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Yi Shen, Yurong Wen, Silvia Sposini, Anjali Amrapali Vishwanath, Ahmed Abdelfattah, et al.. Rational Engineering of an Improved Genetically Encoded pH Sensor Based on Superecliptic pHluorin. ACS Sensors, 2023, 8 (8), pp.3014-3022. 10.1021/acssensors.3c00484 . hal-04288085

HAL Id: hal-04288085

<https://hal.science/hal-04288085v1>

Submitted on 15 Nov 2023

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Rational Engineering of an Improved Genetically Encoded pH Sensor Based on Superecliptic pHLuorin

Yi Shen,* Yurong Wen, Silvia Sposini, Anjali Amrapali Vishwanath, Ahmed S. Abdelfattah, Eric R. Schreiter, M. Joanne Lemieux, Jaime de Juan-Sanz, David Perrais, and Robert E. Campbell*



Cite This: <https://doi.org/10.1021/acssensors.3c00484>



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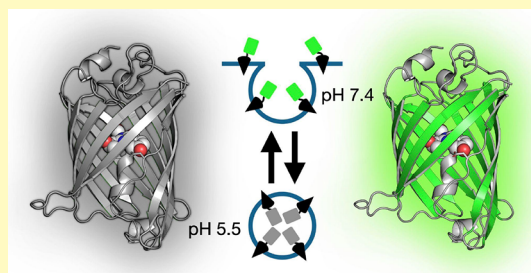
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Supporting Information

ABSTRACT: Genetically encoded pH sensors based on fluorescent proteins are valuable tools for the imaging of cellular events that are associated with pH changes, such as exocytosis and endocytosis. Superecliptic pHLuorin (SEP) is a pH-sensitive green fluorescent protein (GFP) variant widely used for such applications. Here, we report the rational design, development, structure, and applications of Lime, an improved SEP variant with higher fluorescence brightness and greater pH sensitivity. The X-ray crystal structure of Lime supports the mechanistic rationale that guided the introduction of beneficial mutations. Lime provides substantial improvements relative to SEP for imaging of endocytosis and exocytosis. Furthermore, Lime and its variants are advantageous for a broader range of applications including the detection of synaptic release and neuronal voltage changes.

KEYWORDS: pHLuorin, fluorescent proteins, genetically encoded sensors



Genetically encoded sensors based on fluorescent proteins (FPs) are essential tools for studying molecular and cellular physiology.^{1,2} Over the past two decades, an expanded toolkit of FP-based sensors has been engineered to monitor numerous biochemical parameters including the Ca^{2+} concentration, membrane potential, neurotransmitter dynamics, and pH.^{3,4} pH changes are tightly associated with cellular processes such as endocytosis and exocytosis. Using the example of synaptic transmission, the lumen of synaptic vesicles is typically acidified to pH \sim 5.5 by the proton pump activity of vacuolar-type ATPase. Upon fusion of a synaptic vesicle to the plasma membrane, the contents of the vesicle are exposed to the neutral pH (\sim 7.0 to 7.5) of the extracellular environment.⁵ This substantial change in pH allows the process of exocytosis to be visualized using a genetically encoded pH sensor fused with a vesicular membrane-associated protein.^{6,7} Monitoring of endocytosis and exocytosis has provided valuable insights that have helped to elucidate the fundamental biology of neurotransmission and have aided investigations of the underlying mechanism of various neurological diseases.^{8–11} Genetically encoded pH sensors are FPs that demonstrate pH-dependent fluorescence spectrum or intensity change within the physiologically relevant pH range.^{6,12–17} Most naturally occurring FPs exhibit pH-dependent fluorescence changes, but some are much more sensitive in the physiological range than others. For example, the wild-type *Aequorea victoria* green fluorescent protein (GFP) chromophore exists in a pH-dependent equilibrium between protonated and deprotonated states, which absorb maximally near 400 and 488 nm, 46 respectively.

A pH-sensitive GFP variant, ecliptic pHLuorin, was engineered to exhibit dim fluorescence at pH 5.5 when excited at 488 nm while becoming fluorescent at higher pH values, with an apparent pK_a (the pH value at which the fluorescence intensity is 50% of maximal) of 7.1. Fusion of ecliptic pHLuorin to VAMP2 produced synapto-pHLuorin, which enabled the visualization of synaptic vesicle release and neurotransmission.⁶ Incorporating mutations from enhanced GFP (EGFP) led to superecliptic pHLuorin (SEP) with an apparent pK_a of 7.2. SEP is nearly nonfluorescent at pH 5.5 but brightly green fluorescent at pH 7.4. An optimal pK_a and low background fluorescence in the protonated state make SEP a nearly ideal tool for the imaging of exocytosis and endocytosis in living cells.¹² Vesicular membrane proteins fused with SEP have been extensively used to detect the exocytosis of synaptic vesicles, secretory vesicles, and recycling endosomes.^{8,18,19} SEP has also been used to detect the formation of clathrin-coated vesicles (CCVs) using the pulsed pH (ppH) protocol, which reveals the location of receptors that have been newly internalized with high temporal accuracy.^{20,21} A SEP variant, SEP-D (SEP-A227D), serves as the fluorophore of the genetically encoded fluorescent protein voltage sensor ArcLight, which is a fusion

Received: March 14, 2023

Accepted: July 6, 2023

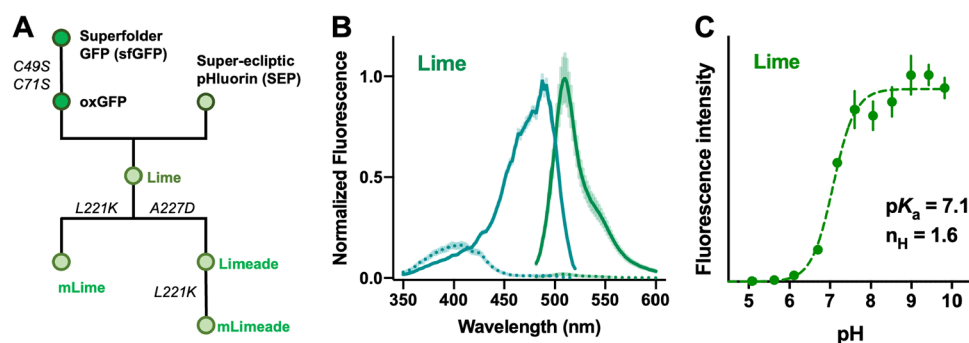


Figure 1. Rational engineering and *in vitro* characterization of Lime. (A) Design and genealogy of Lime and its variants. (B) Fluorescence spectrum of Lime at pH 5.5 (dotted lines) and pH 7.5 (solid lines). (C) pH titration curves of Lime.

Table 1. *In Vitro* Characterization of GFP-Based pH-Sensitive FPs

	extinction coefficient (EC, M ⁻¹ cm ⁻¹)	quantum yield (QY)	molecular brightness (EC × QY/1000)	absorption maxima (nm)	excitation maxima (nm)	emission maxima (nm)	pK _a	n _H	fold change (pH 5.6 to 7.2)
EGFP	57,000	0.60	34	488	488	509	5.5	1.0	N.D. ^a
SEP	37,000	0.80	30	490	488	511	7.0	1.7	66 ± 6
SEP-D	31,000	0.80	25	490	488	511	7.2	1.3	70 ± 1
Lime	45,000	0.77	35	483	488	510	7.1	1.6	82 ± 9
mLime	36,000	0.72	26	483	488	509	7.1	1.6	86 ± 2
Limeade	31,000	0.72	22	483	488	509	7.1	1.5	99 ± 1
mLimeade	29,000	0.77	22	483	488	509	7.1	1.5	98 ± 1

^aN.D., not determined.

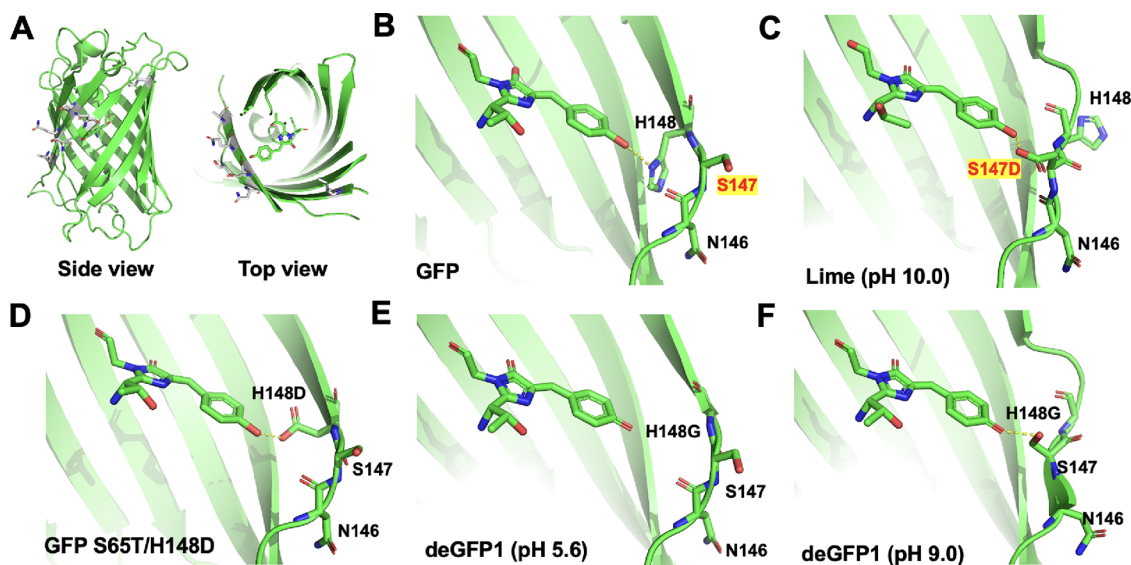


Figure 2. Structural analysis of Lime. (A) SEP mutation positions (from EGFP) are mapped on the structure (left: side view; right: top view) of GFP (PDB 1EMA). The chromophore is shown in green sticks, and mutated residues are shown in gray sticks. (B) In GFP, the side chain of residue S147 points outward from the β -barrel structure. (C) In Lime, the side chain of residue S147D points inward and directly interacts with the chromophore. (D) In the pH-sensitive GFP S65T/H148D variant (PDB 2DUF), H148D is pointing inward and directly interacts with the chromophore. Conformations of residue S147 and H148G in deGFP1 at pH 5.6 (E) (PDB 1JBY) and pH 9.0 (F) (PDB 1JBZ).

69 of the voltage-sensing domain from *Ciona intestinalis* voltage-
70 sensitive phosphatase to SEP-A227D.²²

71 Although widely used, SEP has a few shortcomings such as
72 relatively low brightness and suboptimal trafficking, which
73 limits its utilities in some applications.^{10,23–25} Here, we report
74 the design and characterization of Lime, a rationally
75 engineered SEP variant with higher fluorescence brightness
76 and improved performance. Lime takes advantage of the high
77 brightness and expression of sfGFP²⁶ and is cysteine-free for
78 potentially better compatibility with membrane protein

fusion.²⁷ We determined the X-ray crystal structure of Lime 79
to provide molecular insight into its pH sensitivity. We 80
demonstrated the utility of Lime by imaging endocytosis and 81
exocytosis in cultured cell lines and neuronal activities in 82
dissociated neurons. 83

RESULTS AND DISCUSSION 84

**Rational Engineering and *In Vitro* Characterization of 85
Lime.** Our approach to rationally improving SEP was to 86
incorporate mutations from previously reported GFP variants 87

Table 2. *In Vitro* Characterization of EGFP- and mClover3-S147D Mutants

	extinction coefficient (EC, M ⁻¹ cm ⁻¹)	quantum yield (QY)	molecular brightness (EC × QY, ×1000)	absorption maxima (nm)	excitation maxima (nm)	emission maxima (nm)	pK _a	n _H	fold change (pH 5.6 to 7.2)
EGFP- S147D	32,000	0.53	17	488	488	509	7.0	1.4	43 ± 2
mClover3- S147D	45,000	0.61	27	507	508	518	7.3	1.0	67 ± 2

88 with better characteristics. To improve the brightness and
89 expression of SEP, we changed the GFP scaffold from EGFP to
90 superfolder GFP (sfGFP).²⁶ To make the new variants
91 compatible with oxidative environments such as those within
92 the endoplasmic reticulum (ER) and Golgi, we engineered
93 cysteine-free SEP variants, as previously described for the
94 moxFPs.^{27,28} Based on the two aforementioned rationales, we
95 designed the second-generation SEP by incorporating the
96 sfGFP scaffold and eliminating cysteine residues. We
97 synthesized the DNA encoding this designed construct and
98 named it Lime (Figure 1 and Figure S1). Starting from Lime,
99 we further introduced the most effective GFP monomerizing
100 mutation L221K²⁹ and the key mutation A227D in ArcLight
101 for potential enhancement of pH sensitivity and the ability to
102 be incorporated into genetically encoded voltage indicators
103 (GEVIs).²² These efforts resulted in three more variants:
104 mLime (Lime-L221K), Limeade (Lime-A227D), and mLi-
105 meade (Lime-L221K/A227D) (Figure 1A).

106 To determine the *in vitro* properties of these new variants,
107 we purified Lime, mLime, Limeade, and mLimeade, together
108 with EGFP, SEP, and SEP-D (SEP-A227D from ArcLight) and
109 measured the spectral profile (i.e., absorption maxima,
110 excitation maximum (λ_{ex}), and emission maximum (λ_{em})),
111 photophysical properties (i.e., extinction coefficient (EC) and
112 quantum yield (QY)), and pH sensitivity (i.e., apparent pK_a,
113 apparent Hill coefficients n_H, and fluorescence intensity fold
114 change over pH 5.6 to pH 7.2). At pH 7.5, Lime had λ_{ex} = 488
115 nm and λ_{em} = 510 nm, while at pH 5.5, the λ_{ex} shifted to 400
116 nm, and the green fluorescence emission is mostly quenched
117 when excited at 488 nm (Figure 1B). Based on the
118 fluorescence vs pH response curve, Lime exhibited a pK_a of
119 7.1 and an n_H of 1.6 (Figure 1C). Among all the newly
120 designed variants, Lime exhibited a higher brightness (EC ×
121 QY/1000) compared to SEP (35 vs 30, pH 7.9), and it also
122 had a larger fluorescence change (82-fold vs 66-fold) over the
123 physiological pH range (5.6 to 7.2) (Table 1).

124 **Structural and Mutational Analysis.** During our initial
125 examination of mutations in SEP, we realized that none of the
126 six mutations of SEP relative to EGFP (S147D/N149Q/
127 T161I/S202F/Q204T/A206T) directly interact with the
128 chromophore based on the structure of GFP (PDB 1EMA,
129 Figure 2A). Of the six mutations, five of them (S147D/
130 N149Q/S202F/Q204T/A206T) are located outside the β -
131 barrel structure, and the other mutation T161I resides on the
132 8th strand pointing inside of the β -barrel, yet distant from the
133 chromophore. This led us to speculate about the mechanism
134 by which these mutations might modulate the chromophore
135 pK_a from 5.5 (EGFP) to 7.0 (SEP) (Table 1). A previous study
136 suggested a key role for the S147D mutation in shifting the
137 pK_a, but no detailed explanation at the molecular level was
138 provided.³⁰ To pinpoint the molecular basis of this pK_a shift,
139 we solved the crystal structure of Lime (Table S1). Compared
140 to GFP (PDB 1EMA), which harbors S147 with its side chain
141 directed outward from the β -barrel structure (Figure 2B),³¹ the

crystal structure of Lime at pH 10.0 revealed that the S147D
142 mutation had induced a significant rearrangement. The side
143 chain of S147D has become inward-facing and is directly
144 interacting with the chromophore, which is certain to be
145 influencing the pK_a of the chromophore (Figure 2C). The
146 direct interaction of the side chain of an aspartic acid with the
147 GFP chromophore has been reported previously in GFP
148 S65T/H148D. In this variant, H148D was found to interact
149 with the chromophore via hydrogen bonding and resulted in
150 an elevated pK_a value of 7.9 (Figure 2D).³² The conforma-
151 tional rearrangement of the residue at position 147 has also
152 been observed in deGFP1 (S65T/H148G/T203C). In this
153 variant, the side chain of S147 is outward-facing at pH 5.6 but
154 has flipped to inward-facing at pH 9.0 (Figure 2E,F).³³

To examine possible structure differences at different pH
156 values, we solved structures of Lime at a lower pH of 6.0.
157 Superimposition of the two structures at pH 10 and 6 revealed
158 no major structural rearrangements, with the side chain of
159 S147D pointing inside the FP barrel at both the high and low
160 pH values (Figure S2A). However, the superimposition
161 revealed two relatively subtle structural differences (Figure
162 S2B). First, the chromophore in the higher pH structure
163 adopts a more planar conformation compared to the lower pH
164 structure. The two dihedral angles indicating the chromophore
165 planarity are 8.7 and -5.6° in the pH 10 state, compared with
166 19.9 and -15.0° in the pH 6 state (Figure S2C,D). Second, the
167 carboxylate group on the S147D side chain in the high pH
168 structure sits closer to the chromophore (distance of 2.7 Å)
169 than in the low pH structure (distance of 3.2 Å) (Figure
170 S2C,D). These conformational changes in the chromophore
171 and its proximity to the S147D side chain are likely associated
172 with the large fluorescence change between high and low pH
173 states.

To further confirm the key role of S147D mutation in pK_a
175 modulation, we introduced this single mutation into GFP
176 variants, EGFP (pK_a of 5.5)³⁴ and mClover3 (pK_a of 6.5).³⁵
177 The pH titrations of EGFP-S147D, and mClover3-S147D both
178 revealed a significant increase in apparent pK_a values to 7.0 and
179 7.3, respectively. Thus, the S147D mutation effectively makes
180 EGFP and mClover3 into pH-sensitive GFPs similar to SEP
181 and Lime (Table 2), confirming its ability to modulate the pH
182 sensitivity of GFP variants. It remains to be determined if a
183 similar mutation at the aligned position of FPs from organisms
184 other than *Aequorea* (e.g., W138 of mNeonGreen)³⁶ could
185 have a similar influence on pK_a.

**Comparison of Lime and SEP for Imaging Endocy-
187 tosis and Exocytosis.** We next tested the performance of
188 Lime in live-cell imaging and compared it with SEP. The
189 transferrin receptor (TfR) fused to a pH-sensitive GFP (e.g.,
190 TfR-SEP) has been widely used for the detection of single
191 endocytosis and exocytosis events in cultured cells.^{15,18,20,21,37}
192 We first imaged and quantified endocytic events in the BSC-1
193 cell line using the pulsed-pH protocol with time-lapse total
194 internal reflection fluorescence (TIRF) imaging at 0.5 Hz. We
195

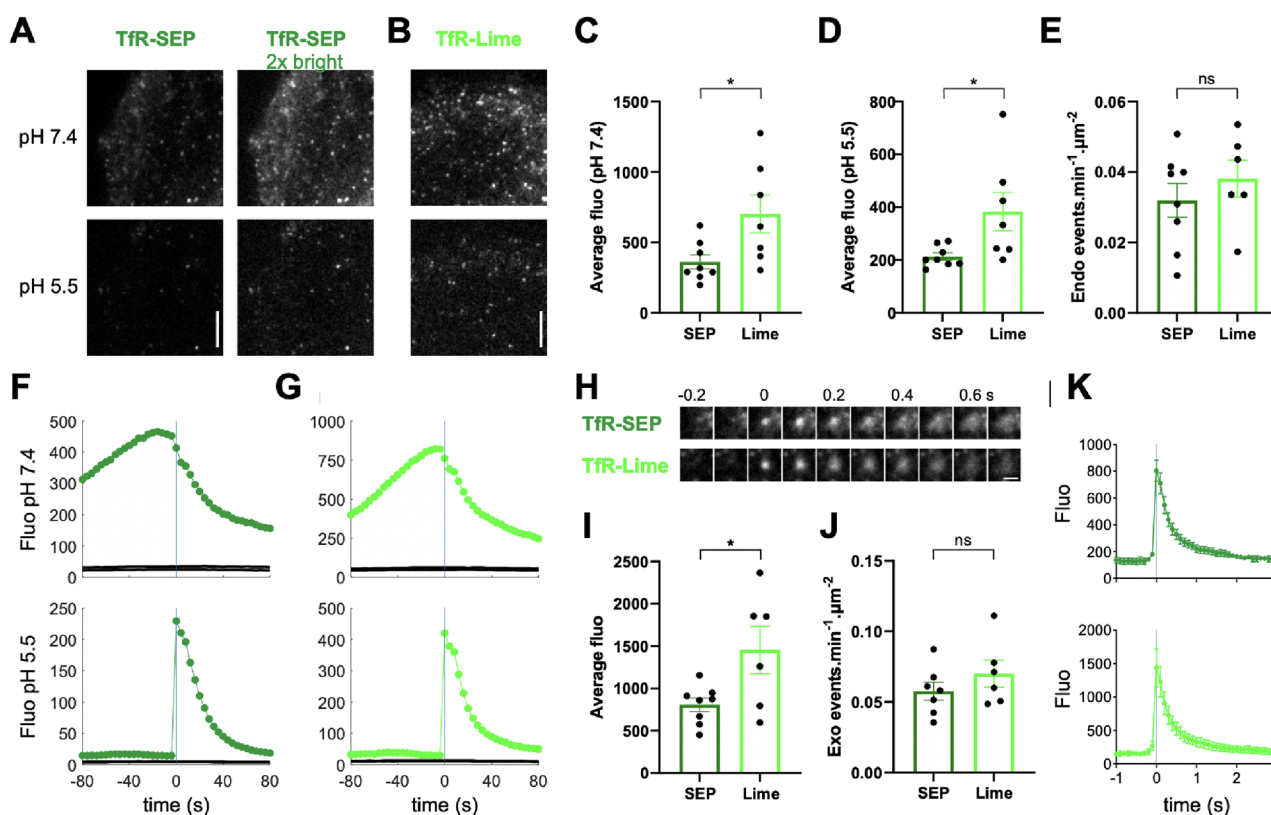


Figure 3. Imaging endocytosis and exocytosis with TfR-Lime. (A,B) Fluorescence images of TfR-SEP (A) and TfR-Lime (B) expressing cells at pH 7.4 and 2 s later at pH 5.5. Scale bar, 5 μm . Fluorescence images of TfR-Lime expressing cells at pH 7.4 and 2 s later at pH 5.5. Scale bar, 5 μm . (C,D) Average fluorescence at the time of scission with TfR-SEP or TfR-Lime at pH 7.4 (C) or pH 5.5 (D) (unpaired *t*-test, $p = 0.027$ and 0.029 , respectively). (E) Frequency of detected endocytic events (unpaired *t*-test, $p = 0.404$). (F,G) Average fluorescence time course of endocytosis events reported by TfR-SEP ((F) 3712 events, 8 cells) and TfR-Lime ((G) 4269 events, 7 cells). Black lines represent 95% confidence intervals for randomized events to determine the level of enrichment at sites of scission. (H) Examples of exocytosis events in consecutive frames for cells transfected with TfR-SEP (top) and TfR-Lime (bottom). Scale bar, 1 μm . (I) Average fluorescence at the time of exocytosis for events with TfR-SEP and TfR-Lime (unpaired *t*-test, $p = 0.027$). (J) Frequency of detected exocytic events (unpaired *t*-test, $p = 0.297$). (K) Average fluorescence time course of exocytosis events reported by TfR-SEP (528 events, 8 cells) and TfR-Lime (721 events, 6 cells), aligned to the time of detection (time 0).

196 used a previously developed algorithm for the determination of
 197 the scission events.^{20,21} Cells expressing TfR-Lime had brighter
 198 fluorescence than the ones expressing TfR-SEP under identical
 199 imaging conditions. A Western blot analysis revealed that the
 200 amounts of TfR-SEP and TfR-Lime in cells were not
 201 significantly different (Figure S3). A two-fold increase in
 202 exposure time was required to obtain images of TfR-SEP with
 203 intensities that were comparable to TfR-Lime (Figure 3A,B).

204 Quantitative analysis of the average fluorescence intensity at
 205 the time of scission revealed that TfR-Lime offers approx-
 206 imately a two-fold improvement in terms of the fluorescence
 207 brightness over TfR-SEP, at both pH = 5.5 and pH = 7.4
 208 (Figure 3C,D). For reasons that remain unclear, the
 209 fluorescence intensities for TfR-Lime endocytic events are
 210 more variable than for TfR-SEP endocytic events. Both TfR-
 211 SEP and TfR-Lime reported similar frequencies of events
 212 detected (Figure 3E), confirming that most endocytic events
 213 can be detected with both reporter proteins.³⁷ The average
 214 fluorescence time course of endocytosis of TfR-SEP and TfR-
 215 Lime reflected similar kinetics, yet again with a substantially
 216 higher fluorescence intensity for TfR-Lime (Figure 3F,G). We
 217 next imaged exocytic events using continuous TIRF micros-
 218 copy imaging at 10 Hz (Figure 3H). An exocytotic event
 219 manifests as sudden bursts of fluorescence due to the change in

pH experienced by the TfR construct followed by dissipation
 of fluorescence as the TfR construct diffuses away from the
 exocytosis site, as previously described.^{18,38} In agreement with
 our results for endocytosis, cells expressing TfR-Lime exhibited
 a significantly higher fluorescence amplitude than TfR-SEP
 (Figure 3I), yet still reported comparable event frequencies,
 and had similar fluorescence decay kinetics at sites of
 exocytosis events, which reflects the rate of protein diffusion
 away from the fusion site (Figure 3J,K). Overall, our results
 indicated that Lime has clear advantages over SEP as a useful
 reporter for TfR exocytosis and endocytic vesicle detection.

Imaging Neuronal Activities with Lime and Its Variants. To evaluate the performance of Lime for imaging neuronal activity, we first attempted to image synaptic vesicle release using synaptophysin-Lime. Lime was incorporated into the intravesicular loop region of vesicle protein synaptophysin.³⁹ Synaptophysin-Lime expressed in dissociated neurons exhibited well-localized fluorescence at the synapse with low background fluorescence (Figure 4A). Under electric stimulation to evoke action potentials (APs), synaptophysin-Lime responded with a fluorescence change $\Delta F/F_0$ of $19.0 \pm 2.9\%$ increase upon 10 stimuli by a field electrode at 10 Hz (Figure 4B, C). Synaptophysin-SEP exhibited a change of $22.6 \pm 2.4\%$ under the same conditions. Synaptophysin-Lime also exhibited

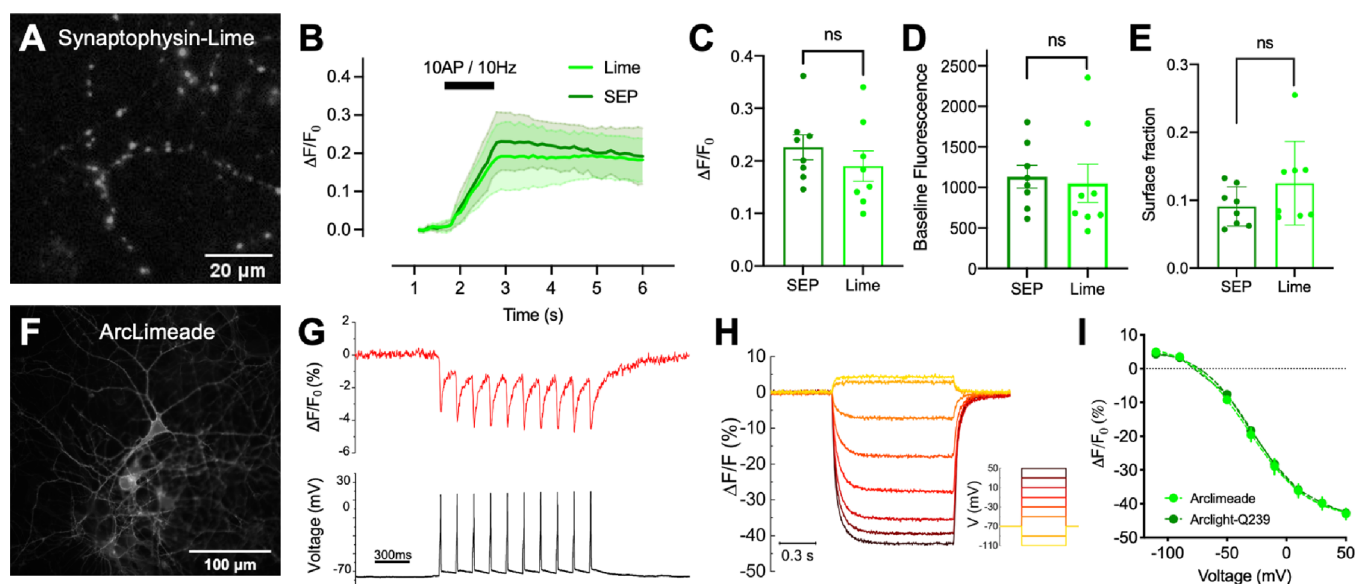


Figure 4. Imaging neuronal activities with synaptophysin-Lime and ArcLimeade. (A) Representative image of neurons expressing synaptophysin-Lime. (B) Synaptophysin-Lime response time course under stimulation of 10 action potentials (AP) at 10 Hz ($n = 8$). Comparison between synaptophysin-Lime and synaptophysin-SEP in terms of fluorescence change upon 10 stimuli by the field electrode at 10 Hz (C), baseline fluorescence (D), and surface fractions (E). (F) Representative image of neurons expressing ArcLimeade. (G) Simultaneous fluorescence imaging (top) and whole-cell patch-clamp membrane voltage measurements (bottom) from cultured neurons expressing ArcLimeade. (H) Representative fluorescence changes of ArcLimeade to voltage steps from -110 to 50 mV, normalized to the fluorescence at -70 mV. (I) Fluorescence change vs membrane voltage (F - V) curve for ArcLimeade and ArcLight-Q239.

244 comparable performance with synaptophysin-SEP in terms of
 245 baseline fluorescence intensities and surface fractions (Figure
 246 4D,E). In contrast to the results with TfR-Lime, synaptophy-
 247 sin-Lime does not exhibit higher brightness than synaptophy-
 248 sin-SEP. The reason for this difference is not known, but it may
 249 be related to the fact that Lime is inserted into a loop region of
 250 synaptophysin but fused to a terminus of TfR.

251 We next attempted to image neuronal membrane potential
 252 changes with Limeade (Lime A227D). We replaced SEP-D in
 253 the ArcLight-Q239 voltage sensor with Limeade to create a
 254 new voltage sensor termed ArcLimeade.²² Expression of
 255 ArcLimeade in dissociated neurons resulted in well-defined
 256 membrane fluorescence (Figure 4F). Membrane depolarization
 257 (-70 to 30 mV) resulted in an $\sim 4\%$ decrease in fluorescence
 258 intensity for both ArcLight and ArcLimeade (Figure 4G). In
 259 response to voltage steps changing from -70 to 50 mV in
 260 cultured neuron cells, ArcLimeade exhibited a total steady-
 261 state fluorescence change $\Delta F/F_0$ of $-43 \pm 1.6\%$, and ArcLight
 262 exhibited an identical change of $-43 \pm 0.8\%$ (Figure 4H).
 263 ArcLimeade retained a sigmoidal fluorescence-voltage rela-
 264 tionship with a $V_{1/2}$ at -32 mV, showing an overall similar
 265 voltage response compared to ArcLight-Q239 (Figure 4I).
 266 Altogether, these results established synaptophysin-Lime and
 267 ArcLimeade as sensitive indicators for the detection of
 268 membrane potential changes associated with neuronal activity.

269 CONCLUSIONS

270 Here, we have reported the rational engineering and
 271 characterization of improved SEP variants. Lime and its
 272 variants were designed based on the combination of cysteine-
 273 free superfolder GFP (oxGFP) and supercliptic pHluorin
 274 (SEP), with the goal of realizing enhanced properties. The
 275 resultant Lime variant is an improved pH-sensitive GFP with
 276 brighter molecular fluorescence and larger fluorescent intensity
 277 change over the physiological pH range.

We solved the atomic structure of Lime, which revealed an
 unexpected orientation rearrangement of residues 147 and 148,
 highlighting the flexibility of these two residues. With the
 identification of the key mutation S147D, we created pH-
 sensitive mutants of EGFP by only incorporating this single
 mutation, which is an effective approach to quickly create pH-
 sensitive GFP fusions from previously constructed EGFP or
 clover-based fusion constructs.

We demonstrated the use of the newly engineered SEP
 variants for imaging endocytosis, exocytosis, and neuronal
 activity. Relative to SEP, Lime exhibited significantly brighter
 fluorescence in the context of TfR fusions for endo- and
 exocytosis imaging. Synaptophysin-Lime and ArcLimeade also
 performed well in synaptic release and membrane voltage
 imaging, respectively. Overall, we believe that Lime and its
 variants are valuable additions to the toolbox of genetically
 encoded sensors.

295 MATERIAL AND METHODS

Protein Engineering and Molecular Biology. The DNA
 encoding Lime was synthesized by IDT. Rational engineering of
 Lime variants was performed via site-directed mutagenesis using
 plasmids encoding Lime as a template. Site-directed mutagenesis
 was performed using a QuikChange Lightning mutagenesis kit (Agilent
 Technologies) or a CloneAmp HiFi PCR premix (Takara Bio).
 Mutagenic primers were designed according to the QuikChange
 mutagenesis guidelines. A mutagenic product was used to transform
 the electrocompetent *Escherichia coli* (*E. coli*) strain DH10B (Thermo
 Scientific). Transformed *E. coli* were plated on agar plates containing
 LB medium supplemented with 0.4 mg/mL ampicillin and 0.02% wt/
 vol L-arabinose. Protein was extracted from overnight liquid culture
 using a B-PER bacterial extraction reagent (Thermo Scientific) as per
 the manufacturer's guidelines. Primary screening for pH sensitivity of
 extracted protein was performed with a Safire2 fluorescence plate
 reader (Tecan) by measuring protein fluorescence intensity in buffers
 with pH 5.5 and pH 7.5. Plasmid DNA was purified with a GeneJET

313 miniprep kit (Thermo Scientific) and then sequenced using a BigDye
314 Terminator Cycle Sequencing kit (Applied Biosystems).

315 **Protein Purification and *In Vitro* Characterization.** To purify
316 Lime and its variants, the electrocompetent *E. coli* strain DH10B was
317 transformed using a Micropulser electroporator (Bio-Rad). Trans-
318 formed bacteria were cultured overnight on agar plates containing LB
319 and ampicillin. Single colonies were picked and grown overnight in 4
320 mL of LB supplemented with ampicillin at 37 °C. For each colony,
321 the 4 mL culture was then used to inoculate 500 mL of LB medium
322 with ampicillin and the addition of 0.02% arabinose and grown
323 overnight at 37 °C. Bacteria were harvested by centrifugation and
324 lysed by sonication. The protein was purified using Ni-NTA (G-
325 biosciences) affinity chromatography. Extinction coefficients were
326 measured by the alkali denaturation method. Fluorescence quantum
327 yields were determined using EGFP as a standard.⁴⁰ Fluorescence
328 intensity as a function of pH was determined by dispensing 2 μ L of
329 the protein solution into 50 μ L of the desired pH buffer in triplicate
330 into a 396-well clear-bottom plate (Thermo Scientific) and measured
331 in a Safire2 plate reader. pH buffer solutions from pH 4 to 10 were
332 prepared according to the Carmody buffer.⁴¹

333 **Crystallization and Structure Determination.** Size-exclusion
334 chromatography-purified Lime protein fractions were pooled and
335 concentrated to 16 mg/mL and used for crystallization trials. Initial
336 crystallization was set up with 384-well plates via sitting drop vapor
337 diffusion against commercially available kits at 20 °C. The Lime
338 protein crystals were grown in multiple conditions and soaked in the
339 buffer of 0.2 M lithium chloride, 0.1 M MES pH 6.0, 20% w/v PEG
340 6000, 0.2 M ammonium phosphate monobasic, 0.1 M Tris pH 10,
341 and 50% v/v MPD. The crystals were cryoprotected with a reservoir
342 supplemented with 20% glycerol in liquid nitrogen. X-ray diffraction
343 data were collected at Beamline 08ID-1. The X-ray diffraction data
344 were scaled using XDS,⁴² and data collection statistics are summarized
345 in Table S1. The Lime pH 10 and pH 6 datasets belonged to the
346 trigonal space group $P3_121$ with one Lime molecule in the asymmetric
347 unit. Molecular replacement was performed with Phaser using GFP
348 protein as a search model.⁴³ The datasets of pH 10 and pH 6 were
349 processed to 2.0 and 2.85 Å with similar unit cell parameters of $a =$
350 109 Å, $b = 109$ Å, and $c = 49.9$ Å. Model building and further
351 refinement were carried out in Coot and Phenix.^{44,45} The final model
352 demonstrated $R_{\text{work}}/R_{\text{free}}$ values of 0.1723/0.2056 and 0.2047/0.2534
353 for pH 10 and pH 6 datasets. All the refinement statistics are noted in
354 Table S1.

355 **Imaging Endocytosis and Exocytosis with Tfr-Lime.** The
356 Tfr-Lime construct was made by replacing SEP with Lime in the
357 previously reported Tfr-SEP construct.³⁷ BSC-1 cells (ECACC no.
358 85011422) were grown in DMEM supplemented with 10% fetal calf
359 serum, 1% sodium pyruvate, and 1% Glutamax and maintained at 37
360 °C in 5% CO₂. Cells were passaged every 2–4 days for maintenance.
361 Cells were transfected in T25 flasks with 1.5 μ g of either Tfr-SEP or
362 Tfr-LIMEDNA using a Fugene 6 (Promega) transfection reagent. Six
363 hours post-transfection, cells were plated onto 18 mm glass coverslips
364 precoated with 0.1 mg/mL poly-L-lysine and imaged 24 h post-
365 transfection. Cells were perfused with HEPES-buffered saline (HBS)
366 solution (135 mM NaCl, 5 mM KCl, 0.4 mM MgCl₂, 1.8 mM CaCl₂,
367 20 mM HEPES, and 1 mM D-glucose) at pH 7.4.

368 TIRF imaging was performed on an inverted microscope (IX71;
369 Olympus) equipped with an Apochromat N oil 60 \times objective (NA
370 1.49), a 1.6 \times magnifying lens, and an EMCCD camera (Quan-
371 tEM:S12SC; Roper Scientific). Fluorescence emission was collected
372 via a 525/50 filter (Chroma). Samples were illuminated by a 473 nm
373 laser (Cobolt) for SEP and Lime imaging with identical laser intensity
374 and camera settings. The ppH protocol for imaging endocytosis was
375 performed as described previously²¹ with a frame rate of 0.5 Hz (100
376 ms exposure time). Cycles of one image at pH 7.4, followed 2 s later
377 by one image at pH 5.5, were repeated for at least 5 min. Imaging of
378 exocytosis events was performed with continuous imaging at 10 Hz
379 for 1 min.

380 To perform a Western blot, BSC-1 cells in 6-well plates were
381 transfected with 0.5 μ g plasmid/well encoding either Tfr-SEP or
382 Tfr-Lime. Cells were lysed 30 h post-transfection in RIPA buffer

supplemented with antiproteases, and 80 μ g of each lysate was loaded 383
and run on a 4–20% polyacrylamide gel. Proteins were transferred to 384
a nitrocellulose membrane and blotted using anti-GFP (Roche ref. 385
11814460001) and antiactin (Sigma-Aldrich ref. A2066) primary 386
antibodies. 387

388 **Analysis of Endocytosis and Exocytosis Events with Tfr-
389 Lime.** Detection and quantification of endocytosis events were
390 conducted using custom-made Matlab (R2018b) scripts that have
391 previously been described.²¹ In short, a sudden, punctate, 391
fluorescence increase appearing in pH 5.5 images was detected as 392
being an endocytic event if (1) it was visible for more than 3 frames 393
(i.e., 8 s) and (2) it appeared at the same location as a pre-existing 394
fluorescence cluster detectable in pH 7.4 images. Candidate events 395
from each cell were validated using a trained support vector machine 396
as described previously.²¹ The event frequency was expressed per cell 397
surface area measured on the cell masks. The average fluorescence 398
intensity was measured in a 4-pixel diameter circle (430 nm) minus a 399
local background (annulus of 4-pixel inner diameter, 10-pixel outer 400
diameter) centered on the detected vesicle (images at pH 5.5) until 401
the vesicle disappears. Causes of vesicle disappearance include 402
movement away from the cell surface and vesicle acidification. Figure 403
3F,G represents averages \pm SEM of the fluorescence (at pH 7.4 and 404
5.5) aligned at the time of vesicle detection (time 0) of all detected 405
events. Detection and quantification of exocytosis events were 406
performed with custom-made Matlab (R2018b) scripts as described 407
previously.⁴⁶ Exocytosis events were detected with an ad hoc 408
threshold in a differential movie and further validated with automated 409
and user-defined criteria. The event frequency was expressed per cell 410
surface area measured on the cell masks. The average fluorescence in a 411
5-pixel diameter area (minus a local background) centered on the 412
appearing vesicle was measured for each event. The decrease in 413
fluorescence reflects diffusion of Tfr in the plasma membrane after 414
exocytosis. 415

416 **Imaging Neuronal Exocytosis with Synaptophysin-Lime.** All 416
procedures followed the European legislation for animal experimenta- 417
tion (directive 2010/63/EU), and animal manipulations were 418
approved by the institutional Ethical Committee. Wild-type rats 419
were of the Sprague Dawley strain CrI:CD (SD), which are bred by 420
Charles River Laboratories worldwide following the international 421
genetic standard protocol (IGS). Hippocampal CA3-CA1 regions 422
without dentate gyrus were isolated from 0- to 2-days-old rats of 423
mixed gender, plated on poly-ornithine-coated coverslips, transfected 424
7 days after plating using calcium phosphate-mediated gene transfer, 425
and imaged 14–21 days after plating as previously described.⁴⁷ These 426
cultures resulted in mixed neuron-astrocyte cultures, which were 427
maintained in culture media composed of MEM (Thermo Scientific), 428
0.5% glucose, 0.1 g/L bovine transferrin (Millipore Sigma), 0.25 g/L 429
insulin (Millipore Sigma), 1% Glutamax (Thermo Scientific), 5–10% 430
fetal bovine serum (Thermo Scientific), and 2% N-21 (Bio-Techne). 431
Culture media was replaced 2–3 days later with culture media 432
containing 2 μ M cytosine β -D-arabinofuranoside (Millipore Sigma) to 433
limit astrocyte overgrowth. Cultures were incubated at 37 °C in a 95% 434
air/5% CO₂ humidified incubator for 14–21 days prior to use. 435
Neuronal live-cell imaging was performed using a custom-built laser- 436
illuminated epifluorescence microscope with an Andor iXon Ultra 437
(model no. DU-897U-CSO-#BV) back-illuminated electron-multi- 438
plying charge-coupled device camera cooled to -90 °C. Experiments 439
were performed at a clamped temperature of 36.5 °C using both an 440
in-line solution heater (640104: SHM-6, multichannel systems) and a 441
chamber heater platform (64-0285 PH-2, multichannel systems). 442
Action potentials (AP) were evoked by passing 1 ms current pulses, 443
yielding fields of approximately 7 V cm⁻¹ via platinum-iridium 444
electrodes using an imaging chamber that allows field stimulation (64- 445
0226 RC-21BRFS, multichannel systems). Cells were continuously 446
perfused at 0.1 mL/min with a Tyrode's solution containing (in mM) 447
119 NaCl, 2.5 KCl, 2 CaCl₂, 2 MgCl₂, and 30 glucose (Sigma-Aldrich 448
G8270), 10 μ M 6-cyano-7-nitroquinoxaline-2,3-dione (CNQX), and 449
50 μ M D,L-2-amino-5-phosphonovaleric acid (AP5) to block 450
postsynaptic AMPA and NMDA receptor responses, buffered to pH 451
7.4 using 25 mM HEPES. Synaptophysin-Lime was generated by 452

453 replacing SEP with Lime in synaptophysin-SEP. Synaptophysin-Lime-
454 expressing neurons were imaged at 10 Hz, and responses to 10 AP at
455 10 Hz were recorded. Images were analyzed using the ImageJ plugin
456 Time Series Analyzer V3, where typically 30–40 regions of interest
457 (ROIs) corresponding to synaptic boutons were selected, and
458 fluorescence was measured over time.

459 **Imaging Neuronal Membrane Voltage with ArcLimeade.**

460 All procedures involving animals were conducted in accordance with
461 protocols approved by the Howard Hughes Medical Institute Janelia
462 Research Campus Institutional Animal Care and Use Committee and
463 Institutional Biosafety Committee. Hippocampal neurons extracted
464 from P0 to 1 Sprague Dawley rat pups were transfected with
465 pcDNA3.1-CAG-ArcLimeade by electroporation (Lonza, P3 Primary
466 Cell 4D-Nucleofector X kit). Neurons were plated onto 24-well glass-
467 bottom plates (MaTek) coated with poly-D-lysine (Sigma). Neurons
468 were cultured for 8–12 days in NbActiv4 medium (BrainBits).
469 Imaging buffer (containing the following (in mM): 145 NaCl, 2.5
470 KCl, 10 glucose, 10 HEPES pH 7.4, 2 CaCl₂, and 1 MgCl₂) was used.
471 Cultures were illuminated with a SPECTRA X light engine
472 (Lumencor) and observed through a 40× oil objective (NA = 1.3,
473 Nikon) on an inverted Nikon Eclipse Ti2 microscope. Excitation and
474 emission light was passed through a FITC filter set (475/50 nm
475 (excitation), 540/50 nm (emission), and a 506LP dichroic mirror
476 (FITC-S050A-000; Semrock)) to image ArcLimeade. Fluorescence
477 was collected by a CMOS camera (ORCA-Flash 4.0, Hamamatsu). A
478 stimulus isolator (A385, World Precision Instruments) with platinum
479 wires was used to deliver field stimuli to elicit action potentials in
480 cultured neurons. For voltage-clamp experiments used to generate
481 fluorescence–voltage curves, voltage steps (from −110 to +50 mV in
482 20 mV increments for 1 s) were applied to cells held at −70 mV. All
483 recordings were done at room temperature.

484 ■ ASSOCIATED CONTENT

485 **Supporting Information**

486 The Supporting Information is available free of charge at
487 <https://pubs.acs.org/doi/10.1021/acssensors.3c00484>.

488 (Table S1) X-ray data collection and refinement
489 statistics, (Figure S1) sequence alignment, (Figure S2)
490 comparison of Lime structures at pH 10 and pH 6, and
491 (Figure S3) comparison of TfR-SEP and TfR-Lime
492 expression levels in BSC-1 cells (PDF)

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537 **Author Contributions**

Y.S. engineered Lime variants, assembled DNA constructs,
performed protein characterization, analyzed data, prepared
figures, and wrote the manuscript. Y.W. performed the protein
crystallization, solved the structures, and analyzed data. S.S.
performed imaging of TfR-Lime, analyzed data, and prepared
figures. A.A.V. performed imaging of synaptophysin-Lime,
analyzed data, and prepared figures. A.S.A. performed imaging
of ArcLimeade, analyzed data, and prepared figures. E.R.S.,
M.J.L., J.d.J.-S., D.P., and R.E.C. supervised the research. All
authors contributed to the editing and proofreading of the
manuscript.

549 **Notes**

The authors declare no competing financial interest.
Plasmids and DNA sequences are available via Addgene. The
Lime structures are deposited in the Protein Data Bank (PDB
IDs 7YV3 and 7YV5). Data supporting the findings in this
research are available from the corresponding author upon
request.

556 ■ ACKNOWLEDGMENTS

This work was supported by grants from the Canadian
Institutes of Health Research (CIHR, FS-154310 to R.E.C.)
and the Natural Sciences and Engineering Research Council of
Canada (NSERC, RGPIN 2018-04364 to R.E.C. and RGPIN-
2016-06478 to M.J.L.) and the Agence Nationale de la
Recherche (LocalEndoProbes, ANR-17-CE16-0012, to D.P.).
Y.W. was supported by the Alberta Parkinson Society
Fellowship and the National Natural Science Foundation of
China (nos. 31870132 and 82072237). S.S. was supported by a
Sir Henry Wellcome Postdoctoral Fellowship (Wellcome
Trust, 218650/Z/19/Z). Data were collected at beamline
CMCF-ID at the Canadian Light Source, a national research
facility of the University of Saskatchewan, which is supported
by the Canada Foundation for Innovation (CFI), the NSERC,
the National Research Council (NRC), the CIHR, the
Government of Saskatchewan, and the University of
Saskatchewan. A.S.A. and E.R.S. were supported by Howard
Hughes Medical Institute. J.d.J.-S. and A.A.V. were supported

575 by the Paris Brain Institute Diane Barrière Chair in Synaptic
576 Bioenergetics, an ERC Starting Grant SynaptoEnergy
577 (852873), and the 2019 ATIP-Avenir program. J.d.J.-S. is a
578 permanent CNRS researcher. Y.S. and R.E.C. thank the
579 University of Alberta Molecular Biology Services Unit for
580 technical assistance.

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