⁹⁹ had no effect. Additionally, we show that the indirect actions of the known KCC2 activators staurosporine and *N*-ethylmaleimide (NEM) involved multiple phosphosites. S31D, T34A, S932A/D, T999A, or T1008A/D abrogated staurosporine mediated stimulation, and S31A, T34D, or S932D abolished NEM-mediated stimulation. This demonstrates for the first time differential effects of staurosporine and NEM on KCC2. In addition, the staurosporine-mediated effects involved both KCC2 phosphorylation and dephosphorylation with Ser⁹³² and Thr¹⁰⁰⁸ being *bona fide* target sites. In summary, our data reveal a complex phosphoregulation of KCC2 that provides the transporter with a toolbox for graded activity and integration of different signaling pathways.

$K^+ - Cl^-$ cotransporter 2 (KCC2)² plays a pivotal role in inhibitory neurotransmission. Under normal physiological conditions, KCC2 mediates outward transport of K^+ and Cl^- , thereby lowering the intracellular Cl^- concentration ($[Cl^-]_i$) in neurons (1–3). This renders the action of GABA or glycine hyperpolarizing as their receptors are ligand-coupled Cl^- channels. KCC2 exists in two isoforms, KCC2a and KCC2b,

which differ in their N termini due to alternative promoters and first exon usage (4). In the adult, KCC2b is the most prominent isoform (5). Mice with disruption of the gene *Slc12a5* encoding both KCC2a and KCC2b die shortly after birth due to motor deficits (6). KCC2b-deficient mice survive up to 3 weeks postnatally (7), whereas KCC2a-deficient mice show no obvious phenotype (8).

Dysregulation of KCC2 is associated with several neurological and psychiatric disorders, including epilepsy, neuropathic pain, spasticity, ischemic insults, brain trauma, schizophrenia, and autism (9–19). This renders KCC2 a prime pharmacotherapeutic target and fosters interest in understanding posttranslational mechanisms of its regulation (20–25). Among those, phosphorelated mechanisms are most intensively scrutinized. The broad-spectrum kinase inhibitor staurosporine enhances KCC2 transport activity in hippocampal neurons (26). *N*-Ethylmaleimide (NEM) enhances KCC transport activity as well and is thought to act on the same regulatory kinases as staurosporine (27–30). In contrast, the protein phosphatase inhibitors calyculin and okadaic acid block KCC activation by cell swelling (31, 32).

Functional characterization of several KCC2 phosphosites demonstrated the importance of phosphorelated regulatory mechanisms (20, 23, 27, 33, 34). Dephosphorylation of the N-terminal phosphosite Thr⁶ of KCC2a (35, 36) or the pan-C-terminal phosphosites Thr⁹⁰⁶ and Thr¹⁰⁰⁶ (numbering according to mouse KCC2b) increases transport activity (27, 37–39). Similarly, phosphorylation of Tyr⁹⁰³ and Tyr¹⁰⁸⁷ decreases cell-surface expression as well as transport activity of Tyr¹⁰⁸⁷ (40–42). In contrast, phosphorylation of Thr⁹³⁴, Ser⁹³⁷, or Ser⁹⁴⁰ increases KCC2 transport activity (27, 43). The latter three phosphorylation sites are encoded in exon 22, which is exclusively conserved throughout vertebrate KCC2 and nontherian KCC4 (27, 33).

Analyses of the underlying regulatory mechanism identified several kinases that interact with KCC2. These kinases include protein kinase C (PKC), with-no-lysine (K) kinases (WNKs), oxidative stress-responsive kinase 1 (OSR1), Ste20p-related proline/alanine-rich kinase (SPAK), and creatine kinase (CKB) (35–37, 43–46). PKC was shown to phosphorylate Ser⁹⁴⁰ (43), and WNKs interact with SPAK/OSR1 to phosphorylate the KCC2a isoform-specific N-terminal residue Thr⁶ and the pan-residue Thr¹⁰⁰⁶ (35–37, 39, 47). WNKs also interact with a yet unknown kinase to phosphorylate Thr⁹⁰⁶ (36, 37, 39). Kinases

This work was supported by Deutsche Forschungsgemeinschaft Grants NO428/14-1 (to H. G. N.) and HA 6338/2-1 (to A.-M. H.). The authors declare that they have no conflicts of interest with the contents of this article.

This article contains Figs. S1 and S2.

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² The abbreviations used are: KCC, $K^+ - Cl^-$ cotransporter; NEM, *N*-ethylmaleimide; PKC, protein kinase C; WNK, with-no-lysine (K) kinase; OSR1, oxidative stress-responsive kinase 1; SPAK, Ste20p-related proline/alanine-rich kinase; HEK, human embryonic kidney; *mm*, *M. musculus*.

Table 1**Phosphosites in PhosphoSitePlus and PHOSIDA**

Dashes indicate no presence in the data base or they were not publicized. *rn*, *R. norvegicus*.

PhosphoSitePlus <i>mmKCC2</i>	PhosphoSitePlus <i>rnKCC2</i>	PHOSIDA <i>mmKCC2</i>	Transport activity measured by (Ref.)
Thr ⁶	—	—	34–36
Ser ²⁵	Ser ²⁵	Ser ²⁵	27, 34
Ser ²⁶	Ser ²⁶	Ser ²⁶	27, 34
—	Ser ³¹	Ser ³¹	—
Thr ³⁴	Thr ³⁴	Thr ³⁴	72
Thr ⁹⁰⁶	Thr ⁹⁰⁶	Thr ⁹⁰⁶	27, 37, 39
Ser ⁹¹³	—	—	—
Ser ⁹³²	—	(Ser ⁹³²)	—
Thr ⁹³⁴	Thr ⁹³⁴	(Thr ⁹³⁴)	27
Ser ⁹³⁷	Ser ⁹³⁷	Ser ⁹³⁷	27
Ser ⁹⁴⁰	Ser ⁹⁴⁰	Ser ⁹⁴⁰	28, 43
Ser ⁹⁸⁸	—	—	—
Thr ⁹⁹⁹	—	—	—
Thr ¹⁰⁰⁶	Thr ¹⁰⁰⁷	Thr ¹⁰⁰⁶	27, 28, 39
Thr ¹⁰⁰⁸	—	Thr ¹⁰⁰⁸	—
Ser ¹⁰²¹	Ser ¹⁰²²	Ser ¹⁰²¹	27
Ser ¹⁰²⁴	Ser ¹⁰²⁵	(Ser ¹⁰²⁴)	27
Ser ¹⁰²⁵	Ser ¹⁰²⁶	Ser ¹⁰²⁵	27

involved in the phosphorylation of the other phosphosites have yet to be identified. Overall, regulation of KCC2 transport activity by phosphorylation involves a variety of phosphosites as well as kinases and phosphatases. This complexity likely serves to match the demand for a fine-grained setting of $[Cl^-]$ to modulate inhibitory neurotransmission and to enable integration of different signaling pathways in neurons (27, 33, 34, 48–50).

Here, we analyzed the impact of *bona fide* phosphosites identified in large-scale phosphoproteomics studies on KCC2 transport activity. These residues were substituted by either alanine or aspartate in mouse KCC2b to block or mimic phosphorylation, respectively. Subsequently, transport activity measurements were performed in HEK-293 cells to determine KCC2 transport activity in the presence of various agents.

Results

Database mining and evolutionary conservation of KCC2 phosphosites

The databases PhosphoSitePlus and PHOSIDA subsume all experimentally observed phosphosites that were identified by MS-based proteomics studies (51, 52). Using KCC2 as query, we identified eight *bona fide* phosphosites, Ser³¹, Thr³⁴, Ser⁹¹³, Ser⁹³², Ser⁹⁸⁸, Thr⁹⁹⁹, and Thr¹⁰⁰⁸, in addition to the previously described phosphosites Thr⁶, Ser²⁵, Ser²⁶, Thr⁹⁰⁶, Thr⁹³⁴, Ser⁹³⁷, Ser⁹⁴⁰, Thr¹⁰⁰⁶, Ser¹⁰²¹, Ser¹⁰²⁴, and Ser¹⁰²⁵ (Table 1). Five of these eight phosphosites, Thr⁶, Ser²⁵, Ser²⁶, Ser³¹, and Thr³⁴ are located in the cytoplasmic N terminus whereby Thr⁶ is contained in both alternative exons 1 of KCC2a and KCC2b and Ser²⁵, Ser²⁶, Ser³¹, and Thr³⁴ are shared by both isoforms. The remaining phosphosites are located in the shared C terminus of both KCC2 isoforms. In the following, we focus our analyses on the two N-terminal Ser³¹ and Thr³⁴ and the three C-terminal Ser⁹³², Thr⁹⁹⁹, and Thr¹⁰⁰⁸ phosphosites as they were so far not characterized.

Multiple sequence alignment of vertebrate KCC subfamily members revealed that these phosphosites cover different patterns of phylogenetic conservation (Fig. 1). The phosphosite Thr¹⁰⁰⁸ is highly conserved throughout all vertebrate KCC isoforms. Thr⁹⁹⁹ is moderately conserved throughout KCC2 and

KCC3 and partially conserved in KCC1 and KCC4. The N-terminal phosphosite Ser³¹ is highly conserved in orthologous KCC2 members and is rarely observed in KCC1 and KCC4, whereas Thr³⁴ is mainly present in therian KCC2. Ser⁹³² is highly conserved in vertebrate KCC2 and nontherian KCC4. This phosphosite is located in exon 22, which also harbors the previously analyzed and highly conserved phosphosites Thr⁹³⁴, Ser⁹³⁷, and Ser⁹⁴⁰ (33).

Expression analyses of KCC2 phosphomutants

To study the posttranslational regulatory impact of phosphorylated Ser³¹, Thr³⁴, Ser⁹³², Thr⁹⁹⁹, and Thr¹⁰⁰⁸ for KCC2b (*Mus musculus* (*mm*)KCC2b) function, we generated two mutants for each phosphosite mimicking the phosphorylated (mutation into aspartate) or dephosphorylated (mutation into alanine) status. This resulted in a total of 10 mutants (KCC2^{S31A/D}, KCC2^{T34A/D}, KCC2^{S932A/D}, KCC2^{T999A/D}, and KCC2^{T1008A/D}). To analyze whether these mutations affect the expression pattern of KCC2, the constructs were transiently expressed in HEK-293 cells. All mutants showed a transfection rate in HEK-293 cells similar to KCC2^{WT} (Fig. S1). Furthermore, immunoreactivity against all mutants was detected at the plasma membrane and in the cytosol (Fig. 2). Only the nucleus was spared. Thus, all mutants were well expressed in HEK-293 cells and therefore suitable for transport activity measurements.

Regulatory role of S932D and T1008A

To investigate the regulatory relevance of the five *bona fide* phosphosites, we determined the transport activity of phosphomimetic (aspartate) and dephosphomimetic (alanine) mutations of *mmKCC2* by Tl⁺ flux measurements. All mutants as well as the KCC2^{WT} displayed at least a 2.9-times increased transport activity compared with mock-transfected cells (Fig. 3, Table 2, and Fig. S2). The loop diuretic furosemide, which specifically inhibits the function of cation-chloride cotransporters (53, 54), blocks most of the flux, demonstrating that the transport activity was largely mediated by KCC2 (see Fig. 5, Table 2, and Fig. S2).

Analogous to the previously described N-terminal Ser²⁵ and Ser²⁶ phosphosites (27), substitution of Ser³¹ and Thr³⁴ by alanine or aspartate did not alter transport activity compared with KCC2^{WT}. Similar results were obtained for the C-terminal mutants S932A, T999A/D, and T1008D. All four mutants showed a transport activity indistinguishable from KCC2^{WT} (Fig. 3 and Table 2). In contrast, substitution of Ser⁹³² by aspartate and Thr¹⁰⁰⁸ by alanine significantly enhanced KCC2 transport activity, albeit to a different extent (Fig. 3 and Table 2). To conclude, phosphorylation of the C-terminal residue Ser⁹³² and dephosphorylation of Thr¹⁰⁰⁸ result in an increased KCC2 transport activity in HEK-293 cells.

No change in abundance and cell-surface expression of KCC2^{S932D} and KCC2^{T1008A}

To analyze whether the enhanced activity of the two phosphomutants is due to increased abundance at the cell surface, we performed biotinylation assays for KCC2^{WT}, S932D, and T1008A (Fig. 4). KCC2^{WT} displayed a cell-surface localization of $16.7 \pm 1.6\%$ compared with the total KCC2 protein amount.

Regulation of KCC2 by multiple phosphosites

	N-terminus		C-terminus				
	[mmKCC2b]	31	34	932	940	999	1008
<i>hsKCC1</i>		P L E A				V G A D K I Q M T W T	
<i>rnKCC1</i>		P L D A				V G A D K I Q M T W T	
<i>mdKCC1</i>		C S E A				A R P E K V Q M T W T	
<i>acKCC1</i>		N T D S				T I P E K I Q M T W T	
<i>ggKCC1</i>		S S E A				T V P E N I Q M T W T	
<i>tgKCC1</i>		S S E A				P V P E N I Q M T W T	
<i>xtKCC1</i>		G S E A				L E L A K I H M T W T	
<i>trKCC1</i>		G A D G				L P S E K V Q M T W T	
<i>drKCC1</i>		S S D A				I L P E K N Q M T W T	
<i>hsKCC3</i>		N S N Y				T Y Q E K V H M T W T	
<i>rnKCC3</i>		N S N Y				T Y Q E K V H M T W T	
<i>mdKCC3</i>		N S N F				T Y Q E K V H M T W T	
<i>acKCC3</i>		N I N Y				T Y Q E K V H M T W T	
<i>xtKCC3</i>		H T D				A V P D R V H M T W T	
<i>trKCC3</i>		N T H V				E H H R R V Q M T W T	
<i>hsKCC2</i>		S T D T	S I T D E S R G S			T D P E K V H L T W T	
<i>rnKCC2</i>		S T D T	S I T D E S R G S			T D P E K V H L T W T	
<i>mmKCC2</i>		S T D T	S I T D E S R G S			T D P E V H L T W T	
<i>mdKCC2</i>		S T D S	S I T D E S R G S			A A P E K V H L T W T	
<i>acKCC2</i>			S I T D E S R G S			A A P E K V H L T W T	
<i>ggKCC2</i>		S T D L	S I T D E S R G S			S A P E K V H L T W T	
<i>xtKCC2</i>		S S E M	S I T D E S R G S			T T Q E K V H L T W T	
<i>tgKCC2</i>			S I T D E S R G S			A A P E K V H L T W T	
<i>drKCC2_1</i>		D H D	S I T D E S R I S			P T S D R V H M T W T	
<i>drKCC2_2</i>		S T D	S I T D S S R G S			T P G T A V Q M T W S	
<i>hsKCC4</i>		N V E V				P T P D K V Q M T W T	
<i>rnKCC4</i>		N V E V				P T P D K V Q M T W T	
<i>mdKCC4</i>		N T D M	S I S N E S R C S			A T P E K V Q M T W T	
<i>acKCC4</i>		N A S M	S I S D E S R S S			T T P E K V Q M T W T	
<i>ggKCC4</i>		S A E M	S I T D E S R G S			A M P E K V Q M T W T	
<i>tgKCC4</i>		C A E L	S I T D E S R G S			A V P E K V Q M T W T	
<i>drKCC4_1</i>		S T S V	S I T D V S R G S			A P T P A T M S	
<i>drKCC4_2</i>		N T D D	S I T D E S R S S			A T P E R V H M T W T	

Figure 1. Evolutionary conservation of phosphosites and their neighboring amino acids in KCC subgroups. Ser³¹, Thr³⁴, and Thr⁹⁹⁹ are moderately conserved in vertebrate KCC subfamily members. The phosphosites Thr¹⁰⁰⁶ and Thr¹⁰⁰⁸ are highly conserved throughout vertebrate KCCs. Ser⁹³², Ser⁹³⁷, Thr⁹³⁴, and Ser⁹⁴⁰ display similar degrees of phylogenetic conservation. They are only present in vertebrate KCC2 and in nontherian KCC4. *hs*, *H. sapiens*; *rn*, *Rattus norvegicus*; *md*, *Monodelphis domestica*; *gg*, *Gallus gallus*; *tg*, *Taeniopygia guttata*; *ac*, *Anolis carolinensis*; *xt*, *Xenopus tropicalis*; *tr*, *Takifugu rubripes*; *Dr*, *Danio rerio*.

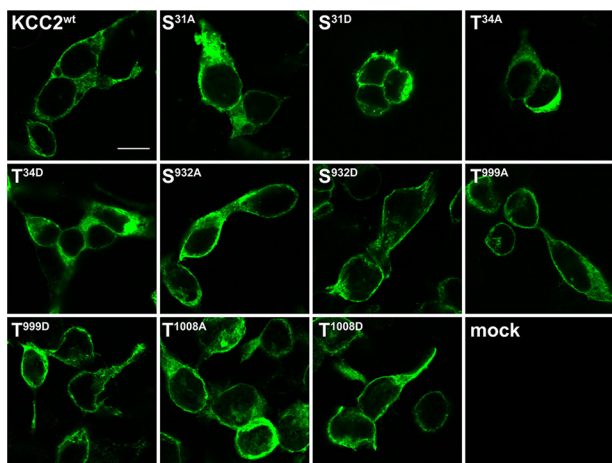


Figure 2. Expression of KCC2^{WT} or KCC2 phosphomutants in HEK-293 cells. The subcellular distribution of KCC2 mutants was indistinguishable from KCC2^{WT} with immunoreactivity outside the nucleus. Photomicrographs were taken with a confocal laser-scanning microscope. Scale bar, 10 μm.

This is in line with previously published results that reported a 12–13% surface localization for rat KCC2 (55, 56). The cell-surface rates of S932D (19.8 ± 2.5%) and T1008A (17.4 ± 0.2%) were indistinguishable from KCC2^{WT}. Thus, the enhanced

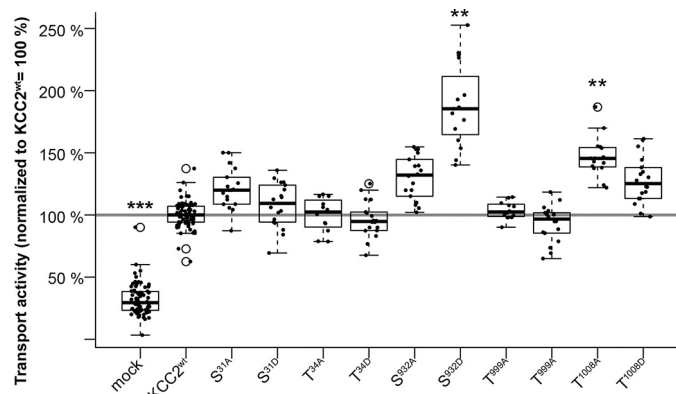


Figure 3. Transport activity of KCC2 phosphomutants. HEK-293 cells were transfected with KCC2^{WT} or KCC2 phosphomutant constructs. Transport activity was determined by performing TI⁺ flux measurements. The TI⁺ flux determined for KCC2^{S31A/D}, KCC2^{T34A/D}, KCC2^{S932A}, KCC2^{T999A/D}, and KCC2^{T1008D} was similar to the flux of KCC2^{WT}. In contrast, KCC2^{S932D} and KCC2^{T1008A} mutants resulted in significantly increased transport activity. The graph represents the data of at least four independent measurements (each consisting of three technical replicates) normalized to KCC2^{WT}. Statistical analysis is presented in Table 2 (**, *p* < 0.01; ***, *p* < 0.001). Circles indicate outliers with respect to the 1.5 × interquartile range of the box plot. Error bars represent S.E.

Table 2

Transport activity under basal conditions and in the presence of furosemide

** $p < 0.01$; *** $p < 0.001$; n.s., not significant.

	Basal conditions (significance in comparison with KCC2 ^{WT})	2 mM furosemide (significance in comparison with untreated samples)
Mock	32 ± 2 (***)	27 ± 2 (n.s.)
KCC2 ^{WT}	100 ± 2 (n.s.)	27 ± 1 (***)
S31A	121 ± 7 (n.s.)	45 ± 7 (***)
S31D	108 ± 7 (n.s.)	32 ± 4 (***)
T34A	100 ± 7 (n.s.)	27 ± 2 (***)
T34D	96 ± 6 (n.s.)	37 ± 4 (***)
S932A	130 ± 7 (n.s.)	24 ± 3 (***)
S932D	188 ± 15 (**)	27 ± 3 (***)
T999A	104 ± 4 (n.s.)	24 ± 2 (***)
T999D	93 ± 6 (n.s.)	26 ± 2 (***)
T1008A	147 ± 7 (**)	27 ± 4 (***)
T1008D	128 ± 8 (n.s.)	23 ± 2 (***)

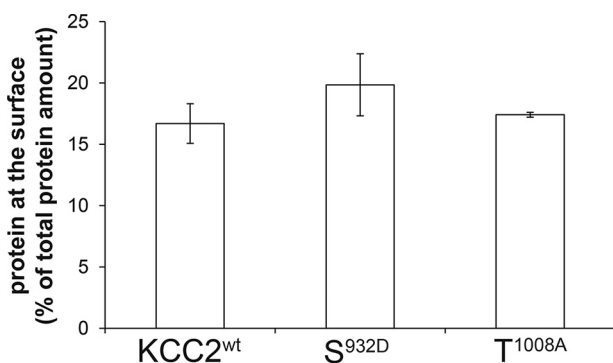


Figure 4. Cell-surface expression of KCC2 phosphomutants. The cell-surface amount of the indicated KCC2 mutants was quantitatively determined by immunoblot analysis. KCC2^{WT} and the KCC2 mutants S932A or T1008A show similar abundance at the surface. The plot depicts the mean of at least three experiments ± S.E. (error bars).

transport activity of S932D and T1008A is caused by intrinsically kinetic effects and not by changes in KCC2 cell-surface abundance.

Staurosporine and NEM differentially affect KCC2 phosphomutants

Staurosporine is a broad kinase inhibitor that generally activates KCCs (27, 57, 58). To investigate whether Ser³¹, Thr³⁴, Ser⁷²⁸, Ser⁹³², Thr⁹⁹⁹, or Thr¹⁰⁰⁸ is an indirect target of staurosporine, we determined the transport activity of the corresponding mutants upon application of 8 μ M staurosporine. S31A, T34D, and T999D mutants were stimulated by staurosporine to a similar extent as KCC2^{WT} (Fig. 5 and Table 3). In contrast, mutations S31D, T34A, S932A/D, T999A, and T1008A/D abrogated stimulation by staurosporine. These data indicate that all five amino acid residues tested, Ser³¹, Thr³⁴, Ser⁹³², Thr⁹⁹⁹, and Thr¹⁰⁰⁸, are involved in the staurosporine-mediated effect.

As described previously, NEM, which generally activates KCCs (27, 57, 58), closely mimics the effect of staurosporine (27). To investigate whether this assumption holds true, we analyzed the impact of NEM on the transport activity of KCC2^{S31A/D}, KCC2^{T34A/D}, KCC2^{S728A/D}, KCC2^{S932A/D}, KCC2^{T999A/D}, and KCC2^{T1008A/D}. As observed for staurosporine, NEM still stimulated transport activity of the mutant T999D and failed to enhance the transport activity of S932D.

Contrary to staurosporine, NEM also enhanced the transport activity of S31D, T34A, T932A, T999A, and T1008A/D, whereas it did not affect the transport activity of S31A, T34D, or S932D. Thus, we demonstrate for the first time that staurosporine and NEM can differentially affect KCC2-mediated transport activity.

Discussion

The main function of KCC2 is to establish a low intracellular [Cl⁻] as this is required for the hyperpolarizing action of GABA and glycine. Decreased Cl⁻ extrusion by dysregulated KCC2 activity has been associated with a variety of disorders (12, 18, 19, 23, 25). One potent mechanism to rapidly and reversibly regulate the intrinsic transport rate and cell-surface abundance of KCC2 is phosphorylation and dephosphorylation of serine, threonine, and tyrosine residues (23). Recently, some progress in our understanding of the regulatory impact of specific phosphosites (27, 34, 35, 39, 41, 43) and underlying kinases and phosphates (35–37, 43–46) has been made.

Here, we focused on the functional characterization of *bona fide* phosphorylation sites of KCC2 that were identified by MS analysis of brain tissue. Site-directed mutagenesis in combination with transport activity measurements identified a potent role of Ser⁹³² and Thr¹⁰⁰⁸ in phosphoregulation. Phosphorylation of Ser⁹³² (mimicked by S932D) and dephosphorylation of Thr¹⁰⁰⁸ (mimicked by T1008A) increase KCC2 activity. In principle, such an increase can arise from an increased cell-surface abundance of the protein or from an intrinsic conformational change (20, 23). Surface biotinylation experiments demonstrated that surface abundance of S932D and T1008A were indistinguishable from KCC2^{WT}. Thus, their increased transport activity resulted from intrinsically kinetic changes. Similar results were reported previously for the mutants T934D and S937D (27).

Ser⁹³² is located within exon 22, which is exclusively present in vertebrate KCC2 and nontherian KCC4. This exon also harbors the previously characterized phosphorylation sites Thr⁹³⁴, Ser⁹³⁷, and Ser⁹⁴⁰ (27, 43). Dephosphorylation of Thr⁹³⁴ and Ser⁹³⁷, mimicked by mutation to alanine, results in transport activity similar to KCC2^{WT}, and phosphorylation of both residues, as mimicked by mutation to aspartate, intrinsically increases KCC2 transport activity (27). Furthermore, PKC-directed phosphorylation of Ser⁹⁴⁰ enhances KCC2 cell-surface stability and increases ion transport, whereas mutation of Ser⁹⁴⁰ to alanine results in transport activity that is equal to or decreased compared with KCC2^{WT} (34, 43, 59). Thus, phosphorylation of each phosphosite so far described in exon 22 stimulates KCC2 function. Exon 22 phosphosites are therefore in strikingly contrast to non-exon 22 phosphosites such as Thr⁹⁰⁶ and Thr¹⁰⁰⁶. The latter two are highly conserved throughout KCCs, and their dephosphorylation increases KCC2 transport activity (27, 34, 37, 39). In addition, Thr¹⁰⁰⁸, analyzed in the present study, that is near Thr¹⁰⁰⁶ conforms to this observation as dephosphorylation augments KCC2 activity as well. Thus, KCC2 harbors two main regulatory principles in which phosphorylation of exon 22-specific phosphosites and dephosphorylation of highly conserved KCC phosphosites outside exon 22 increase KCC2 transport activity. Therefore, con-

Regulation of KCC2 by multiple phosphosites

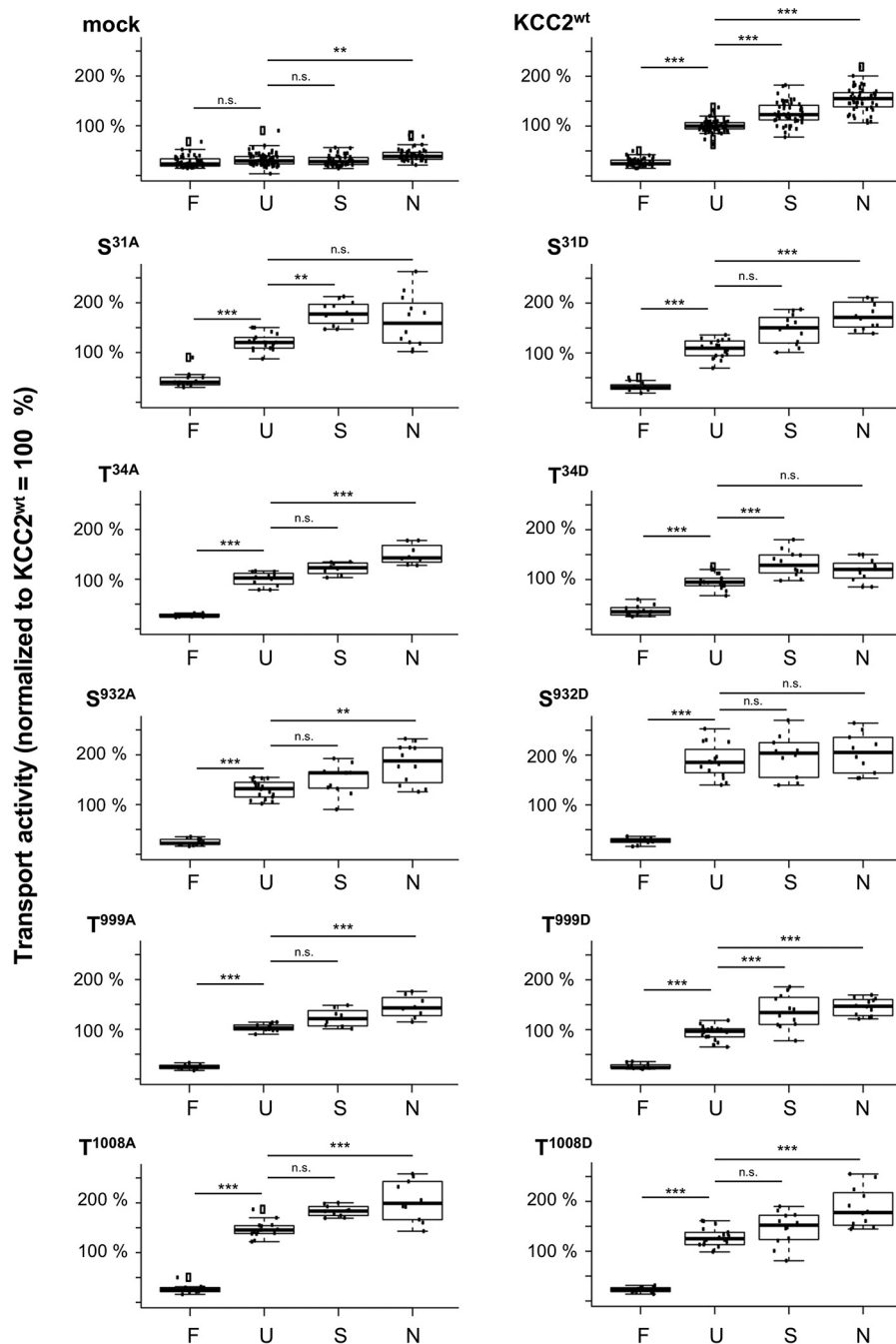


Figure 5. Effect of furosemide, staurosporine, or NEM on transport activity of KCC2 phosphomutants. HEK-293 cells were transfected with KCC2^{WT} or KCC2 phosphomutant constructs. Transport activity was determined by performing TI⁺ flux measurements. Furosemide, staurosporine, or NEM was added 15 min prior to measurement. KCC2^{WT} and all phosphomutants were significantly inhibited by furosemide. KCC2^{WT}, KCC2^{S31A}, KCC2^{T34A}, and KCC2^{T999D} were significantly activated by staurosporine. KCC2^{WT}, KCC2^{S31D}, KCC2^{T34A}, KCC2^{S932A}, KCC2^{T999A/D}, and KCC2^{T1008A/D} were significantly activated by NEM. The graph represents data of at least four independent measurements (each consisting of two (treated cells) or three (untreated cells) technical replicates) normalized to KCC2^{WT}. Statistical analysis is presented in Table 3. **, $p < 0.01$; ***, $p < 0.001$; n.s., not significant. F, furosemide; U, untreated cells; S, staurosporine; N, NEM. Squares indicate outliers with respect to the $1.5 \times$ interquartile range of the box plot. Error bars represent S.E.

trary to other KCC isoforms, which are only up-regulated upon dephosphorylation (39, 60), posttranslational regulation of KCC2 is more complex. This likely equips KCC2 with a more fine-grained phosphoregulatory mechanism as well as an enlarged capacity to integrate multiple signaling cascades compared with other KCC isoforms.

So far, the underlying regulatory mechanisms that lead to phosphorylation and dephosphorylation of specific KCC2

phosphosites have only be partially identified. Ser⁹⁴⁰ is phosphorylated via PKC (43). The phosphosites Thr⁶ of KCC2a and Thr⁹⁰⁶ and Thr¹⁰⁰⁶ are regulated by the WNK-SPAK/OSR1 phosphorylation cascade (35–37, 39, 47). Toward the identification of kinases involved in the phosphosites analyzed in this study, we treated HEK-293 cells with staurosporine or NEM. In general, both enhance KCC2 transport activity (27, 28, 56, 61, 62). Recent analyses by Deeb and co-workers (28) demonstrated

Table 3**Transport activity in the presence of staurosporine or NEM****, $p < 0.01$; ***, $p < 0.001$; n.s., not significant.

	Basal conditions (significance in comparison with KCC2 ^{WT})	8 μ M staurosporine (significance in comparison with untreated samples)	1 mM NEM (significance in comparison with untreated samples)
	%	%	%
Mock	32 \pm 2 (***)	30 \pm 2 (n.s.)	41 \pm 2 (**)
KCC2 ^{WT}	100 \pm 2 (n.s.)	126 \pm 4 (***)	153 \pm 5 (***)
S31A	121 \pm 7 (n.s.)	179 \pm 9 (**)	163 \pm 20 (n.s.)
S31D	108 \pm 7 (n.s.)	147 \pm 12 (n.s.)	182 \pm 18 (***)
T34A	100 \pm 7 (n.s.)	122 \pm 6 (n.s.)	150 \pm 9 (***)
T34D	96 \pm 6 (n.s.)	132 \pm 10 (***)	118 \pm 9 (n.s.)
S932A	130 \pm 7 (n.s.)	151 \pm 11 (n.s.)	183 \pm 15 (**)
S932D	188 \pm 15 (*)	198 \pm 18 (n.s.)	204 \pm 17 (n.s.)
T999A	104 \pm 4 (n.s.)	123 \pm 8 (n.s.)	145 \pm 10 (***)
T999D	93 \pm 6 (n.s.)	136 \pm 13 (***)	145 \pm 7 (***)
T1008A	147 \pm 7 (**)	184 \pm 5 (n.s.)	205 \pm 17 (***)
T1008D	128 \pm 8 (n.s.)	146 \pm 13 (n.s.)	187 \pm 15 (***)

that NEM leads to increased phosphorylation of Ser⁹⁴⁰ and decreased phosphorylation of Thr¹⁰⁰⁷ (numbering according to rat KCC2b). The latter might be explained by the observation that NEM also reduces the phosphorylation level of SPAK, which is involved in phosphorylation of Thr¹⁰⁰⁷ (28). Interestingly, NEM cannot stimulate the transport activity of T1007E, indicating that the induced activation of KCC2 is mediated by dephosphorylation of Thr¹⁰⁰⁷ (28). Here, we show that the phosphomutants S31A, T34D, and S932D also abolish the NEM-mediated increase in KCC2 transport activity. Our results reveal that more than one phosphosite partakes in NEM-induced activation of KCC2.

Previous data indicate that NEM and staurosporine act via the same regulatory mechanism (27). This actually holds true for Thr⁹³⁴ and Ser⁹³⁷ (27). Our analyses demonstrate for the first time that NEM and staurosporine can differentially impact KCC2 transport activity. NEM did not enhance transport activity of S31A and T34D, whereas staurosporine did not stimulate S31D, T34A, S932A/D, T999A, and T1008A/D. This points to partially different regulatory mechanisms being involved in stimulation of these phosphosites.

Furthermore, two categories of phosphosites were identified. The first category consists of the transport activity–regulatory phosphosites Ser⁹³² and Thr¹⁰⁰⁸ where mutation to either alanine or aspartate abrogated stimulation by staurosporine. This is expected for a site directly targeted by the staurosporine-mediated action. In line with this result, alteration of the phosphorylation status increased activity (S932D and T1008A). Together, these data strongly suggest that both amino acid residues are *bona fide* target sites of proteins affected by the kinase inhibitor. Additionally, these results reveal that staurosporine acts by triggering both phosphorylation (S932D) and dephosphorylation (T1008A). In the case of Thr¹⁰⁰⁸, this kinase inhibitor might inhibit a kinase that opposes KCC2 activation by phosphorylation of this site. In the case of Ser⁹³², the kinase inhibitor might indirectly inhibit a phosphatase that dephosphorylates this site and thereby opposes KCC2 activation. It is currently unclear why mutation of either site alone abolished significant stimulation by staurosporine. One explanation is a functional cross-talk of both sites. Furthermore, we still noted a trend toward stimulated activity of the single mutants.

The second category consists of Ser³¹ and Thr³⁴ for staurosporine and NEM, Thr⁹⁹⁹ for staurosporine, and Ser⁹³² for

NEM. In these cases, only mutation into one amino acid residue (alanine or aspartate) abrogated stimulation, whereas mutants containing the other amino acid residue replacement were still sensitive to the respective agent. One explanation is that the kind of substitution at these sites defines accessibility to other phosphosites such as Ser⁹³² or Thr¹⁰⁰⁸ in the case of staurosporine. One conformational state occludes hidden sites (S31A, T34D, and S932D for NEM and S31D, T34A, and T999A for staurosporine), resulting in no further activation of KCC2. The other conformational state deoccludes hidden sites (S31D, T34A, and S932A for NEM and S31A, T34D, and T999D for staurosporine), leading to stimulation upon staurosporine or NEM treatment, respectively. Thus, (de)phosphorylation of specific phosphosites likely results in different conformational states of KCC2 termini that have a long-range effect on other phosphosites. They therefore indirectly regulate the transport activity of KCC2. This hypothesis is in line with previous work of Forbush and co-workers (63, 64). They provided evidence that phosphorylation of N-terminal NKCC1 phosphosites leads to movements of transmembrane domains 10 and 12 relative to each other (63, 64). Furthermore, the existence of long-range effects on the phosphostatus of KCC2 is supported by the observation that the mutation R1049C causes a significant >50% decrease in Ser⁹⁴⁰ phosphorylation (11). Full understanding of this issue likely requires the 3D structure of KCC2 to modulate the impact of different phosphosites.

In conclusion, a detailed functional analysis of KCC2 amino acid residues revealed a complex phosphoregulatory landscape. Full understanding of phosphoregulation therefore requires a 3D model of KCC2 and the interacting effectors to simulate the competitive (de)phosphorylation events and the associated conformational changes. In addition, mass spectrometric characterization of KCC2 phosphosites under different treatments would be of advantage. These types of analyses will clarify how single and combined (de)phosphorylation events influence the conformational changes of KCC2 and thus its transport activity. Initial progress toward this goal has been made and revealed a flexible multidomain organization of KCC2 (65). Furthermore, future studies should address the role of phosphosites in KCC2 trafficking. Most studies, including our own, analyze phosphosites in nonneuronal cells with a simplified morphology compared with the high degree of compartmentalization in neurons. The N terminus of KCC2, for instance, is required for

Regulation of KCC2 by multiple phosphosites

Table 4

Forward primers for site-directed mutagenesis

for, forward.

	Sequence (5' to 3')
S31A for	CTTCATCAACGCCACGGACACGG
S31D for	TCCCTTCATCAACGACACGGACACGGAGAAG
T34A for	CAACAGCACGGACGGAGAGGGCAG
T34D for	CTTCATCAACAGCACGGACGATGAGAAGGGCAGAGAGTACG
S932A for	GGAACGGGAGATCCAGGCCATCACAGACGAGTCT
S932D for	GGGAACGGGAGATCCAGGACATCACAGACGAGTCTC
T999A for	GGGAGAGGGAGGCAGACCCAGAGG
T999D for	CGAGGGGAGAGGGAGGATGACCCAGAGGTGCATC
T1008A for	AGGTGCATCTTACCTGGGCCAAGGATAAGTCAAGT
T1008D for	GAGGTGCATCTTACCTGGGACAAGGATAAGTCAAGTGGC

cell-surface delivery in neurons (66). Interestingly, this part contains various phosphorylation sites with unknown function.

Experimental procedures

Bioinformatics analyses

To identify native phosphosites from proteomics approaches, the two databases PhosphoSitePlus (<http://www.phosphosite.org>)³ (52) and PHOSIDA (51) were screened using KCC2 as query. Both databases contained experimentally observed posttranslational modifications obtained by mass spectrometric analyses.

KCC protein sequences for a diverse selection of organisms were obtained from a combination of BLAST searches against GenBankTM and data mining of the Ensembl database and the Joint Genome Institute (<http://www.jgi.doe.gov/>). The protein sequences of human KCC1 (NP_005063.1), KCC2 (NP_065759.1), KCC3 (NP_598408.1), and KCC4 (NP_006589.2) were used as queries. For each protein in each target species, we saved all sequences with an E-value of at least 10^{-2} . These sequences were then reverse blasted (BLASTp or translated BLAST) against the *Homo sapiens* protein database, and only those protein sequences were retained that showed the same CCC protein sequence of *H. sapiens* that was used as a query sequence as the best hit (E-value of at least 10^{-2}). Each obtained sequence was then aligned at the amino acid level using the default settings in MUSCLE (67) as implemented in SeaView v.4.4.2 (68) and manually improved by eye thereafter.

Construction of expression clones

Site-directed mutagenesis of mouse expression clones for KCC2b (GenBank accession NM_020333.2) was performed according to the QuikChange mutagenesis system (Stratagene, Heidelberg, Germany). Forward oligonucleotides for the generation of the mutations are given in Table 4. Only sequence-verified clones were used for this study.

Cell culture

For immunocytochemistry, K^+ - Cl^- cotransporter activity measurements, and cell-surface biotinylation assays, HEK-293 cells were transiently transfected with the respective construct using polyethylenimine (Sigma-Aldrich). 3 h prior to transfection the medium was replaced. Briefly, 400 μ l of Dulbecco's modified Eagle's medium (Invitrogen), 18 μ l of polyethyleni-

mine, and ~ 4.5 μ g of DNA were mixed and incubated for 15 min at room temperature prior to transfection. For K^+ - Cl^- cotransport activity measurements, HEK-293 cells were plated in a 0.1 mg/ml poly-L-lysine-coated 96-black well culture dish (Greiner Bio-One, Frickenhausen, Germany) at a concentration of 100,000 cells/well 24 h after transfection. The remaining cells were plated on a 0.1 mg/ml poly-L-lysine-coated glass coverslip. After ~ 18 h, coverslips were processed for immunocytochemical analyses to determine transfection rates, which were routinely between 20 and 30% (Fig. S1).

Immunocytochemistry

For immunocytochemistry, all steps were performed at room temperature. HEK-293 cells grown on poly-L-lysine-coated coverslips were fixed for 10 min with 4% paraformaldehyde in 0.2 M phosphate-buffered saline (PBS). After three washing steps in PBS, cells were incubated with blocking solution (2% BSA, 10% goat serum in PBS) for 30 min. Primary antibody solution (anti-KCC2 N1-12; 1:1,000; Neuromab) was added in carrier solution (0.3% Triton X-100, 1% BSA, 1% goat serum in PBS) for 1 h. After washing three times in PBS, the secondary antibody, which was conjugated to a fluorescent probe (Alexa Fluor 488 goat anti-mouse; 1:1,000; Thermo Fisher Scientific, Bremen, Germany), was incubated for 1 h. After three washes in PBS, cells were mounted onto glass slides with Mowiol (Roth, Karlsruhe, Germany) and DAPI (Roth; 1:1000). Photomicrographs were taken using a TCS SP8 confocal laser-scanning microscope (Leica, Wetzlar, Germany).

Determination of K^+ - Cl^- cotransport

KCC2 transport activity was determined by Cl^- -dependent uptake of Tl^+ in HEK-293 cells as described previously (27, 55, 56). To initiate the flux measurement, the medium in the 96-well culture dish was replaced by 80 μ l of preincubation buffer (100 mM *N*-methyl-D-glucamine chloride, 5 mM HEPES, 5 mM KCl, 2 mM $CaCl_2$, 0.8 mM $MgSO_4$, 5 mM glucose, pH 7.4) with 2 μ M FlouZin-2 AM dye (Invitrogen) plus 0.2% (w/v) Pluronic F-127 (Invitrogen) and incubated for 48 min at room temperature. Cells were then washed three times with 80 μ l of preincubation buffer and incubated for 15 min with 80 μ l of preincubation buffer plus 0.1 mM ouabain to block Na^+/K^+ -ATPase activity. This was done for three technical replicates for each construct. Afterward, the 96-well plate was placed into a fluorometer (Fluoroskan Accent, Thermo Scientific), and each well was injected with 40 μ l of $5\times Tl^+$ stimulation buffer (12 mM Tl_2SO_4 , 100 mM *N*-methyl-D-glucamine chloride, 5 mM HEPES, 2 mM KCl, 2 mM $CaCl_2$, 0.8 mM $MgSO_4$, 5 mM glucose, pH 7.4). Fluorescence was measured in a kinetic-dependent manner (excitation, 485 nm; emission, 538 nm; one frame in 6 s in a 200-s time span) across the entire cell population in a single well. By using linear regression of the initial values of the slope of Tl^+ -stimulated fluorescence increase, transport activity was calculated (55, 56).

The effects of the kinase inhibitor staurosporine or NEM were determined by adding 8 μ M staurosporine or 1 mM NEM to the preincubation buffer 15 min prior to flux measurement. This was done for two technical replicates for each construct, and at least four independent measurements were performed

³ Please note that the JBC is not responsible for the long-term archiving and maintenance of this site or any other third party-hosted site.

for each construct. To specifically block transport activity of cation-chloride cotransporters, the loop diuretic furosemide (2 mM) was added to the preincubation buffer. Again, this was done for two technical replicates for each construct, and at least four independent measurements were performed for each construct.

Statistical analyses

Transport activity of each phosphomutant was tested against the control sample (WT), both under control treatment (untreated), using two-sample unequal-variances *t* test after Welch test (69). Because three technical replicates were measured from each independent preparation, we deflated the number of degrees of freedom according to the actual sample size (number of independent preparations) to avoid pseudoreplication. The resulting *p* values were corrected using the Benjamini–Hochberg method (70), which controls the false-discovery rate in multiple comparisons.

For each phosphomutant, we compared the flux measured under four different treatment conditions (untreated, furosemide, staurosporine, and NEM) in a nested analysis of variance where we set the treatment condition as the fixed effect and the replicates as nested random effects. The mixed effects were modeled with the *lme* function from the R package *nlme*, and Tukey post hoc analysis was performed with the *glht* function from the R package *multcomp*. The *p* values from the post hoc comparisons were adjusted using Holm's sequential Bonferroni correction (71). Note that only *p* values <0.01 were considered to reduce the chances of false positives (type I errors).

Cell-surface biotinylation

KCC2 cell-surface levels were assessed by surface biotinylation as described previously (55, 56). For this purpose, 90–95% confluent 10-cm culture dishes of transfected HEK-293 cells were treated with the membrane-impermeant Sulfo-NHS-SS-Biotin (Thermo Fisher Scientific) according to the provided protocol. After several washes and cell lysis, biotinylated proteins were recovered by a NeutrAvidin-agarose column. After three rounds of washes, biotinylated proteins were eluted in sample buffer. Aliquots of the cell homogenate and of the eluate were collected and analyzed by immunoblot analysis.

To quantify the amount of KCCs expressed at the cell surface, dilution series of each sample were loaded onto a 10% SDS-polyacrylamide gel system. After separation and electrotransfer onto polyvinylidene difluoride membranes, membranes were incubated with N1–12 antibody (1:1,000). After incubation for 2 h at room temperature, membranes were washed four times with TBS-T (20 mM Tris, 150 mM NaCl, 1% Tween, pH 7.5), and the secondary antibody donkey anti-mouse IgG-horseradish peroxidase (Santa Cruz Biotechnology, Heidelberg, Germany) was applied for 2 h. After washing, bound antibodies were detected using an enhanced chemiluminescence assay (GE Healthcare) and a LAS-3000 documentation system (Fujifilm, Düsseldorf, Germany). Quantification of the bands was performed using MultiGauge software V3.1 (Fujifilm). The cell lysate corresponds to the total protein amount and was set to 100%. Only data with recovery values of

100 ± 20% were included in our analysis. Four to six biological replicates were performed for each construct. Data are given as mean ± S.D. Significant differences between the groups were analyzed by Student's *t* test.

Author contributions—A. C., W. B., M. W., H. G. N., and A.-M. H. data curation; A. C., W. B., M. W., and A.-M. H. formal analysis; A. C., M. W., H. G. N., and A. M. H. validation; A. C., W. B., and A.-M. H. investigation; A. C. and M. W. visualization; A. C. and A.-M. H. methodology; A. C., H. G. N., and A.-M. H. project administration; A. C., M. W., H. G. N., and A.-M. H. writing-review and editing; H. G. N. and A.-M. H. conceptualization; H. G. N. and A.-M. H. supervision; H. G. N. and A.-M. H. funding acquisition; H. G. N. and A.-M. H. writing-original draft.

Acknowledgment—We thank M. Reents for excellent technical support.

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Regulation of KCC2 by multiple phosphosites

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