1 SUPPLEMENTARY INFORMATION

3 Supplementary Table 1: Determination of the equilibration time for dialysis experiments. To

determine the time required for the equilibration, dialysis units were set up with one chamber containing
100 μM AgNO₃ and the other containing only buffer. AgNO₃ concentration was measured after 24, 48,
72, and 96 hours by ICP-MS and is reported as a percentage of total metal content in both the chambers
along with the standard error.



9	Time (hours)	% Metal content in Dialysis unit			
10		Chamber 1	Chamber 2		
11	24.00	64.52 ± 2.62	35.48 ± 1.02		
12	48.00	50.73 ± 0.73	49.28 ± 0.33		
13	72.00	49.16 ± 0.33	50.84 ± 3.40		
14	96.00	49.97 ± 0.82	50.03 ± 1.80		

- 1 Supplementary Figure 1: Schematic overview of the CusR/CusS two-component system. A) CusS is
- 2 shown as a dimer with domains labels. B) The amino acid sequence of the *E. coli* histidine kinase CusS
- 3 with transmembrane helices and domains indicated in color as predicted by KeGG database
- 4 (<u>http://www.genome.jp/dbget-bin/www_bget?eco:b0570</u>) and HMMTOP and TMHMM transmembrane
- 5 topology prediction software (this work). The numbers in the sequence indicate the position of the
- 6 domain in the full-length CusS.
- 7 A)



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B)

10 11	1	mvskpfqrpf	sla <mark>trltffi</mark>	slatiaaffa	<mark>fawi</mark> mihsvk	vhfaeqdind	lkeisatler
12 13	61	vlnhpdetqa	rrlmtlediv	sgysnvlisl	adsqgktvyh	spgapdiref	trdaipdkda
14 15	121	qggevyllsg	ptmmmpghgh	ghmehsnwrm	inlpvgplvd	gkpiytlyia	lsidfhlhyi
16 16 17	181	ndlmnk <mark>limt</mark>	asvisilivf	<mark>ivllav</mark> hkgh	apirsvsrqi	qnitskdldv	<mark>rldpqtvpi</mark> e
18 10	241	<mark>leqlvlsfnh</mark>	<u>mieriedvft</u>	<mark>rqsnfsadia</mark>	heirtpitnl	itqteialsq	srsqkeledv
20	301	lysnleeltr	makmvsdmlf	<mark>laqadnn</mark> qli	pekkmlnlad	evgkvfdffe	alaedrgvel
22	361	rfvgdkcqva	gdplmlrral	snllsnalry	tptgetivvr	cqtvdhlvqv	ivenpgtpia
23 24 25	421	pehlprlfdr	fyrvdpsrqr	kgegsgigla	ivksivvahk	gtvavtsdar	gtrfvitlpa
26	TM helices						
27	HAMP						
28	dimerization	/phosphoaccept	or				
29	ATPase						
30	30.187 clone	d consor doma	in				

30 39-187-cloned sensor domain

Supplementary Figure 2: Sedimentation velocity analytical ultracentrifugation analysis of CusS_s
 samples in the presence of Zn(II) and Ni(II). The c(s) distribution plots show one sedimentation species
 for each sample.

