Displacement of extracellular chloride by sulfated glycosaminoglycans of the brain's
extracellular matrix[*]

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and extracellular structural features regulated on differing time scales to properly function both
individually and as part of a larger information storage and retrieval system, and how failure to
do so leads to seizure and epilepsy.

Key Points Summary

- Extracellular chloride concentrations in the brain were measured using a new chloride-
sensitive organic fluorophore and two photon fluorescence lifetime imaging.
- *In vivo*, the extracellular chloride concentration was spatially heterogenous and only half
of the CSF chloride concentration
- Stable displacement of extracellular chloride by immobile extracellular anions was
responsible for the low extracellular chloride concentration
- The changes in extracellular chloride were of sufficient magnitude to alter the
conductance and reversal potential of $GABA_A$ chloride currents
- The stability of the extracellular matrix, the impact of the component immobile anions
including sulfated glycosaminoglycans on extracellular chloride concentrations, and the
consequent effect on $GABA_A$ signaling suggests a previously unappreciated mechanism
for modulating $GABA_A$ signaling.

Abstract

GABA is the primary inhibitory neurotransmitter. Membrane currents evoked by $GABA_A$
receptor activation have uniquely small driving forces: their reversal potential (E_{GABA}) is very
close to the resting membrane potential. As a consequence, $GABA_A$ currents can flow in either
direction, depending on both the membrane potential and the local intra and extracellular
concentrations of the primary permeant ion, chloride (Cl). Local cytoplasmic Cl concentrations
vary widely due to displacement of mobile Cl ions by relatively immobile anions. Here we use
new reporters of extracellular chloride (Cl^-_o) to demonstrate that Cl is displaced in the
extracellular space by high and spatially heterogenous concentrations of immobile anions
including sulfated glycosaminoglycans (sGAGs). Cl^-_o varies widely, and the mean Cl^-_o is only
half the canonical concentration, i.e. the Cl concentration in the cerebrospinal fluid.   These
unexpectedly low and heterogenous Cl^-_o domains provide a mechanism to link the varied but
highly stable distribution of sGAGs and other immobile anions in the brain's extracellular space
to neuronal signal processing via the effects on the amplitude and direction of $GABA_A$
transmembrane Cl currents.

Introduction

$GABA_A$ synapses comprise the primary output for inhibitory interneurons in the brain (Hu *et al.*,
2014; Tremblay *et al.*, 2016). A unique feature of $GABA_A$ synapses are the very small driving
forces for ion flux through open $GABA_A$ receptor-operated membrane channels. The reversal
potential for the primary permeant ion, chloride, is usually within a few mV of the neuronal
resting membrane potential (RMP) (Thompson *et al.*, 1988) and may even be positive to RMP
(Staley & Mody, 1992; Tyzio *et al.*, 2008). This low driving force makes possible a novel form of
synaptic plasticity at $GABA_A$ synapses: the direction of current flow, i.e. the effect of $GABA_A$
receptor activation on the resting membrane potential, can be reversed by low millimolar
alterations in the local chloride concentration (Coombs *et al.*, 1955). Such physiological
variance is routinely observed in individual studies (Ebihara *et al.*, 1995; Huberfeld *et al.*, 2007)
and is likely to underlie the 25 mV range of reported group mean reversal potentials in 20 recent
studies of evoked $GABA_A$ currents recorded with gramicidin perforated patch electrodes in area
CA1 of the hippocampus (tabulated in (Rahmati *et al.*, 2021). This variance has substantial
effects on synaptic signaling: the reversal potential of $GABA_A$ currents evoked in a single
pyramidal cell by stimulation of 8 different presynaptic interneurons also varied by over 20 mV
(Rahmati *et al.*, 2021).

We have proposed that the intracellular chloride concentration (Cl^-_i) is not monotonic across the
neuronal cytoplasm, but rather varies inversely with the local concentration of macromolecular
anions that comprise the vast majority of intracellular anions (Glykys *et al.*, 2014a; Rahmati *et*
al., 2021). This phenomenon is known as Donnan exclusion (Marinsky, 1985; Helfferich, 1995;
Fatin-Rouge *et al.*, 2003; Epsztein *et al.*, 2018; Gao *et al.*, 2022). Mobile ions, in this case Cl,
are repelled by relatively immobile ions such as proteins with negative surface charges. Many
proteins such as gephyrin that are associated with $GABA_A$ synapses bear large negative
surface charges (Sola *et al.*, 2001), suggesting that variance in the $GABA_A$ reversal potential
(E_{GABA}) is determined by local fixed cytoplasmic charge densities. However, E_{GABA} is not
determined solely by Cl^-_i but rather by the ratio of intra- to extracellular permeant ions. This

raises the possibility that spatial variance in the extracellular Cl concentration (Cl_o^-) could also
be an important determinant of E_{GABA}.

The displacement of Cl^- by fixed negative charges should also occur in the extracellular space,
where the high negative charge density of several classes of functionalized macromolecules are
anchored to the cell membrane either directly or indirectly. Gangliosides typically bearing one to
three – or more, though rarely – carboxylate groups in the form of sialic acid groups are present
in the extracellular space of human cerebral cortex (Schnaar *et al.*, 2014) and are concentrated
within the synaptosomal fraction (Svennerholm, 1980). Together with the polysulfated
glycosaminoglycans (GAGs) that are a major constituent of the extracellular matrix (Karamanos
et al., 2021), which have been reported to be as high as the Cl^- concentration in the CSF (Urban
et al., 1979; Chahine *et al.*, 2005; Morawski *et al.*, 2015), we calculate that total extracellular
fixed anions are in excess of 50mM (see Methods; Schnaar *et al.*, 2014). Thus some to all of the
local Cl_o^- could be displaced, depending on local anionic density and the degree of GAG
sulfation. Such displacement has been most clearly demonstrated in the chondroitin sulfate-rich
matrix of cartilaginous tissue, where the negative charge density of the extracellular matrix can
reach 400 meq / liter (Lesperance *et al.*, 1992), but dozens of mM of Cl_o^- are also displaced by
sulfated GAGs in tissues such as skin (Titze *et al.*, 2004). Mucous, which comprises the
extracellular space for airway epithelial cells, is also rich in polysulfated GAGs that displace
about half of the Cl_o^- (Reuter *et al.*, 1998). Given this evidence for sulfated GAGs displacing Cl_o^-
and the commercial availability of exogenous matrix metalloprotease (MMP) analog
chondroitinase, we chose to focus on the role of extracellular sulfated GAGs and, in particular,
the role of chondroitin sulfate.

Many findings suggest that the brain Cl_o^- is lower than the canonical value. Xray emission
spectroscopy of the extracellular space has demonstrated sulfate concentrations as high as 100
mM (Morawski *et al.*, 2015). Astrocytic buffering of Cl_o^- (Egawa *et al.*, 2013) would not be
necessary if Cl_o^- were indeed > 100 mM. The gating of Group II and III metabotropic glutamate
receptors, kainate receptors, acid-sensing membrane ion channels, and the transport rate of the
GlyT1 glycine transporter are all strongly modulated by Cl_o^- over the entire range of 1 - 100 mM
(Kuang & Hampson, 2006; Plested & Mayer, 2007; Kusama *et al.*, 2010; DiRaddo *et al.*, 2015;
Tora *et al.*, 2018; Zhang *et al.*, 2021). Such strong modulation by low Cl_o^- would not make
sense if Cl_o^- was uniformly > 100 mM.

Studies of Cl_o^- are few, particularly in live mammalian tissue, and have been carried out with ion-
sensitive electrodes that sample only one microenvironment (Nicholson & Kraig, 1975). Our
prior work suggested that the local chloride concentration varies widely as a function of the local
concentration of immobile anions (Rahmati *et al.*, 2021). Earlier results from our group (Glykys
et al., 2014a) have suggested that physiological Cl_o^- is lower than that measured with ion-
sensitive electrodes, and we hypothesized that the large sample sizes provided by fluorometric
imaging techniques might provide the most robust measure of the extracellular chloride
distribution.

Although a fluorometric study of Cl_o^- would provide a noninvasive means to establish the
distribution of chloride in the extracellular space, no suitable Cl-sensitive organic fluorophores
exist, and transgenic fluorophores such as SuperClomeleon (Grimley *et al.*, 2013) and
CloPhensor (Sato *et al.*, 2017) are not distributed in the extracellular space. We therefore
developed a chloride-sensitive fluorophore (Normoyle *et al.*, 2024) from previously described
organic backbones (Biwersi *et al.*, 1992; Biwersi *et al.*, 1994) that satisfied the following criteria.

First, the fluorophore should be sensitive to Cl in the range of the extracellular chloride
concentration i.e., up to 100 mM; available fluorophores have been optimized for the low
millimolar chloride concentrations of the cytoplasm. Second, the fluorophore should report Cl
independently of the concentration of fluorophore. Ratiometric fluorophores suitable for the
extracellular space do not exist, so we used **F**luorescence **L**ifetime **Im**aging (FLIM) (Kaneko *et*
al., 2004) to remove the dependence of the fluorescence emission on fluorophore
concentration. Third, the fluorophore should be constrained to the extracellular space, for which
dextran conjugation is optimal (Xiao *et al.*, 2008; Tønnesen *et al.*, 2018). Fourth, the
fluorophore should be excited by wavelengths that are not damaging to brain tissue, i.e. below
the ultraviolet range and in the visible or infrared range. Fifth, many Cl sensors are also
sensitive to pH (Kuner & Augustine, 2000; Grimley *et al.*, 2013), so a pH-insensitive fluorophore
would be ideal. Finally, the fluorophore needs to be sufficiently bright so that its emission can be
reliably distinguished from autofluorescence.

Here, we utilize a newly synthesized Cl-sensitive fluorophore that meets these 6 criteria to
demonstrate: stable Donnan exclusion of chloride by immobile extracellular anions such as
sulfates fixed to GAG-like carbohydrate polymers; directly measured Cl^-_o of *in vitro* and *in vivo*
brain tissue that is much lower than cerebrospinal or plasma chloride; a remarkable spatial
variance in Cl^-_o; and, as evidence that Cl^-_o is determined by Donnan exclusion of Cl by sulfated
moieties such as GAGs, Cl^-_o increases after release of immobile sulfates by exogenous
chondroitinase.

Methods

Ethical Approval: All animals are housed in a facility with on-call veterinary team and have free
access to food water in accordance with MGH IACUC animal welfare board regulations,
conforming to Grundy 2015 principles and regulations (protocol 2018N000221). Isofluorane
anaesthesia was induced by inhalation through a nosecone at 5mL/min and maintained at 1-
2mL/min for the duration of the experiment, checking frequently for signs of adequate
anaesthesia. All surgeries performed were acute (non-survival) experiments after which mice
were administered maximum anaesthesia (5mL/min isofluorane) and euthanized by
decapitation.

General: Chemicals were purchased from Sigma-Aldrich (St Louis, MO) unless otherwise noted.
Solutions are brought up in distilled water unless otherwise noted. Standard aCSF was brought
up in 18MΩ water and consisted of (in mM): NaCl 126; KCl 3.5; $CaCl_2$ 2; $MgCl_2$ 1.3; NaH_2PO4
1.2; Glucose 11; $NaHCO_3$ 15. Low chloride aCSF variant was identical except that sodium
gluconate was substituted for NaCl, resulting in 10mM Cl^-. Calibration solutions were made by
mixing appropriate proportions of standard aCSF with low chloride aCSF such that a chloride
and gluconate sum total of 136mM was maintained while Cl^- ranged from 10 to 136mM.
Colorimetric assays were read using a Wallac Victor-2 1420 spectrophotometer with a halogen
continuous wave light source and spectral line filters at listed wavelength +/- 5 to 10nm.
Centrifugation steps were accomplished in a tabletop Eppendorf 5417R microcentrifuge. Reflux
apparatus for synthesis consisted of a recirculating cooling bath (Fisher Scientific) filled with
ethylene glycol cooling a 24/40 double-lumen coiled reflux tube (Ace Glassware, Vineland, NJ)
with a 500mL round bottom flask (Corning) heated with a heating mantle regulated by a timed
power controller (Glas-Col #O406 and #104A PL312, respectively).

Synthesis of ABP-dextran: The process of optimizing a bright, redshifted, pH-insensitive
fluorophore that is responsive to chloride concentration over a dynamic range inclusive of
expected extracellular chloride concentrations is beyond the scope of this paper and has been
published separately (Normoyle et al., 2024). Synthesis techniques closely followed those of the
Verkman group when synthesizing related compounds (Verkman, 1990; Biwersi et al., 1992)
and conjugating to dextran (Biwersi et al., 1992). Briefly, N(4-**A**mino**B**utyl)**P**henantridinium
(ABP) was synthesized by a reflux of equimolar amounts of phenanthridine and N(4-
bromobutyl)phthalimide in acetonitrile followed by a second reflux in 6N HCl to hydrolyze
phthalate. Product was twice recrystallized from 95% ethanol before conjugation to cyanogen
bromide-activated 10,000g/moL (10KDa) dextran, producing 10KDa ABP-dextran with an
approximate molar labeling ratio of 4.4.

Sulfation of agarose: We modified the method of Fuse and Suzuki (Fuse & Toshiya, 1975) to
add sulfate groups to the repeating disaccharide units of agarose. The goal of maximizing
sulfation must be balanced with the consequent erosion of gel properties such as gelation and
water holding capacity; in our hands, the maximum sulfation we could achieve while retaining
gelation at 5% (w/v) was when using a 6:1 molar ratio of sulfuric acid to agarose disaccharide.
When cast at 5% (w/v), this worked out to ≈50mM sulfate in resultant gels (49.2+/-0.289mM; for
sulfate measurement see next section). This roughly matches calculated estimates of fixed
negative charges from a collection of bulk biochemical studies quantifying the content of sulfate
groups (proteoglycans and sulfatides) and carboxylic acid groups (sialic acid-bearing glycolipids
and proteins) in brain (Schnaar et al., 2014). Schnaar et al. (2014) summarized the components
of the brain's extracellular matrix as follows: proteoglycans represent 0.45mM disaccharide
monovalent negative charge equivalents and sulfatides represent 5.8mM charge equivalents,
while sialic acid groups on gangliosides account for 3.9mM, and sialic acid bound to protein
comprises 1.3mM. In total, these distinct sources of extracellular negative charge bound to lipid,
protein, and sugar components of the extracellular matrix amount to 11.45mM sequestered into
the 20% of total volume that is extracellular. This gives a total expected fixed extracellular
anionic charge equivalent of 57.3mM in the brain's extracellular space. Proteoglycans, including
chondroitin sulfate, account for 2.3mM of total extracellular fixed charge (0.45mM corrected for
extracellular space being 20% of total). Despite this, we focus on chondroitin sulfate digestion of
live tissue due to experimental accessibility and the ability to use commercially available
chondroitinase. It is also for practical reasons that we model the complex extracellular matrix
using sulfated agarose because of the experimental expediency of adding sulfate to a
polymerizable sugar. We stress again that there is a limit to how much sulfate can be added to
agarose while retaining its ability to polymerize, and the following describes a sulfated agarose
with sulfate content near or at this limit. Briefly, agarose was added to a well-dried Erlenmeyer
flask and dissolved in DMSO at a concentration of 4%(w/v) at room temperature before being
cooled to 4°C with stirring. Addition of 4:1 mixture of acetic anhydride / glacial acetic acid, also
pre-chilled to 4°C, was added to agarose/DMSO mixture (0.4 volumes) in 4°C coldroom.
Vigorous mixing by handheld rotation was necessary to thin the gelatinous mixture to a slurry
and allow stirring at 4°C for 15 minutes; gentle heat transfer from experimenter's hands helped
loosen the initial gel but care is taken to return the mixture to 4°C. Sulfuric acid (15.6M) is then
added slowly at a 6:1 molar ratio to agarose repeating disaccharide units, taking care to keep
temperature between 4-10°C. Mixture is then moved to ambient temperature and allowed to stir
for 15 minutes before reaction is stopped by neutralization with 10M NaOH after again cooling
to 4°C and maintaining temperature between 4-10°C in coldroom. Sulfated agarose is then

dialyzed at ambient temperature in 12-14KDa dialysis tubing (SpectraPor S432703) against 15
volumes of 50mM Tris pH 7.4 once, then against distilled water changed twice daily until
dialysate clarifies. Agarose is then precipitated in 95% ethanol cooled to 4°C >4hours; over-
dialysis may hinder ethanol precipitation due to a lack of sufficient counter-ion presence.
Precipitate is then vacuum filtered and oven-dried at 50°C. Material is loosened with polished
glass pestle and stored at ambient temperature in sealed glass vial until use. Note that careful
temperature and pH control is necessary throughout exothermic processes to maintain gelation
characteristics of the product.

<u>Measurement of sulfate concentration in polysaccharide gels</u>: $BaCl_2$-gelatin turbidimetric method
(Torres *et al.*, 2021) was used to quantify the sulfate content of gel materials. Sulfated agarose
product or commercially available agarose or agar powder was dissolved in 0.5M HCl at a
concentration of 5% (w/v) in 2mL screw-top microtubes with gasket (Fisher Scientific). Tubes
are then placed in a heat block at 100-110°C for 3hours with periodic vortex mixing, hydrolyzing
the sugar backbone and releasing sulfate. All samples had varying amounts of insoluble dark
brown precipitated sugar, which was clarified at 20,000 x g for 10 minutes. Standards are
diluted from 1M Na_2SO_4 stock in 0.5M HCl. $BaCl_2$-gelatin reagent is freshly prepared by
dissolving 30mg gelatin in 10mL distilled water at 80°C for 10minutes, then promptly adding
100mg $BaCl_2$ and vortex mixing. $BaCl_2$-gelatin is then allowed to cool passively before use.
Samples are prepared by combining 1 part sample (diluted as desired), 1 part $BaCl_2$-gelatin,
and 3 parts 0.5M HCl. Assay is performed in a glass-bottom 96-well plate reading absorbance
at 405nm. Multiple sample dilutions were prepared and concentrations were calculated only
from dilutions whose readings were well within the dynamic range of the standards.

<u>Measurement of Cl^- in agar or agarose gels (chemical method)</u>: Chloride was measured
colorimetrically using mercury(II) thiocyanate ($Hg(SCN)_2$) / iron(III) nitrate ($Fe(HNO_3)_3$)
absorbance method of Florence and Farrar (Florence & Farrar, 1971) to infer Cl^- from $Fe(SCN)_3$
production through the two-step reaction,

$$[Hg(SCN)_2 + 2Cl^- \rightleftharpoons HgCl_2 + 2SCN^-]x3$$

$$[3SCN^- + Fe(NO_3)_3 \rightleftharpoons Fe(SCN)_3 + 3(NO_3)^-]x2$$

reading $Fe(SCN)_3$ absorbance at 490nm. Briefly, agar or agarose gels cast at 5% (w/v) in 3.5cm
Petri dishes were drained by gravity and then Kimwipes were used to gently wick away
remaining excess fluid at sides of dish. Similar amounts of each sample are transferred to 2mL
screw-top microtubes with gasket (Fisher Scientific) and 1 gel volume, estimated by weight, of
7.8M nitric acid (HNO_3) is added (final $[HNO_3]$ = 3.9M). Samples are then placed in a heat block
at 100-110°C for 3hours with periodic vortex mixing, hydrolyzing the sugar backbone to break
down the gel lattice. All samples had varying amounts of insoluble dark brown precipitated
sugar, which was clarified at 20,000 x g for 10 minutes. A portion of supernatant or KCl
standard, diluted with 0.3M HNO_3, was combined with one-tenth volumes of 0.4M $Fe(NO_3)_3$ (in
4M nitric acid) and saturated $Hg(SCN)_2$ (in ethanol), triturated, and allowed 20minutes for
reaction to reach endpoint. Stock solutions are used within 1week. Multiple sample dilutions
were prepared and concentrations were calculated only from dilutions whose readings were well
within the dynamic range of the standards. Final concentrations are adjusted to account for
dilution from original gel sample volume.

<u>Fluorescence Lifetime Imaging (FLIM)</u>: Time-correlated single-photon counting (TCSPC) FLIM
measurements were obtained using a custom laser-scanning two-photon rig driven by custom
ScanImage software (MBF Bioscience, Williston, VT) equipped with a MaiTai Ti:Sapph laser
(SpectraPhysics) and high-sensitivity PMT detectors (Hamamatsu C6438-01) as described
previously (Normoyle *et al.*, 2024). Briefly, ABP-dextran was excited at 760nm and emitted
photons were subjected to a 445/58 bandpass filter (Chroma) prior to detection using a high-
sensitivity PMT. ABP-dextran was used at 500microgram/mL (50μM) in aCSF unless otherwise
noted. A fluorescence lifetime is calculated for each pixel by measuring the time it takes for an
emitted photon to be detected, binning these photons according to arrival time, and to these
data a first-order exponential equation is fit to derive the rate constant representing the
fluorescence lifetime (Gehlen, 2020). The presence of a quencher will shorten fluorescence
lifetime to an extent which is linearly related to quencher concentration through the Stern-
Volmer equation,

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$$\frac{\tau_o}{\tau_i} = 1 + [Q]k_{SV}$$

where τ_o / τ_i represents the unquenched lifetime divided by the shortened lifetime at a given
quencher concentration ([*Q*]) (Gehlen, 2020). The Stern-Volmer constant (k_{SV}) of the resultant
line relates the concentration of quencher to the shortening of fluorescence lifetime. Photons
were collected over an acquisition period of 60 seconds (*in vivo* and agarose gels) to 90
seconds (*in vitro* slice cultures) and the lag between incident laser pulse and resulting photon
detection recorded. The population of photons in each individual pixel is fit to an exponential to
yield a lifetime value and summed to yield an intensity value using the FLIMJ plug-in for ImageJ.
Further image processing, calculations, and statistics were accomplished using built-in functions
and custom routines developed in Matlab (v2018b and v2022a; Mathworks, Natick, MA). For
composite image generation, see *Image processing in Matlab* section below.

<u>Calibration of ABP-dextran</u>: ABP-dextran is synthesized, conjugated, and calibrated as
described previously (Normoyle *et al.*, 2024). Briefly, we calibrated 50μM ABP-dextran against
aCSF with varying chloride concentrations by preparing standard aCSF (in mM: NaCl 126; KCl
3.5; CaCl$_2$ 2; MgCl$_2$ 1.3; NaH$_2$PO4 1.2; Glucose 11; NaHCO$_3$ 15) and a low-chloride aCSF in
which NaCl was replaced with sodium gluconate. We mixed appropriate amounts of each to
vary chloride concentrations (10-136mM) while maintaining the sum of sodium chloride and
sodium gluconate at 136mM. Although k_{SV} values did not differ appreciably between ABP-
dextran batches nor when measured using different FLIM-capable microscopes, out of an
abundance of caution we used a single batch of ABP-dextran and obtained FLIM calibration
parameters specific for this batch of fluorophore and the custom microscope used for all
experiments reported in this manuscript. Because calibrations done in aCSF have a minimum
Cl$^-$ of 10mM as described, the unquenched lifetime (τ_o) used for Stern-Volmer calculations is
approximated as the y-intercept (Cl$^-$ = 0mM) of a best-fit curve of the raw calibration data;
empirically, a biexponential fit was used. Each concentration of Cl$^-$ in the calibration curve has a
normally distributed set of ABP-dextran lifetime values with a near-constant relative standard
deviation (RSD = standard deviation divided by mean) (Normoyle *et al.*, 2024). All calculations
are otherwise done as described under *Fluorescence Lifetime Imaging (FLIM)* section above.

<u>Animals</u>: All animal protocols were approved by the Massachusetts General Hospital
Institutional Animal Care and Use Committee (protocol 2018N000221). Wild type mice (C57bl/6;
Jackson Labs 000664) of either sex were used for this study. Mouse pups remained in the

home cage with the dam under standard husbandry conditions until postnatal day 6 to 8 (P6–8)
when organotypic slice cultures were prepared, or until P26-30 when a cortical window was
surgically placed.

<u>In vitro organotypic slice cultures and imaging:</u> Organotypic hippocampal slice cultures were
prepared either as glass-mounted (Berdichevsky *et al.*, 2016) or membrane insert-mounted
(Stoppini *et al.*, 1991) cultures. Briefly, in either case hippocampi are obtained from P6-8 mice
and cut to 400μm thick slices. These are then gently transferred to a 6-well dish containing
either a membrane insert (Millipore) or a poly-L-lysine coated coverslip (Electron Microscopy
Sciences), are fed twice weekly with 1mL neurobasal-A media supplemented with 500μM
Glutamax, 2% B-27, and 0.03mg/mL gentamycin (all from Invitrogen), and are incubated at
35°C in a 5% CO_2 incubator. Cultures are typically imaged between DIV 12-21 in aCSF warmed
to 33°C and bubbled with 95%O_2 / 5% CO_2 perfused at a rate of approximately 100mL/hour
unless otherwise noted. Slices were pretreated with media containing 500μg/mL ABP-dextran in
incubator for 1-2 hours prior to perfusing with aCSF containing 136mM chloride and the same
concentration of ABP-dextran, plus 100nM tetrodotoxin (TTX). Slices were allowed to equilibrate
in perfusate for 20-30 minutes before imaging, equaling at least 2 hours of total exposure to
ABP-dextran prior to initiation of imaging. Two photon images were captured on a perfusion-
enabled stage with a 20x water-immersion objective, NA 0.95, and analyzed as described (see
Image processing in Matlab section below).

<u>*In vivo* murine cortical window imaging</u>: Using a modified method based on that of Che and De
Marco Garcia (Che & De Marco García, 2021), we placed cortical windows in young adult mice
(P26-30) for acute (non-survival) imaging in accordance with Massachusetts General Hospital
Institutional Animal Care and Use Committee policies and procedures (protocol 2018N000221).
Briefly, anaesthetized mice were immobilized with standard ear bars and nosepiece until custom
headbar is placed. A section of scalp is removed to expose a roughly 1cm section of skull.
Acrylic dental cement powder (Lang Dental, Wheeling IL) mixed with cyanoacrylate adhesive is
used to fix the headbar to the exposed skull at 4 o'clock to Bregma, creating a 5mm diameter
working area just lateral to midline. A 2.5mm round section of skull and underlying dura is
removed and a 3mm No. 1 coverslip is placed over the exposed cortex. Coverslip has 10μL
concentrated ABP-dextran / agarose mixture (1%w/v low gelation temperature agarose, Sigma-
Aldrich, with 10mg/mL ABP-dextran in aCSF) pipetted from 42°C heat block immediately before
inversion and placement over cortex. One hour is allowed before image acquisition for ABP-
dextran diffusion into cortex from overlying agarose (between cortex and coverslip), producing
signal similar to that seen with 50μM ABP-dextran in vitro. During this time the warmed
breadboard with immobilization apparatus and anesthetized mouse is transferred to the
microscope table for *in vivo* imaging. This custom-made gantry-type microscope accommodates
the breadboard as a stage for *in vivo* imaging. Two photon images were captured with a 16x
water-immersion long focal distance objective, NA 0.80, and were analyzed as described (see
Image processing in Matlab section below).

<u>Agarose or agar gel Cl$^-$ determination using ABP-dextran FLIM:</u> Cl$^-$ within an agar or agarose
gel was measured using the two-photon rig described above in the *in vivo* section, except with a
4x (NA 0.28) objective. Using an 8-well microchamber with silicone dividing gasket (Ibidi,
Grafelfing, Germany), gels were cast in aCSF containing ABP-dextran and subsequently
transferred to a single Petri dish where they were equilibrated with aCSF containing ABP-
dextran for at least 1 hour prior to imaging. FLIM measurements were taken as described,

generally one field per quadrant at a depth of between 50-100microns. Importantly, the gasket
separating gels of differing compositions was removed such that all gels in an experiment were
bathed in the same aCSF with the same Cl⁻. Where gels were kept for more than 1 day, they
were prepared in aCSF without glucose and kept refrigerated between readings to prevent
fouling.

<u>Chondroitinase treatment of organotypic hippocampal slice cultures</u>: Chondroitinase ABC
(ChABC; AMSBIO, #E1028-02) was brought up in aCSF containing 0.1% bovine serum albumin
(BSA) to a concentration of 1U/mL. Slices grown on membrane inserts were treated for 1hour
either with aCSF containing ChABC or sham aCSF containing only the 0.1% BSA vehicle. Both
experiment and control had 0.5mg/mL ABP-dextran (50μM), and FLIM imaging was done using
the two-photon rig described in the *in vivo* section above. At the conclusion of imaging, the
aCSF was collected for detection of liberated chondroitin sulfate.

<u>Measurement of sulfated glycosamioglycans (sGAGs) liberated in aCSF</u>: Blyscan 1,9-
dimethylmethylene blue-based kit (Biocolor, #B1000) was utilized for measurement of sGAGs
including chondroitin sulfate proteoglycans (CSPGs). After treatment with aCSF containing
ChABC or BSA vehicle as detailed above, aCSF was collected and measured as directed
against standards of bovine trachea chondroitin (Blyscan kit standard) with appropriate amounts
of 10x stocks of aCSF and 0.1% BSA to obtain concentrations identical to samples. 1,9-
Dimethylmethylene blue reagent absorbance is read at 650nm.

<u>Measurement of chondroitin sulfate by liquid chromatography / mass spectroscopy (LC-MS)</u>:
aCSF containing either chondroitinase or vehicle was recovered after incubation with slice (see
above), volume recovered carefully noted before freezing at -20°C, and shipped over dry ice
with blinded labels for analysis. The samples were filtered using 3K MWCO spin filter units (Pall
Corporation Nanosep with 3K Omega Ref: OD003C34) at 14000 RPM at 10°C for 20minutes.
The flow through containing CS disaccharides was dried in speed vac. The dried flow through
were reconstituted in 200µl ultrapure distilled water (Invitrogen, Cat # 10977-015) and 100µl
was dried taken for $^{12}C_6$ aniline tagging by reductive amination method (Lawrence *et al.*, 2008).
Briefly, the CS disaccharides were dissolved in 17µl of $^{12}C_6$ aniline followed by addition of equal
volume of freshly prepared 1 M NaCNBH$_3$ (Sigma-Aldrich) in dimethyl sulfoxide: acetic acid
mixture (65:35, v/v). The reaction mixture was kept at 70°C for 45min and then transferred to
dry oven at 37°C for overnight reaction (16 h). After aniline tagging samples were dried in
speed-vac for 48h to remove excess reagents. The samples were then dissolved in 17µL of LC-
MS grade water (Honeywell), centrifuged at 7000g for 5min. 5µL of the sample was taken and
mixed with 5µL reconstitution buffer containing known amount of internal standard (5µl of the
reconstitution buffer contains, 1 µl of 10X LC-MS buffer-A (80 mM acetic acid and 50 mM
dibutylamine; Sigma-Aldrich), 2 µl of $^{13}C_6$ aniline-tagged CS disaccharide internal standard
mixture (20pmole each) and 2 µl LC-MS grade water. CS disaccharides were analyzed by LTQ
Orbitrap Discovery (Thermo Scientific) mass spectrometry attached with liquid chromatography
system (Ultimate3000, Thermo-Dionex). All disaccharides were separated on a reverse phase
C18 column (1mm x 150mm, 5µm, Targa, Higgins Analytical) using buffer containing dibutyl
amine as ion-pairing reagent, followed by detection of disaccharides on mass spectrometer in
negative ionization mode. The chromatographic steps were: 100% buffer-A (8mM acetic acid,
5mM DBA) for 10 min followed by stepwise increase of buffer-B amount; 17% buffer-B (70%
methanol, 8 mM acetic acid, 5 mM DBA) for 10 min; 32% buffer B for 15 min; 40% buffer B for

15 min; 50% buffer B for 15min; 60% buffer B for 15 min; and 100% buffer A for 10 min. Flow
rate was kept at 50µL per min.

<u>Calculation of ECM sulfate lost after chondroitinase digestion</u>: In order to contextualize the Cl^-_o
increase we observe after chondroitinase treatment of OHSCs, we used our HPLC-derived data
and approximated OHSC volume to derive a reasonable expected Cl^-_o value for comparison.
HPLC data was obtained from collected chondroitinase (or sham) digestion aCSF of a known
volume. Chondroitin disaccharide concentration and sulfate content were found analytically, and
a total chondroitin and total sulfate amount were calculated from mean values of chondroitin
sulfate content (0.2mg/mL), sample volume (0.725mL), sulfation ratio (0.95 sulfate per
disaccharide), and a monosulfated disaccharide molar mass of 481.4g/moL. Given mean OHSC
thickness of 266µm and typical OHSC dimensions of 3x1.5mm, we calculate the best
approximation of extracellular volume (20% of total slice volume) to be 0.293mL. The organic
sulfate content lost from total ECS volume comes out to 1.65mM when assuming full-depth
uniform chondroitinase digestion, or 8.8mM assuming depth-dependent digestion affecting only
50µm nearest the chondroitinase reservoir (i.e., nearest the perfusate). For comparison to
measured Cl^-_o, we assume the molar relationship between sulfate lost and chloride gained to be
1:1.

<u>Image processing in Matlab</u>: ABP-dextran fluorescence lifetime is converted to Cl^-_o as described
above. Composite Cl^-_o images, depicting Cl^-_o values via colormap while incorporating structural
data through brightness adjustment, were produced using custom Matlab routines that apply
normalized intensity data to Cl^-_o images in a manner similar to commercial FLIM software. Note
that intensity images were generated by summation of photons for each pixel across 32 time
bins after excitation, resulting in a higher intensity background than is typical in standard two-
photon images.

Pixel exclusion: We sought to perform as little processing of either intensity or lifetime data as
possible, using statistical methods to objectively exclude pixels greater than three standard
deviations from the mean of either property. Any remaining pixels reflecting a fluorescence
lifetime outside the calibrated range (0-150mM Cl^-), as happens in pixels with poor data quality
typically due to low signal, were also excluded. More specifically, pixels were excluded if ABP-
dextran lifetimes were in excess of the mean at 0mM chloride, or if lifetimes were shorter than
twice the standard deviation less than the mean at 150mM (calculated from calibration data).
This yielded total objective exclusion of 0.1-0.5% of pixels in a given image, which were set to
black. Subjective exclusions were done either by manually drawn regions of interest (ROI) to
exclude areas of perfusate at the margins of OHSCs or large blood vessels *in vivo*, or else by
image-specific thresholding to exclude low-intensity areas coinciding with apparent somatic
silhouettes. All exclusions were performed prior to analysis of extracellular Cl^-_o. To ensure that
somatic silhouette-defined pixels, in particular, were not a subpopulation of pixels possibly
reflecting ABP-dextran in an atypical compartment (e.g., the intracellular space), multiple
analyses of excluded versus included pixels were performed to confirm faithful extracellular
ABP-dextran signal and appropriateness of pixel exclusion (see Results).

Neuronal tracing analysis: Where somatic borders were traced for analysis, these were not
dependent upon thresholding but were traced manually where neurons within the focal plane
could be confidently identified based upon morphology. Traces followed the exterior aspect of
the visually apparent border between bright and dim signal (see Results). Data was linearized
and is presented as the pixelwise change in Cl^-_o versus linearized distance, the latter calculated

from pixel centerpoints. Comparison control data is derived by applying the same traces over
calibration solution images, in which stochastic pixel to pixel differences are isolated (e.g.,
machine noise, Brownian motion artifact, etc). *In vivo* analysis was optimized for more
superficial L1 cortical imaging and demonstration of ABP-dextran exclusion from vasculature
and intracellular space, but a limited number of L2/3 neurons were also identified *post hoc* by
their silhouettes formed through ABP-dextran exclusion within deeper fields. Morphological
identification at this suboptimal optical zoom was only possible where pyramidal neurons were
well within the chosen focal plane, producing demonstrably pyramidal silhouettes. This yielded a
limited dataset on which we repeated perineuronal tracing analysis as an initial *in vivo*
conformation of our better-optimized *in vitro* studies.

Regions of interest (ROIs) selection: ROIs are defined using intensity images for OHSCs either
as a differentiation between tissue and surrounding bath, or this plus a regular division of the
field (i.e., quarters or eighths) as indicated. ROI fields containing a majority of excluded pixels
(e.g., perfusate) are excluded from analysis. ROIs are defined *in vivo* as cortical regions
between anatomical landmarks, such as large vessels, which are easily identified through their
exclusion of ABP-dextran. ROIs are then converted to masks and applied to fluorescence
lifetime or Cl^-_o images. ROIs in fields in which somatic silhouettes are evident are distinguished
from ROIs that are too superficial to contain discernable silhouettes such as cellular (Layer 2/3)
or acellular (Layer 1) cortical fields, respectively.

Statistics: Statistical analysis was done with Matlab 2022a, with access to statistical toolbox
functions. Individual tests used and *p*-values are detailed in figure legends. Corresponding *p*-
value levels are indicated within figures by asterisks and listed in figure legends. Where sample
sizes are small, we first determined whether we could assume normal distributions using the
Jarque-Bera test (Matlab built-in function jbtest); where non-parametric tests were required, we
utilized Mann-Whitney ranked sum or Kolmogorov-Smirnov tests as noted. *In vivo* statistical
analysis of cortical Cl^-_o was accomplished with ROI mean values, but because ROI size and
number varies between groups we report mean+/-standard deviation of all analyzed pixels in
addition to the ROI mean+/-standard error associated with ANOVA analysis. In the interest of
transparency we elected to display violin plots of all pixels analyzed overlaid with ROI mean+/-
standard error, using ANOVA analysis of the latter to determine significance of findings.

Data availability statement: All data files used to generate the figures in the paper can be found
on GitHub under KieranNormoyle/NeuronalChloride2023.

Results

Non-invasive measurement of extracellular chloride using ABP-dextran: ABP is a novel Cl-
sensitive fluorophore compatible with <u>F</u>luorescence <u>L</u>ifetime <u>IM</u>aging (FLIM) that we have
optimized to be bright, red-shifted, and sensitive to chloride concentrations through the range
that would be encountered in in the extracellular space. We conjugated ABP to a 10,000 Dalton
(10KDa) dextran resulting in an amine-bonded moiety (Figure 1A) that is resistant to pH
changes in the physiological range (Normoyle *et al.*, 2024) and is restricted to the extracellular
space (see below). We validated the ability of ABP-dextran to reliably report chloride
concentration by correlating the shortening of ABP-dextran fluorescence lifetime to chloride
concentration (Figure 1B) through the Stern-Volmer relationship (Figure 1C), generating a k_{SV} of
15.9M^{-1} for ABP-dextran used in these experiments. The fluorescence lifetime of ABP-dextran is
not dependent upon the concentration of ABP-dextran, only the concentration of chloride.

Chloride concentration also affects ABP-dextran intensity, such that high chloride
concentrations not only shorten the emission lifetime but also reduce the intensity of emission.
However, the concentration of chloride can be calculated (independently of the local ABP-
dextran concentration) as long as sufficient photons are collected to calculate fluorescence
lifetime in a given pixel.

Sulfated agarose gels as an *in vitro* model of perineuronal space: We recently observed that
differing concentrations of chloride juxtaposed to one another were stable on time scales of at
least 100 minutes due to the presence of immobile anionic charges present in the neuronal
cytoplasm (Rahmati *et al.*, 2021), an effect known as Donnan exclusion (Marinsky, 1985;
Helfferich, 1995; Fatin-Rouge *et al.*, 2003; Epsztein *et al.*, 2018; Gao *et al.*, 2022). We tested
whether Donnan exclusion was also operative in the extracellular space as a consequence of
the abundant fixed negative charges present on extracellular glycolipids and glycoproteins
(Schnaar *et al.*, 2014), focusing in particular on the sulfate moieties of the glycosaminoglycans
that comprise the bulk of the extracellular matrix in the brain (Karamanos *et al.*, 2021). This
matrix is most frequently visualized as the perineuronal lattice-like structures around all neurons
and first described by Golgi in 1898 (Golgi, 1898; Celio *et al.*, 1998). More recently the term
'perineuronal nets' has been applied to a specific extracellular structural motif associated with
some interneurons and recognized by specific agents such as *wisteria floribunda* agglutinin
(WFA); however, perineuronal space contains a ubiquitous, if variable (Deepa *et al.*, 2006),
abundance of negatively charged moieties (Schnaar *et al.*, 2014) and Donnan exclusionary
effects remain ubiquitous even as specific perineuronal environments vary among neuron
subtypes. The process of Donnan exclusion does not require an ongoing energy input, although
this issue has been contested (Glykys *et al.*, 2014b; Voipio *et al.*, 2014). We therefore modeled
the brain's extracellular matrix using a reduced system to remove the possibility of active
buffering of Cl^-_o by astrocytes (Egawa *et al.*, 2013) or other cellular or vascular elements. We
used gels of sulfated agarose to mimic the sulfated glycosaminoglycans such as the chondroitin
sulfate-decorated aggrecan family members that are prominent in the perineuronal matrix.
Agarose is a nominally sulfate-free linear glycopolymer that is a major component of agar
(Figure 2B; bars 1 and 2) that was used as a chemically homogenous starting material for
covalent sulfate linkage. We optimized the method of Fuse and Suzuki (Fuse & Toshiya, 1975)
to balance the gelatinizing properties of agarose with the dispersive, hydrophilic Donnan effects
arising from incorporation of the charged sulfate groups (Gregor, 1951; Helfferich, 1995). We
obtained a sulfated agarose that could be used to cast gels with 50 mM effective sulfate
concentration (Figure 2B, bar 3; 49.8+/-0.9mM sulfate across three batches [mean+/-SD])
covalently linked to the polymerized agarose lattice. Gels cast from sulfated agarose serve as a
simple *in vitro* model of the perineuronal extracellular space, allowing us to investigate the ability
of covalently linked anions attached to a three-dimensional matrix to displace mobile chloride
ions.

We measured the chloride concentrations within non-sulfated agarose gels vs. sulfated agarose
gels, each equilibrated in aCSF, and compared these to the chloride concentration in the
surrounding aCSF using either a standard colorimetric iron(III) thiocyanate assay (Figure 2C,
dark gray bars) or ABP-dextran FLIM imaging (Figure 2C, light gray bars). Agarose gels with
fixed anions in the form of covalently bound sulfate had significantly decreased chloride
concentrations versus both control aCSF and non-sulfated agarose gels (Figure 2C, right pair vs
left and center pairs, respectively) measured either with the standard chemical assay (dark gray
bars; $p = 0.00264$ and $p = 0.00354$ by Student's paired *t*-test, respectively) or ABP-dextran FLIM

(light gray bars; $p < 0.001$ by Student's paired t-test for either comparison). We measured a
small chloride increase within non-sulfated agarose gels vs control aCSF in either assay,
representing an insignificant increase when using the standard chemical assay (8.05+/-6.14mM,
mean+/-standard deviation; $p = 0.190$ by Student's paired t-test) and a smaller yet statistically
significant increase when measured using ABP-dextran FLIM (4.95+/-0.51mM, mean+/-
standard deviation; $p = 0.00328$ by Student's paired t-test). Later ABP-dextran FLIM
experiments comparing aCSF perfusate to non-sulfated gels show no such difference (see
below and Figure 2E). This Cl$^-$ increase is curious but is quantitatively small and qualitatively
distinct from the Cl$^-$ decrease we see in sulfated agarose gels (3.5% increase from non-sulfated
gel vs. aCSF control compared to a 40.7% decrease from sulfated agarose gel vs. aCSF
control, respectively), meaning that any effect would be a small overestimation of Cl$^-$ within
sulfated agarose gels. The overall agreement of results derived from both assays lends
confidence to the reliable performance of ABP-dextran FLIM versus standard chemical
colorimetric methods of Cl$^-$ measurement.

Next we placed separately cast non-sulfated and sulfated gels adjacent to each other and
equilibrated in the same aCSF bath with ABP-dextran (Figure 2D; schematic in Figure 2A).
ABP-dextran FLIM measurements of chloride concentration within the non-sulfated and sulfated
gels demonstrated significant chloride concentration differences between gels that had no fixed
anionic charge to displace mobile chloride (non-sulfated agarose; Figure 2D light blue bars) vs.
gels that had covalently bound sulfate groups (sulfated agarose; Figure 2D dark blue bars). The
chloride concentrations were inversely proportional to the sulfate concentration in the gel, were
significantly lower for sulfated gels at each time point (each $p < 0.001$), and were stable for over
three weeks (agarose gel comparisons: each $p = 1.0000$; sulfate gel comparisons: 2-4hours vs
24hours $p = 1.0000$, 3weeks vs 2-4 hours and 24 hours $p = 0.211$ and $p = 0.113$, respectively;
ANOVA with Bonferroni correction). These findings support the displacement of mobile chloride
ions by the sulfates fixed to the gel (Figure 2D) by Donnan exclusion. We next imaged both non-
sulfated and sulfated gels immediately juxtaposed to one another, along with aCSF perfusate, in
the same field (Figure 2E) and demonstrated that the presence of sulfate groups covalently
bound within the polymerized gel results in a significantly decreased chloride concentration
relative to both non-sulfated gels and aCSF perfusate (Figure 2E, bar 3 vs bar 2 and bar 1,
respectively; each $p < 0.001$ by Student's paired t-test). Non-sulfated agarose gels
demonstrated no difference versus aCSF perfusate ($p = 0.0647$ by Student's paired t-test).

Demonstration of chloride displacement in living systems: To test whether Donnan exclusion is
also operative in the extracellular matrix of the brain, we studied mouse hippocampal
organotypic slice cultures. We tested whether extracellular perineuronal fixed anions, such as
the chondroitin sulfate moieties of aggrecan family proteoglycans (Frantz et $al.$, 2010;
Karamanos et $al.$, 2021), displace chloride in this living system. After incubation with ABP-
dextran and equilibration with aCSF containing ABP-dextran and 136mM chloride, we measured
extracellular chloride concentration using ABP-dextran FLIM and found that Cl^-_o was
unexpectedly low and heterogenous (46.7 +/- 18.8 mM, calculated from 25.8×10^6 pixels across
32 fields of 7 slices). Representative fields are shown in Figure 3A (ABP-dextran intensity) and
Figure 3B (Cl^-_o composite image, quantified in Figure 3C). Paired analysis of slices pre- and
post-ABP-dextran incubation confirmed that autofluorescence signals in pixels in pre-ABP
images did not contribute to the unexpectedly low values of Cl^-_o obtained from post-ABP
images. This is because pre-ABP pixels that had both sufficient photon count to allow lifetime

calculation and lifetimes within the calibrated range of ABP-dextran had short lifetimes whose
effect would be to increase the reported Cl^-_o, not decrease it.

Perineuronal traces along the outer edge of neuronal silhouettes (Figure 3B, white dashes)
were used to analyze the spatial change in Cl^-_o in the extracellular space immediately adjacent
to the neuronal cytoplasmic membrane. Pyramidal neuron silhouettes were identified
morphologically and pixels underlying the extracellular margin (i.e., perineuronal) traces were
linearized for analysis. We compared the size of the effects of fixed anions on local Cl^-_o to
Brownian and machine noise arising from FLIM of ABP-dextran in bulk solutions with similar
mean Cl^-_o. The pixel-to-pixel change in Cl^-_o (ΔCl^-_o) versus distance in the presence of fixed
anions in the perineuronal space (Figure 3D, blue) was much larger than the ΔCl^-_o versus
distance in the absence of fixed anions in bulk solution containing ABP-dextran and a single
concentration of Cl^- (Figure 3D, red). Figure 3E shows similar data for a larger cohort of
perineuronal tracings and their corresponding aCSF solution counterparts (72 neurons traced
from 6 OHSCs). We found a consistently increased probability of greater ΔCl^-_o per micron in the
extracellular space where fixed extracellular anions were present compared to the perfusate
aCSF (Figure 3E, blue vs red).

We further analyzed dim pixels typical of the neuronal silhouettes, which had not already been
statistically excluded and displayed as black. These dim pixels retain their Cl^-_o colormap values
but are often so dim they are difficult to appreciate visually (e.g., Figure 3B). They are included
in presented images in the interest of transparency but were excluded from Cl^-_o analysis after
applying an empirically derived threshold value that best approximates the clearest silhouettes
in each image. We reasoned that these pixels represented photons originating from extracellular
ABP-dextran above or below the focal plane, likely present due to the higher-background FLIM-
derived intensity images (Figure 4A) which represent a summation of all photons in each pixel.
Because Cl^-_o is derived from the intrinsic, intensity-independent property of fluorescence
lifetime, structural context is lost in Cl^-_o images (Figure 4B) and must be reestablished by
incorporation of intensity information into a composite image (Figure 4C). This is not unique to
Cl imaging; commercial FLIM software creates intensity-lifetime composite images in a similar
manner. In our images we first converted from fluorescence lifetime to Cl^-_o to allow the use of a
linear colormap for readers' ease of interpretation (see Methods).

The dim, excluded pixels occurring in neuronal silhouettes offered an opportunity to assess
whether they were in fact caused by out-of-focus extracellular ABP-dextran, consistent with
recent super-resolution imaging of the extracellular space utilizing a 10KDa dextran-linked
fluorophore in addition to unconjugated fluorophore (Tønnesen *et al.*, 2018). If true, this would
produce a similar, if wider (Normoyle *et al.*, 2024), distribution of Cl^-_o values. Conversely, if the
dim, excluded pixels were autofluorescent in origin or were reflective of low Cl^-_i reported by
ABP-dextran leaked into neurons, then we would find a right-shifted, high-Cl^-_o distribution or a
left-shifted, low-Cl^-_o distribution, respectively.

<u>Verification of ABP-dextran extracellular compartmentalization:</u> We used two approaches to
assess the Cl values reported in the dimmest pixels. We first compared all pixels below the
exclusion threshold to all pixels above the threshold. Only pixels outside the actual slice (i.e.,
perfusate pixels) and those pixels with lifetimes outside the calibrated range of ABP-dextran
were not considered. We found that included and excluded pixels had histograms with similar
characteristics, such as mean and mode, although excluded pixels were fewer in number and
had a wider distribution (Figure 4D, blue vs gray). There is neither a high-Cl^-_o peak indicative of

autofluorescence nor is there a low-Cl_o peak indicative of intracellular signal in either included
pixels or excluded pixels. Notably, there are virtually no included pixels in the typically
intracellular range (i.e., ≤15mM Cl^-), and such pixels are far more likely to be excluded from
analysis (Figure 4D, gray arrow). We conclude that intensity-excluded pixels are not a low- or
high-Cl_o subset, which would seem to preclude errant Cl_i signal. However, we wanted to rule
out any possible non-extracellular signal more specifically as most pixels at these resolutions
are expected to contain a portion of both neuropil and extracellular space.

As a second means to evaluate the Cl values reported in the dimmest pixels, we assessed
pixels within individual somatic silhouettes. Visually apparent somatic edges are ideal to
compare extracellular ABP-dextran signal in the bright perineuronal exterior of silhouettes to
ostensibly intracellular pixels inside the silhouette margins. The fact that the brightest of these
pixels are located nearest the outer silhouette margin and the least intense pixels are located
toward silhouette centers supports our hypothesis that this signal is extracellular in origin from
outside the focal plane. Alternatively, if ABP-dextran leaked inside cells, despite its conjugation
to 10KDa dextran, we would expect that such an intracellular signal would be brightest in the
silhouettes formed by cells firmly within the focal plane (i.e., with the most ABP-containing
cytoplasm in the focal plane). After the objective pixel exclusion step (intensity greater than
three standard deviations from the mean, or lifetime outside the calibrated range), we compared
Cl_o in the perineuronal margin within one micron external to the traced border to those pixels
inside the traced border. In this way our analysis was restricted to only those cells
morphologically identified as pyramidal neurons adequately centered in the focal plane. Pixels
from inside the silhouette are greater in number than perineuronal extracellular pixels in this
analysis, yet we saw no subpopulation of intracellular chloride values (i.e., in the range of 15mM
Cl^-) that would be expected if this signal were originating from 'leaked' intracellular ABP-dextran
(Figure 4E). Signal from the one micron external to the perineuronal perimeter is five times as
bright on average as pixels from within the silhouette (Figure 4F), which helps explain why the
excluded intracellular signal has a wider distribution of Cl_o values (Normoyle *et al.*, 2024). If no
intracellular leakage of ABP-dextran can be detected even within in-focus neuronal somatic
silhouettes, where such signal is expected to be strongest if it were present, one can infer that
neuropil will not contribute any such signal in pixels containing both neuropil and extracellular
space. While we look forward to future experiments with greater spatial resolution, we conclude
that neither objectively excluded pixels nor those excluded by intensity thresholding are
indicative of low- or high-Cl_o subsets. Further, we provide ample evidence supporting the fidelity
of ABP-dextran in its reporting of chloride exclusively in the extracellular space.

<u>Demonstration of chloride displacement by chondroitin sulfate:</u> We then confirmed that fixed
anions, including chondroitin sulfate glycoproteins, are a significant contributor to the observed
difference between expected and measured Cl_o by measuring Cl_o before and after treatment
with chondroitinase. Analogous to matrix metalloproteases, chondroitinase is a bacterial
enzyme that cleaves the sulfated glycopolymer chondroitin. Chondroitinase treatment
significantly increased Cl_o in organotypic hippocampal slice cultures (Figure 5A&B; pre- and
post-digestion, respectively). Cl_o increased on average 8.3+/-3.3mM (mean+/-standard
deviation) in freely diffusible extracellular chloride within the slice culture (Figure 5A vs 5B;
quantified in 5D-F) and was significantly greater in chondroitinase digested slices than in sham
digested slices (Figure 5B vs 5C; quantified in 5F). This increase in Cl_o coincides with a
significant decrease in the extracellular fixed anions within the slice culture. While chondroitin
sulfate is targeted in this experiment, proteoglycans collectively make up less than 10% of the

extracellular fixed charge; gangliosides and sulfatides make up the balance (Schnaar *et al.*,
2014). The actual decrease in fixed anion concentration in the extracellular space was
estimated from the concentration of chondroitin sulfate released into the perfusate after
chondroitinase treatment (Figure 5G) and confirmed by HPLC analysis (Figure 5H). Quantitative
estimates of fixed anionic charge in the perineuronal space are few in the absence of a
quantitative fluorescent or histological sensor. Those present in the literature are either based
on novel techniques (Marinsky, 1985) or else are extrapolated from non-neuronal tissues also
rich in chondroitin sulfate (Urban *et al.*, 1979; Chahine *et al.*, 2005). We estimated the expected
Cl^-_o increase after chondroitinase digestion using HPLC-derived measurements of released
chondroitin disaccharides and OHSC volume (see Methods). Careful *in vitro* studies of
chondroitinase have concluded that only approximately 50% of total chondroitin sulfate is
accessible to chondroitinase (Lin *et al.*, 2008). This is likely not due to a diffusion restriction
(Hrabetová *et al.*, 2009) and more likely is related to enzyme activity, perhaps due to variance in
local matrix structures. Our own empirical observations in OHSCs, in agreement with others'
published observations (e.g. Orlando and colleagues, especially Figure 5C therein) (Orlando *et*
al., 2012) indicate that chondroitinase activity decreases with distance from its diffusive
reservoir and full activity is restricted to an estimated 50μm; as such we only measure Cl^-_o to a
depth of 50μm. Rather than seek definitive conclusions about the enzymatic efficiency of
chondroitinase at this time, we performed calculations for each case. If all digested chondroitin
sulfate indeed came from only the most superficial 50μm of our OHSCs, the Cl^-_o increase
expected in this same superficial 50μm is calculated to be 8.8mM (see Methods). This agrees
well with experimental mean Cl^-_o values calculated from regular subfields of pre- and post-
chondroitinase digestion, 8.8mM versus 8.3+/-3.3mM (Figure 5E), or when using the full field to
calculate the minimum and maximum range of Cl^-_o increases from 0.6-16.1mM (Figure 5D; pre-
digestion mean minus standard deviation to post-digestion mean plus standard deviation).
Further, we find that even if we assume chondroitin sulfate is lost uniformly from the full
thickness of the OHSC and recalculate a smaller expected Cl^-_o increase of 1.65mM, this still lies
within the empirically measured range of 0.6-16.1mM. These observations are consistent with
the expected inverse relationship between fixed extracellular anions such as sulfate and mobile
Cl arising from Donnan exclusion. They are also consistent with the fact that chondroitin sulfate,
while experimentally accessible, only accounts for a minority of total expected perineuronal fixed
anionic charge despite being the dominant sGAG in the perineuronal space. Estimations
employing bulk biochemical measurements from rat brain (Schnaar *et al.*, 2014) suggest that
the actual fixed anionic charge contribution from chondroitin sulfate is approximately 2mM
equivalent charge (see Methods) in agreement with our findings and consistent with the
electrophysiological findings of others (Klein *et al.*, 2018). It would be advantageous to similarly
estimate a predicted Cl^-_o based upon local sulfate concentrations and compare this to empirical
Cl^-_o measurements similar to our sulfated agarose experiments (Figure 2E), but without direct
and independent measurement of the extracellular sulfate content of OHSCs this is not currently
feasible. In summary, the immobile ions associated with the extracellular matrix displace mobile
anions such as chloride consistent with the well-established effects of Donnan equilibrium
forces, such that Cl^-_o is much lower and less uniform than would otherwise be expected.

<u>Chloride displacement in the perineuronal space *in vivo*</u>: To test whether Donnan exclusion of
Cl^-_o by sulfated GAGs and other fixed anions was significant *in vivo*, we performed live 2 photon
imaging of P26-30 mice via a cortical window (Figure 6A). Direct application of high
concentrations of ABP-dextran into the non-sulfated agarose overlying the neocortex (Figure

6B) resulted in a robust ABP fluorescence signal from the extracellular space of the brain
parenchyma, similar in intensity to 50μM ABP-dextran used *in vitro*. Control measurements
were obtained from the agarose above the cortex, which had been brought up in aCSF (136mM
Cl^-) and allowed to equilibrate with *in vivo* CSF. Notable exclusion of ABP-dextran fluorescence
emission from blood vessels (Figure 6C,D&E) and cell bodies (Figure 6D) was observed. Areas
of locally elevated Cl^-_o and overall bright signal seen in OHSCs (Figures 3-5) were absent *in*
vivo (Figure 6), suggesting these features are specific to *in vitro* preparations. At several
microns in size, we reason the areas seen in OHSCs are most likely damaged areas where
intracellular space makes up less than the typical 80% of volume allowing ABP-dextran access
to a greater proportion of volume, so that the signal is bright despite quenching by the high Cl^-_o
in these spaces. ECM damage would also be likely in such circumstances and would be
expected to result in a loss of extracellular immobile anions, limiting the Donnan exclusionary
force and leading to relatively high concentrations of Cl^-_o. This combination would be expected
to result in a paradoxically bright, short-lifetime ABP-dextran signal yielding an unusually intense
high Cl^-_o area. Given the absence of these features *in vivo*, we speculate that these areas are
the result of slicing trauma but longitudinal studies will be needed to adequately categorize
them. Regions of interest (ROIs) were defined using intensity images before rendering
composite images so that only structural information was considered; an example intensity and
composite image pair can be seen in Figure 6C&E. Perineuronal tracing analysis was repeated
for the limited number of layer 2/3 neurons we could identify by morphology and confirmed that
perineuronal $\Delta[Cl^-]_o$ per micron *in vivo* is similar to *in vitro* findings (Figure 6D inset, F&G;
compare to Figure 3D&E). Cortical Cl^-_o was less than half the chloride concentration measured
in the overlying agarose (48.1 +/- 17.0mM, calculated from 68 ROIs and 4 animals, versus
135.4 +/- 5.0mM in agarose between cortex and coverglass). Cl^-_o in cellular and acellular fields
displayed in Figure 6C,D&F were not significantly different from each other (Figure 6E entries
2&3, respectively), nor were either significantly different from all ROIs collected from this animal
(entry 4) or from all animals (entry 5; each p = 1.0000 by ANOVA with Bonferroni correction),
while all were significantly different when compared to aCSF measured above the cortex (each
p < 0.001 by ANOVA with Bonferroni correction). Regional mean Cl^-_o values were approximately
45-55mM (Figure 6E) but there was notable spatial variation between regions and even within
regions, similar to *in vitro* OHSC results and consistent with local Donnan exclusion of Cl^-_o by
local variation in fixed anions such as sulfated GAGs. Future experiments will be optimized for
higher resolution imaging, but our results suggest that the well-established heterogeneity of
sulfation patterns around neurons represent a means by which neurons and supporting cells
can indirectly modulate Cl^-_o through Donnan forces in a manner similar to how cytoskeletal
components, in particular actin, have been recently shown to influence local intracellular Cl^-_i
(Rahmati *et al.*, 2021).

Discussion

We demonstrate stable Donnan exclusion of chloride by fixed anions in a transport-free system
of sulfated agar using FLIM of a novel fluorophore, ABP-dextran, and validate these
measurements with direct chemical assays of sulfate and chloride (Figure 2). FLIM of ABP-
dextran demonstrated that Cl^-_o in the brain is less than half the Cl concentration in the
cerebrospinal fluid and plasma (Figures 3-6). This low Cl^-_o arises from Donnan exclusion of
chloride by fixed anions including sulfated glycosaminoglycans (sGAGs), because release of
sGAGs by chondroitinase results in an increase in Cl^-_o that varies with the amount of sulfates
released (Figure 5). Major findings are confirmed *in vivo* (Figure 6).

<u>Limitations of this study</u>

The finding that Cl^-_o is much lower than expected in the extracellular space of living brain tissue is based on FLIM of a new Cl-sensitive fluorophore, ABP-dextran (Normoyle *et al.*, 2024). These results are in contrast to the higher values measured using ion sensitive electrodes (Jiang *et al.*, 1992; Kroeger *et al.*, 2010), a discrepancy that we cannot definitively explain at this time. The ABP-dextran fluorophore is based on a validated structure (Biwersi *et al.*, 1992) and was calibrated against Cl, other anions, and direct chemical analysis of chloride concentrations in situ (Figures 1&2). ABP-dextran FLIM accurately reported Cl values in sulfated carbohydrate polymers (Figure 2), so it is unlikely that the gangliosides, sGAGs or other anions in the extracellular environment (Figure 1C) affected the accuracy of the ABP-dextran FLIM. ABP-dextran overcomes several barriers to accurate measurement of extracellular chloride, including sufficient sensitivity in the relevant range of chloride concentrations, competition with autofluorescence, and exclusion from the cytoplasmic space, where lower chloride values would be encountered. ABP-dextran was clearly excluded from the intracellular space (Figure 3A&B; Figure 4A&C; Figure 6D) and blood vessels (Figure 6C,D&E). Experiments were focused on establishing the utility of ABP-dextran as an extracellular-specific sensor and did not include transgenic fluorophores that could have measured Cl^-_i and marked neurons for *in vivo* analysis. We speculate that the difference between our non-invasive, novel fluorophore-based measures and the implanted ion-sensitive electrode measures of Cl^-_o may arise from the large difference in sample sizes, where microelectrodes sample a single microenvironment while the fluorometric technique samples millions. It is much easier to perceive the wide distribution of Cl^-_o with the larger sample size (Figure 4D), and to appreciate the average Cl^-_o. A study directly comparing fluorometric and microelectrode techniques would be of great interest.

<u>Stable Donnan exclusion</u>

An important finding in this study is that Cl microdomains established by Donnan exclusion are stable for weeks, and do not require active transport to be maintained (Figure 2). This phenomenon is well-established in biophysics (Epsztein *et al.*, 2018; Gao *et al.*, 2022), but is more confusing in neuronal physiology where membranes with time-varying ionic permeabilities and transporters create a more complex environment (Voipio *et al.*, 2014; Doyon *et al.*, 2016; Düsterwald *et al.*, 2018; Rahmati *et al.*, 2021). A point of particular confusion is the role of active Cl transport vs. Donnan exclusion in maintaining a particular E_{GABA} in the face of GABA-gated Cl flux that alters the local Cl concentration. After a GABA-gated Cl influx, and re-establishment of local charge balance by cationic flux via voltage- and ligand-gated cation channels, the local cytoplasm will contain excess chloride salts. This Cl has two fates: either excess salt diffuses through the cytoplasm to re-establish a new equilibrium with fixed charges, or the excess salt is transported back across the membrane by cation-chloride cotransporters (Brumback & Staley, 2008; Lewin *et al.*, 2012; Doyon *et al.*, 2016; Beckstein & Naughton, 2022). The transporters are required to re-establish the original steady state volume, but in the absence of transport, diffusion maintains local Cl concentrations remarkably well (Brumback & Staley, 2008; Rahmati *et al.*, 2021). In the absence of membrane Cl salt transport, this diffusion of excess Cl salts will be associated with either a cytoplasmic volume increase from associated water influx or an increase in the mean Cl concentration in the cytoplasm. At pathologically high rates of Cl influx, membrane chloride salt transport becomes rate-limiting (Staley & Proctor, 1999; Jedlicka *et al.*, 2011; Lewin *et al.*, 2012; Doyon *et al.*, 2016), and chloride concentrations become sufficiently labile to depolarize E_{GABA} (Barker & Ransom, 1978; Alger & Nicoll, 1982;

Huguenard & Alger, 1986; Staley *et al.*, 1995). Thus Donnan exclusion *establishes* the local
value of E_{GABA}, and active transport *maintains* that value (and neuronal volume) in the face of
synaptic Cl flux (Glykys *et al.*, 2014a). The same principals should apply to the local
extracellular chloride concentrations described here, with astrocytic chloride buffering (Egawa *et*
al., 2013) and diffusion between the extracellular fluid, the CSF, and vascular spaces
(Rasmussen *et al.*, 2022) taking the place of neuronal membrane cation-chloride cotransport.
Importantly, because E_{GABA} is set by the ratio of Cl^-_o to Cl^-_i (as given by the Nernst equation)
and neurons can actively adjust intracellular immobile anions (Rahmati *et al.*, 2021), there is no
Cl^-_o level that expressly precludes hyperpolarizing inhibition because proportional Cl^-_i reduction
allows E_{GABA} to be maintained at any given value (Figure 7). Multi-ion modeling from our group
has previously demonstrated similarly modest changes in E_{GABA} with Cl^-_o reduction that can be
counteracted by even more modest Cl^-_i changes (Glykys *et al.*, 2017).

<u>Low extracellular Cl</u>

The Cl^-_o measured by ABP FLIM is less than half of the canonical Cl^-_o. Such a low value of Cl^-_o
should affect not only E_{GABA} but also the inhibitory $GABA_A$ conductance, because there are only
half as many ions to carry the outward membrane currents (i.e. inward Cl- flux) (Coombs *et al.*,
1955). Shouldn't such a low value of Cl^-_o have been obvious from electrophysiological studies?
E_{GABA} is determined by the ratio of Cl^-_i to Cl^-_o (Coombs *et al.*, 1955; Staley, 2023). If either
concentration is known, the other can be determined from E_{GABA}. However if both Cl^-_i and Cl^-_o
are determined by the concentrations of local immobile anions, neither can be set
experimentally and thus E_{GABA} cannot be used to determine either Cl^-_i or Cl^-_o; only the ratio can
be inferred from the Nernst equation. Similarly, although the conductance of inward Cl flux
(outward membrane current) is determined in part by Cl^-_o, it is also determined by the $GABA_A$
permeability, i.e. the number of open membrane channels and their capacity for ion flux. Thus
membrane currents are not sufficient to determine Cl^-_o (Coombs *et al.*, 1955). Control of the
ionic milieu is greater in single-channel recordings, but whether the complement of immobile
anions is physiological under these conditions is difficult to determine, and even in these
conditions there is substantial uncertainty regarding local ionic concentrations (Li *et al.*, 2015).
The effects of variable Cl^-_i and Cl^-_o have on E_{GABA} have been explored (Glykys *et al.*, 2017), but
high resolution spatiotemporal correlation of all three parameters will provide exciting new
insights into dendritic signal processing.

<u>Cl^-_o microdomains</u>

The extracellular matrix of the brain is often depicted as perineural nets surrounding
parvalbumin neurons that are detected by specific agglutinins and antibodies (Celio & Blümcke,
1994). However, these assays detect very specific motifs of glycoproteins and
glycosaminoglycan sulfation; using more permissive ionic methods, a highly anionic
extracellular matrix can be seen to surround virtually all neurons (Golgi, 1898; Glykys *et al.*,
2014a; Morawski *et al.*, 2015). This extracellular matrix fills the extracellular space, which
comprises about 20% of the brain's volume (Syková & Nicholson, 2008; Tønnesen *et al.*, 2018).
We have focused our analysis on the sGAG moiety of proteoglycans because these are
prominent constituents of perineuronal extracellular matrix (Tønnesen *et al.*, 2018; Karamanos
et al., 2021), are found in both dense and more diffuse neuronal extracellular matrix (Deepa *et*
al., 2006), and are readily perturbed experimentally with commercially available enzymes.
GAGs are polymers of widely varied length comprised of sugars and substituted sugars (N-
acetylglucosamine, glucuronic acid, and galactose) that are synthesized without templates. Up

to 3 sulfates are added to the sugar moieties before export to the extracellular space. This
enables the creation of a stable but highly variable spatial distribution of dense, fixed anionic
charge in the extracellular matrix. Figure 3 demonstrates that this variance is substantial at the
level of resolution of light microscopy. We have previously demonstrated reduction of fixed
extracellular anions after chondroitinase treatment (Glykys et al., 2014a), and others have
demonstrated small but significant depolarizing shifts of E_{GABA} after chondroitinase treatment
(Klein et al., 2018). However, the distribution of fixed anions at the extracellular face of $GABA_A$
receptors, and the corresponding Cl^-_o, is currently unknown. The effects of variable Cl^-_o and Cl^-_i
have on E_{GABA} have been explored (Glykys *et al.*, 2017), but high resolution spatiotemporal
correlation of all three variables would allow more descriptive modeling in complex solutions.

Physiological implications

Along with Cl^-_i microdomains (Rahmati *et al.*, 2021), Cl^-_o microdomains in the region of the
extracellular openings of $GABA_A$ receptor-operated channels are a critical determinant of both
E_{GABA} and the $GABA_A$ conductance. The wide range of Cl^-_o values established via Donnan
exclusion by sulfated GAGs (Figures 2, 3, 4, 5 and 6) makes possible a substantial variety of
effects of $GABA_A$ receptor activation based on the direction of chloride flux. These effects range
from hyperpolarizing inhibition through shunting inhibition through excitation by activation of low
threshold calcium currents and removal of the magnesium block of the NMDA receptor. In
addition, the effects of Cl^-_o on the quantity of charge that is carried by $GABA_A$ membrane
currents (the conductance) (Coombs *et al.*, 1955) makes possible a broad range of strengths of
$GABA_A$ synapses that is independent of the number or subunit composition of receptors or their
posttranslational modifications.

The turnover of the macromolecules comprising the extracellular matrix is very slow (Tsien,
2013), on the order of months to years based on rodent experiments (Margolis & Margolis,
1973) as well as the rate of deterioration of patients with genetic defects of GAG catabolism
(Héron *et al.*, 2011; Hampe *et al.*, 2020; Seo *et al.*, 2020). This slow turnover provides a
mechanism for long-lasting influences on synaptic GABA signaling. Some elements of GAG
synthesis are activity dependent (Sidharthan *et al.*, 2013), but currently nothing is known about
the insertion of GAGs into the extracellular matrix, in situ modification, and the capacity for
directed alterations of Cl^-_o microdomains in the regions of $GABA_A$ receptors and synapses. Thus
the role of extracellular chloride microdomains in synaptic signal processing and memory
remains to be discovered.

Pathological implications

Cytotoxic cerebral edema: If Cl^-_o is normally only half of the value of Cl in CSF and plasma, then
the capacity for Cl^-_o to increase acutely may be an important and hitherto unappreciated
element of the pathophysiology of cerebral edema (Glykys *et al.*, 2017). Matrix
metalloproteinases (MMPs) are released and activated after neuronal injury and death (Zhang
et al., 2016). Release of sulfates in sGAGs from the extracellular matrix would reduce the
Donnan exclusion of Cl by fixed sulfates. This would result in an acute increase of Cl^-_o as in
Figure 4. The action of equilibrative cation-Cl cotransporters would then lead to a
corresponding increase in chloride salts in the cytoplasm of neighboring healthy neurons, with
attendant volume increases. This novel mechanism of cytotoxic edema could potentially be
ameliorated by pharmacological MMP inhibition. Alternatively, inhibition of the influx of chloride

salts that cross the BBB from the vascular space (Jha *et al.*, 2019) would limit the influx of Cl
into the extra and intracellular spaces.

Post Traumatic Epilepsy: Richard Miles and colleagues demonstrated that GABA$_A$ receptor
activation could be excitatory in human brain tissue resected for control of medically intractable
epilepsy (Cohen *et al.*, 2002). However, the pathomechanism has never been elucidated
(Huberfeld *et al.*, 2007; González, 2016; Karlócai *et al.*, 2016). Gliosis is the most common
finding in medically intractable epilepsy (Thom, 2014). In glial scars, reactive astrocytes
synthesize new matrix elements (Roll & Faissner, 2014; Song & Dityatev, 2018). If the
replacement matrix was more heavily sulfated than the original, as would be expected from the
firm texture that is responsible for the name "scar" (Lesperance *et al.*, 1992), then in areas of
gliosis Cl_o^- would be low. Low Cl_o^- could contribute to degradation of GABA$_A$ receptor mediated
inhibition, frank excitation, and failure of anticonvulsants whose action are predicated on intact
synaptic inhibition. Thus replacement of the extracellular matrix and distortion of extracellular
chloride microdomains could comprise an important mechanism of medically intractable
epilepsy after brain injury.

Future studies

The findings that Cl_o^- is both lower than expected and spatially heterogenous opens the door for
many investigations into the mechanisms by which Cl_o^- is set, such as the synthesis, export, and
in situ modification of sulfated GAGs. The activity dependence of these mechanisms and the
effect of Cl_o^- microdomains on synaptic signaling are additional areas of investigation.
Pathologically, the impact of changes in Cl_o^- in both acute edema and long-term complications
such as epilepsy may provide much-needed therapeutic insights into these frequently-
intractable conditions.

Figure 1 Characterization and Calibration of Chloride-Sensitive Fluorophore ABP. *A)* N-(**a**mmonium)-**b**utyl **p**henanthridine (ABP) is synthesized in-house and conjugated to activated 10KDa dextran, a glucose polymer, at a molar ratio of 4.4. *B)* Representative calibration of ABP-dextran fluorescence lifetime versus Cl⁻ demonstrating ABP-dextran sensitivity to chloride-induced quenching. Calibration of ABP-dextran fluorescence lifetime vs Cl_o^- is displayed as a violin plot with mean +/- standard deviation overlaid. ABP-dextran lifetime at 0mM chloride (τ_o) is extrapolated using a best-fit approach (see Methods). *C)* Stern-Volmer plot demonstrates a linear relationship between ABP-dextran fluorescence lifetime and concentration of chloride and was used to convert lifetimes to chloride concentrations. The ratio of unquenched ABP-dextran fluorescence lifetime (τ_o) to ABP-dextran lifetime at a given concentration of quencher (τ) is plotted versus concentration of quencher (τ_o/τ vs [Q⁻]). The slope of the linear regression is the Stern-Volmer constant (k_{SV}) which allows conversion of ABP-dextran lifetime to concentration of quencher, specifically Cl⁻ (blue circles / black line; k_{SV}=15.9M⁻¹). Four biologically relevant anions were found to have no experimentally relevant effect on ABP-dextran fluorescence lifetime: bicarbonate (k_{SV}=1.21M⁻¹), gluconate (k_{SV}=0.70M⁻¹), methyl sulfonate (k_{SV}=0.18M⁻¹), and phosphate (k_{SV}=0.11M⁻¹). Gluconate was subsequently used as a chloride substitute in non-standard aCSF formulations used for calibrations.

Figure 2 **Effects of immobile sulfate on Cl⁻ in a volume of agarose gel.** ***A)*** Experimental
schematic demonstrating how polysaccharide gels, cast in aCSF separately, were equilibrated
in aCSF after transfer to a common vessel. Gels were either equilibrated with aCSF containing
ABP-dextran, processed for chemical analysis, or subjected to multiple investigations in tandem
(see Methods). ***B)*** We covalently bound sulfate groups to algal biopolymer agarose and cast
this as a gel in aCSF to model perineuronal interstitial matrix that is rich in chondroitin sulfate-
decorated glycosaminoglycans. We compared sulfated agarose gel to native agar and agarose
gels, achieving a 250-fold increase in sulfate content compared to commercially available agar
(bar 3 vs bar 1, respectively; $p < 0.001$, Student's paired t-test of at least three gel pieces' mean
of technical replicates; note discontinuous y-axis). Commercially available agarose, which is
intended as a sulfate-free product, had no measurable sulfate content (bar 2) and subsequently
was used as a control gel. ***C)*** Chloride concentration was reduced in sulfated agarose gels. Cl⁻
was measured using both a standard colorimetric assay (dark gray bars) and ABP-dextran FLIM
(light gray bars) in aCSF control (leftmost pair), within non-sulfated agarose gel (center pair) and
within sulfated agarose gel containing ≈50mM (49.2+/-0.289mM) covalently bound sulfate
(rightmost pair). Measured chemically or using ABP-dextran FLIM, Cl⁻ in sulfated agarose gels
differed significantly from aCSF ($p = 0.00264$ and $p < 0.001$, respectively) and non-sulfated
agarose gels ($p = 0.00354$ and $p < 0.001$, respectively), while Cl⁻ measured in non-sulfated
agarose gels was not significantly different from aCSF when measured by chemical assay ($p =$
0.190) but registered a small but significant difference (3.5% increased Cl- relative to aCSF, $p =$
0.00328) when measured with ABP-dextran FLIM. Chemical assay and aCSF FLIM data points
are averages of three technical replicants, while gel values are averaged measurements from
each quadrant of a given gel, each compared using Student's paired t-test. ***D)*** Significant
chloride concentration differences between agarose gels with 50mM covalently bound sulfate
(dark blue) and non-sulfated agarose gels (light blue) do not equilibrate with time but instead are
stable for as long as experimentally observed (> 3 weeks). ANOVA testing with Bonferroni
correction demonstrates that Cl⁻ significantly differs between native agarose and sulfated
agarose at all time points (overall and each pair $p < 0.001$) while neither agarose (each $p =$
1.0000) nor sulfated agarose gels (from left to right, $p = 1.0000$; $p = 0.2119$; $p = 0.1129$) change
significantly with time. Cl- measurements from each quadrant of a given gel are averaged to
generate each data point. ***E)*** Demonstration of stable juxtaposition of significantly different
chloride concentrations at equilibrium. Separately cast sulfated and non-sulfated gel pieces are
placed in a single vessel as described in ***A*** and equilibrated in common aCSF with ABP-dextran.
Sulfated agarose gels (dark blue) again contain significantly lower Cl⁻ than do non-sulfated
agarose gels (light blue; $p < 0.001$) or perfusate aCSF (gray; $p < 0.001$) in this representative
experiment, while Cl⁻ within non-sulfated agarose gels is again not significantly different than
perfusate aCSF ($p = 0.0647$). , Fields from each quadrant of each gel co-incubated in a single
vessel with shared aCSF are analyzed using Student's paired t-test. *Statistical significance*
indicated on graph for p-values <0.05 (*); <0.01 (**); <0.001 (***); "ns" indicates "not significant".
Error bars reflect standard deviation from the mean. Use of parametric tests confirmed
appropriate via Jarque-Bera test (see Methods).

Figure 3 Cl⁻ **in the extracellular space is not uniform and is considerably lower than aCSF perfusate.** *A)* High-magnification OHSC intensity image of ABP-dextran excluded from cell bodies in the pyramidal cell layer (CA1; scale bar 20μm). *B)* Chloride-composite image again demonstrating the exclusion of ABP-dextran from intracellular spaces as well as the non-uniformity of Cl^-_o in the pyramidal cell layer of a representative OHSC. Representative pyramidal cell visible just above and left of image center, identified by ABP-dextran exclusion and morphology of resulting silhouette, is one of 6-10 neurons per field deemed to have a regular and nearly-continuous border analyzed as described in *D&E* (scale bar 20μm). *C)* Histogram of full field Cl^-_o in OHSC pictured in *B*, demonstrating non-uniformity visually apparent in *B*. Notably, Cl^-_o = 44.5+/-15.9mM despite perfusate [Cl⁻] = 136mM (across all depths of this slice Cl^-_o = 49.7+/-18.5mM; mean +/- SD). *D)* Change in chloride ($\Delta[Cl^-]_o$) plotted against distance in the perineuronal space (blue line) or the same trace overlaid onto a calibration aCSF FLIM image (red line) corresponding to the perineuronal trace in *B*. $\Delta[Cl^-]_o$ of calibration aCSF (red) encapsulates machine and experimental noise, and $\Delta[Cl^-]_o$ in the perineuronal space (blue) exceeds that of control in this representative neuron. *E)* Perineuronal $\Delta[Cl^-]_o$ per micron calculated from many neurons' circumferential traces demonstrates that the variability of perineuronal Cl^-_o in living *in vitro* system exceeds the variability of control aCSF (72 neurons versus matched calibration aCSF controls from depths of 20-100μm in this representative OHSC; p < 0.001, by Kolmogorov-Smirnov test). *Cl^-_o image rendering and presentation details can be found in Methods and in subsequent figures. Scale bars A&B: 20μm.*

<u>Figure 4</u> Generation of composite chloride images and cell body masking for pixel
quantification. *A)* ABP-dextran intensity data of an OHSC, derived by taking the total number
of photons detected in each pixel throughout the acquisition period, is used to inform on tissue
structure. Image series *A-C* corresponds to Figure 3B and its traced neuron example. Neuron
silhouette traced in *B&C* is indicated with a white asterisk. *B)* Cl_o^- calculated from ABP-dextran
lifetime. The loss of discernible structure is due to the fact that the intensity of the ABP-dextran
signal has no effect on the Cl_o^- calculated from fluorescence lifetime (see Methods). Areas
corresponding to cell body silhouettes in *A* have notable pixelation with relatively high apparent
Cl_o^- values interspersed with black pixels, the latter indicating statistical exclusion due to low
signal intensity (see Methods). *C)* In order to observe Cl_o^- with spatial context restored, we use
intensity data to inform the brightness of the raw chloride data in *B*, generating a composite
image in which the color corresponds to Cl_o^- and brightness is attenuated based on the intensity
of the signal in each pixel (see Methods). The most popular proprietary FLIM software packages
use similar methods of composite data display. Note that prior to Cl_o^- analysis a further intensity-
based thresholding step excludes pixels from inside somatic silhouettes in the focal plane, and
pixels not corresponding to the slice (i.e., perfusate, top left) are also excluded by manually
drawn ROI (masks not shown). *D)* Histogram of Cl_o^- in all analyzed pixels (blue) versus pixels
excluded through thresholding step, principally marking somatic silhouettes (gray) in this
representative OHSC, demonstrating no secondary peak at typical Cl_i^- values (i.e., =< 15mM).
Further, this range of low Cl_o^- values is more likely excluded (gray) than included (blue) in our
analysis (indicated by gray arrow). *E&F)* To further verify the cellular exclusion of ABP-dextran,
we looked specifically at the margins of well-defined somatic silhouettes, such as the example
marked across *A-C*, to search for signs of intracellular ABP-dextran leakage. We compared
perineuronal pixels up to 1mm outside neurons to those pixels which lie inside the somatic
margins of 72 neurons but were not excluded prior to thresholding (statistically excluded pixels
are not considered; see Methods). Consistent with out-of-focus extracellular ABP-dextran, we
found similar calculated Cl_o^- values between the two groups (*E*) with the expected wider
variance in the less intense intracellular signal (*F*; see text). *Scale bar: **A-C** 50μm.*

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<u>**Figure 5**</u> **Chondroitinase treatment removes fixed perineuronal anions and attenuates Cl^-_o**
displacement. Cl^-_o composite images of representative mouse hippocampus slice cultures
imaged in culture media (Cl$^-$ ≈ 64mM) with 1mg/mL ABP-dextran (100mM ABP-Dextran) before
(**A**) and after (**B**) treatment with bacterial MMP analog chondroitinase, or after sham digestion
(**C**); shared colorbar for **A-C** at right. **D)** Histograms of [Cl$^-$]$_o$ corresponding to **A&B** demonstrate
pre-chondroitinase digestion (dark blue) and post-chondroitinase digestion (light blue) [Cl$^-$]$_o$
populations of pixels are significantly different ($p < 0.001$ by Kolmogorov-Smirnov paired-sample
test). **E)** When images from **A&B** are broken into regularly shaped regions of interest and
analyzed as paired groups, pre-chondroitinase and post-chondroitinase are again significantly
different (46.7+/-2.7mM vs 55.0+/- 5.0mM, respectively, mean+/-SD; $p = 0.0152$ by Wilcoxon
rank sum test). **F)** Violin plot of data from **A&B** (dark and light blue, respectively) vs grouped
sham-digested slice data (gray) demonstrating that Cl^-_o increases significantly after chondroitin
sulfate is removed by digestion, whether compared to pre-digestion of the same slice or a sham
digestion (each $p < 0.001$ by Kolmogorov-Smirnov paired-sample test). **G)** Measurement of
glycosaminoglycans, including chondroitin sulfate, released into the perfusate after OHSCs are
treated with chondroitinase (vs sham digestion) using a commercial colorimetric assay. A
significantly higher concentration of polyanionic glycosaminoglycans are found in the
extracellular fluid after chondroitinase digestion ($p = 0.00632$ by Student's paired t-test),
consistent with the release of chondroitin sulfate from extracellular matrix within slice cultures
and a resultant increase in Cl^-_o. **H)** HPLC analysis confirms the presence of chondroitin sulfate
released into digestion buffer after chondroitinase treatment (mean = 0.20μg/mL); there was no
detectable chondroitin sulfate in sham digests, negating formal significance testing. *A-C scale*
bars 50μm; all slice cultures were DIV14-21 at time of experiment; cultures were grown directly
*on glass with the exception of **G** where cultures were grown on membrane inserts (see*
Methods); significance values noted graphically for p-values <0.05 (*); <0.01 (**); <0.001 (***);
*"ns" indicates "not significant". Note that data contained in **D-F** labeled 'pre' and 'post' are*
*derived from OHSCs in **A** and **B**, respectively.*

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<u>**Figure 6**</u> *In vivo* Cl^-_o in mouse neocortex is consistent with *ex vivo* findings. *A&B)*
Schematic of *in vivo* imaging set-up, using a surgically implanted headbar to immobilize P26-
P30 mouse pup for imaging through 3mm coverglass window overlaying 1% agar brought up in
aCSF containing ABP-Dextran and 136mM chloride laid directly on exposed cortex. *C)* Intensity
image of mouse L1 cortex (depth 54μm) demonstrating ABP-dextran diffusion into parenchyma
and exclusion from vessels. *D)* Intensity image of L2/3 cortex 138μm deep to *C*, demonstrating
ABP-dextran exclusion from cells and vessels; large vessels appear blurred because their
widest diameter exists superficial to this field (depth 192μm). Inset is 7x zoomed portion of
corresponding chloride composite image, one of three fields from this animal from which we
identified and analyzed pyramidal neurons in a manner similar to Figure 3. *E)* Region of interest
(ROI) selections shown numbered in Cl^-_o composite image, corresponding to intensity image in
C, demonstrates exclusion of large vessels from ROIs but is otherwise permissive. *F)* Change in
chloride (Δ[Cl$^-$]$_o$) plotted against distance in the perineuronal space (blue line) or the same trace
overlaid onto a calibration aCSF FLIM image (red line) of the representative neuron traced in *D*
inset (white dashes). *G)* Perineuronal Δ[Cl$^-$]$_o$ per micron calculated from 11 L2/3 neurons'
circumferential traces demonstrates that the variability of perineuronal Cl^-_o *in vivo* exceeds the
variability of control aCSF (p < 0.001, by Kolmogorov-Smirnov test; 11 neurons from 3 fields of
1 animal; see *Methods*), consistent with our *in vitro* findings. *H)* Cl^-_o in mouse neocortex is
significantly lower than the CSF Cl$^-$ as shown in this violin plot of all ROI pixels with population
mean (black dashed lines) and overlaid mean+/-standard error of ROIs analyzed. Compared to
agarose brought up in 136mM aCSF overlying the cortex (leftmost violin plot: 135.4+/-5.0mM;
mean+/-standard deviation of all analyzed pixels), *in vivo* mouse cortex had significantly lower
Cl^-_o whether measured in cellular fields such as in *C* or in acellular fields such as in *D* (plots 2
and 3: 48.9+/-6.7mM and 55.0+/-17.9mM, respectively). This was true when considering all
ROIs in all fields from the animal from which *C&D* were taken (plot 4: 47.2+/-14.9mM), and
when considering all fields from all animals used in this study (plot 5: 48.1+/-17.0mM).
Statistically comparing discreet ROI means by ANOVA analysis with Bonferroni correction (red
overlay indicating mean+/-standard error of ROIs), all groups demonstrated a statistically
significant difference vs control (p < 0.001) but were not significantly different vs each other (p =
1.0000). Note that ROIs are too numerous to display for all groups, and we have instead
overlaid the mean+/-standard error (red lines) associated with ANOVA analysis of ROIs. Violin
plot means (dashed black lines), reflecting aggregated pixels from all ROIs, appear on the
graph; associated standard deviations are listed above but are not explicitly labeled on graph.
*Scale bars **C,D&E**: 50μm; inset scale bar D: 5μm; significance values noted graphically for p-*
values <0.05 (*); <0.01 (**); <0.001 (***); "ns" indicates "not significant".

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Figure 7 E_{GABA} is maintained at any Cl^-_o given proportionate change in Cl^-_i. The reversal

potential of chloride across GABA$_A$Rs (E_{GABA}) is given by the Nernst equation, $E = \frac{RT}{zF} \ln \left(\frac{Clo}{Cli}\right)$. At

constant temperature the only variables that determine E_{GABA} are Cl^-_o and Cl^-_i, or rather the only

single variable is the ratio of Cl^-_o to Cl^-_i. Using the Nernst equation to model E_{GABA} across the

physiological range of Cl^-_i at several Cl^-_o values, we unsurprisingly find that hyperpolarizing

E_{GABA} values can be achieved at any Cl^-_o value. Lower Cl^-_o values simply need a proportionately

lower Cl^-_i value to achieve a given E_{GABA}, which neurons are capable of by increasing

intracellular immobile anions such as cytoskeletal biopolymers (Rahmati *et al.*, 2021). In the

examples given above, the Cl^-_i necessary to maintain E_{GABA} of -85mV (dashed red line) varies

from 1mM to 6mM as Cl^-_o is varied from 20mM to 120mM. More complex multi-ion modeling will

be facilitated with higher resolution and spatiotemporally correlated measurements of Cl^-_o and

Cl^-_i in proximity across the neuronal membrane.

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Author Contributions: KPN, KPL, KE and KJS conceived of and designed the approach and execution of these experiments. KPN and KJS are responsible for specific experimental design, interpretation of experiments, and manuscript preparation. KPL designed and built the two-photon microscopes and operational software that made this work possible. MAM and LL lent expertise and support for in vivo experiments, including training KPN in mouse cranial window surgery. LL and FHS provided expertise and critical input during experimental interpretation and manuscript writing. MP and BPC designed and executed HPLC experiments specific to this manuscript. This research was made possible by NINDS funding to KJS (NIH R01 NS040109, R35 NS116852 and P01 NS127769).

Authors' Translational Perspective: We hypothesized that if measured non-invasively, the extracellular chloride concentration (Cl^-_o) would be less than CSF chloride values ($\approx$110mM) due to Donnan exclusion by heterogeneously distributed extracellular anions so that Cl^-_o would be lower than expected and heterogenous. We found that Cl^-_o has a mean value much lower than previously appreciated ($\approx$50mM) and is indeed heterogenous. Our data further demonstrates that the loss of heterogenous sulfated glycosaminoglycans (sGAGs) in extracellular matrix results in an increased Cl^-_o as the Donnan equilibrium rebalances. Together with our previous work demonstrating heterogenous intracellular chloride (Cl^-_i), our data suggests the variance of GABA reversal potential (E_{GABA}) we and others have observed is due to the heterogeneity of the concentrations of the primary permeant anion, Cl^-, on both the intra- and extracellular side of the channel. Stable variations of perisynaptic Cl^-_o or Cl^-_i potentially allows for the tuning of E_{GABA} at individual GABA$_A$ synapses and suggests a mechanism for information storage. Pathophysiological alteration of Cl^-_o would be expected to occur when sGAG-containing extracellular matrix is damaged, such as when matrix metalloproteases (MMPs) are released following neuronal injury or death. The expected increase in extracellular chloride salts, in turn leading to equilibrative intracellular increases, represents a new mechanism of cytotoxic edema.

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Figure 1

Figure 2

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