Inward $H^+$ pump xenorhodopsin: Mechanism and alternative optogenetic approach

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Generation of an electrochemical proton gradient is the first step of cell bioenergetics. In prokaryotes, the gradient is created by outward membrane protein proton pumps. Inward plasma membrane native proton pumps are yet unknown. We describe comprehensive functional studies of the representatives of the yet noncharacterized xenorhodopsins from Nanohaloarchaeota family of microbial rhodopsins. They are inward proton pumps as we demonstrate in model membrane systems, Escherichia coli cells, human embryonic kidney cells, neuroblastoma cells, and rat hippocampal neuronal cells. We also solved the structure of a xenorhodopsin from the nanohaloarchaeon Nanosalina (NgXeR) and suggest a mechanism of inward proton pumping. We demonstrate that the NgXeR is a powerful pump, which is able to elicit action potentials in rat hippocampal neuronal cells up to their maximal intrinsic firing frequency. Hence, inwardly directed proton pumps are suitable for light-induced remote control of neurons, and they are an alternative to the well-known cation-selective channelrhodopsins.

INTRODUCTION

All cells maintain a particular concentration of ions $H^+$, $K^+$, $Na^+$, and $Cl^-$ in the cytoplasm, which is crucial for life. Ion gradients across cell membranes are maintained by ion transporters, which are integral membrane proteins. In many archaea, bacteria, and unicellular eukaryotes, these gradients are created (among other mechanisms) by light-driven microbial rhodopsins, seven transmembrane $\alpha$ helix proteins comprising a cofactor chromophore named retinal ($I$). Proton gradients are maintained by outward proton pumps, and they play a crucial role in providing energy for most biochemical reactions ($2$). Although a light-driven proton-pumping rhodopsin [bacteriorhodopsin (BR)] was discovered long ago in archaea ($3$) and similar rhodopsins have now been found in other domains of life throughout soil, hypersaline, marine, and freshwater habitats, all known proton-pumping rhodopsins are outwardly directed ($1$). The same is true for non-rhodopsin proton pumps. Another inwardly directed cell plasma membrane rhodopsin proton pump was described very recently in a marine bacterium, Parvularcula oceani, during submission of the present manuscript ($4$). However, in that work ($4$), two major questions remained unanswered. First, the structure of xenorhodopsins (XeRs) and the true proton pathway and molecular mechanism of inward pumping are still not known. Second, their possible application in electrically excitable cells was not demonstrated (optogenetics). The question of whether these depolarizing ion pumps were powerful enough to achieve a similar remote control of neuronal cells as the well-known light-gated channelrhodopsins remained unanswered. In addition, the photocycle of XeR from P. oceani is about 10 times slower than that of XeR from Nanosalina (NgXeR), which also means that this protein cannot be used to elicit action potentials in neuronal cells at a high firing frequency.

In 2011, a new class of microbial rhodopsins, distinct from other rhodopsin types, was discovered ($5$). The authors of that work found several new homologs of Arabadopsis sensory rhodopsin (ASR) ($6$). The members of the class were named XeRs. Among these proteins were XeRs from a new major lineage of Archaea, specifically the nanohaloarchaeon Nanosalina sp. J07AB43 and Nanosalinarum sp. J07AB56 with 89% amino acid identity between them but with only 34% amino acid identity to ASR. By analyzing the amino acid sequence alignment, the authors concluded that XeRs do not share specific features common to proton pumps or halorhodopsin pumps. However, they are similar to ASR because they lack a common Asp at the donor position, as with the sensory rhodopsins known at that time.

We extended the analysis (figs $S1$ and $S2$) and found that XeRs have remarkable differences from conservative amino acid residues usually found in other microbial rhodopsins. Arg$^{22}$ (numbering is in accordance with BR amino acid sequence) is extremely conservative among rhodopsins, whereas in almost all XeRs from Nanohaloarchaeota, this place is occupied by Trp. In XeR, we find a probe for the highly conserved Asp$^{212}$. The positions of classical proton acceptors (Asp$^{225}$ and donors (Asp$^{226}$) in proton pumps are Asp and Ala, respectively, that is, XeRs have the WDSAPK motif, which is very different from that of conventional proton pumps such as BR (RDTDDK). Moreover, contrary to ASR where a proposed soluble transducer protein (ASR transducer) is encoded by a gene in the same operon, in nanohaloarchaeal genomes, there are only putative Na$^+/H^+$ antiporter genes adjacent to the XeR ones ($5$).
We characterized three proteins from the XeR family, namely NsXeR (5), HrvXeR (7), and AlkXeR (8), and found out that all these three proteins are inwardly directed proton pumps. All Nanohaloarchaea are extremely halophilic (live in saturated sodium chloride). NsXeR (5) was found in a metagenome from brines in Lake Tyrrell (Australia), whereas HrvXeR (7) was sequenced in a crystallizer pond of a solar saltern in Spain, and AlkXeR (8) comes from alkaline (pH > 9) brines in Siberia. With one of these proteins, we performed a comprehensive function and structure study, and the results are described below. Moreover, we found that the light-induced depolarizing current by NsXeR is sufficient for reliable activation of neuronal cells with high temporal accuracy. Therefore, NsXeR as a proton pump is attractive for optogenetic studies because of the cation-independent activity and represents an alternative to the well-known cation-selective channelrhodopsins (9).

RESULTS AND DISCUSSION

Functional characterization of XeRs

**pH changes in Escherichia coli suspensions**

The protein NsXeR was heterologously expressed in *E. coli* C41 strain. The pH of the cell suspension increased upon illumination and decreased when the light was turned off (Fig. 1A). The effect of the pH change was completely abolished by the addition of carbonyl cyanide *m*-chlorophenylhydrazone (CCCP). Similar experiments performed with other proton pumps as BR gave the opposite behavior of pH upon illumination of the cells. Two other members of the XeR family, HrvXeR and AlkXeR, studied in the present work gave the same results as NsXeR (Fig. 1A). Thus, pH experiments provide evidence that Nanohaloarchaea rhodopsins are inwardly directed proton pumps.

**pH changes in liposome suspension**

Purified NsXeR was reconstituted in soybean liposomes (10). The pH changes upon illumination showed acidification of the solution outside the membrane (Fig. 1B). These pH changes were abolished when CCCP was added to the suspension. Because in similar experiments outwardly directed proton pumps [such as BR and proteorhodopsin (PR)] show the opposite pH behavior (11), we conclude that NsXeR is a real inwardly directed proton pump. What is interesting is that, in a wide range of pH values (between pH 5 and 9), our experiments still show inward proton pumping (Fig. 1C).

**Absorption spectra, retinal isomer composition, and photocycle**

The absorption maximum of NsXeR in solubilized form is 565 nm (Fig. 2A). It is similar for HrvXeR (562 nm), whereas the homolog AlkXeR is a red-shifted variant (577 nm; Fig. 2A). For NsXeR, the position of the maximum does not shift when the pH of the buffer is varied in the range from 4.5 to 9.0. NsXeR does not exhibit light and dark adaptation, as indicated by the absence of spectral changes. The same holds true for retinal extraction experiments (12) that show a predominant fraction of all-trans retinal independent of preillumination (Fig. 3).

Transient absorption changes of NsXeR (pH 7.5, T = 20°C) are shown at three characteristic wavelengths—378, 408, and 564 nm—with NsXeR prepared in two different ways: in nanodiscs (red) and in single lipid vesicles (blue) (Fig. 2B). The results of global fit using five exponents are shown in Fig. S3. The photocycle of NsXeR in nanodiscs is faster (27 ms) than that of NsXeR in lipid vesicles (50 ms). The photocycle of NsXeR in nanodiscs is shown in Fig. 2C.

The photocycle of NsXeR contains a microsecond-duration phase, which is usually assigned to the multistep reaction of release of the energized ion (the H+ in our case) and a millisecond-duration phase, consisting of relaxation and reuptake of the ion. However, the NsXeR photocycle reveals some distinct features, which, to our knowledge, have never been reported in the previous studies of retinal proteins (fig. S3). After the microsecond phase of the photocycle (P1, P2, and P3) that includes archetypal intermediates with the K- and L-like spectral shifts (P1, λmax = 570 nm; P2, λmax = 530 nm), in the millisecond time domain, we obtained two spectrally and kinetically different M intermediates (P4 and P5). The first M-form (P4) has a characteristic three-band absorption spectrum with the maximum at 360, 378, and 398 nm. This state with the half-time of 2 ms in nanodiscs (3 ms in lipid vesicles) converts to the state P5 with a single maximum at 392 nm. Both intermediates should correspond to the deprotonated state of the retinal Schiff base.
Protein structure, proton uptake and release regions, and active center

NsXeR crystals were grown using the in meso method (13). The structure was refined to a resolution of 2.5 Å. Crystallographic statistics is shown in table S1. P21_21_21 space group crystals contain one trimer of NsXeR in the asymmetric unit (fig. S4).

The light-driven inward proton pump XeR has seven transmembrane α helices (A to G) and a cofactor retinal covalently bound to Lys213 via the Schiff base. The helix A is preceded with a small N-terminal α helix, which caps the protein on the extracellular side (fig. S5).

Comparison with BR structure (14) [Protein Data Bank (PDB): 1C3W] indicates considerable differences in helix localization and form, which are shown in Fig. 4A and fig. S6. A and G helices are significantly distorted. XeRs have a conservative residue Pro209 (position in NsXeR), which is located at the position of Asp212 in BR. Our experiments showed that its replacement with Asp makes the protein unstable. If changed to glycine, the pumping activity markedly decreases (table S2). Thus, Pro209 is crucial for proton pumping.

Proton uptake region and active center

NsXeR has a proton uptake cavity (Fig. 5), which is accessible from the bulk through the residue Gln122. The cavity is filled with water...
molecules. The putative proton donor Asp\textsuperscript{76} is available from that cavity through the residue Tyr\textsuperscript{199}. Mutations of Asp\textsuperscript{76} to Glu, Ser, Thr, and Asn do not allow the protein to fold correctly (mutants were not colored; table S2). This is evidence of not only functional but also significant structural role of these amino acids. Ser\textsuperscript{55} is located close to Asp\textsuperscript{76}, and it may stabilize this residue. Substitution of Ser\textsuperscript{55} with alanine (Ala\textsuperscript{53} in BR) also breaks protein folding. Asp\textsuperscript{76} is connected to the Schiff base through the water molecule \textit{w1} (the Asp\textsuperscript{76}-w1 distance is 2.9 Å, which indicated its crucial role in protein structure stabilization. The structure and experiments with mutated amino acids provide insights into the mechanism of inwardly directed proton transport. A putative pathway of proton translocation is shown in Fig. 5, and more details are shown in fig. S7 (C to H). Upon illumination, retinal isomerizes, the Schiff base deprotonates, and the proton is translocated to the cytoplasmic side of the protein close to the Schiff base and serves as a Schiff base proton acceptor. The structure and experiments with mutated amino acids provide insights into the mechanism of inwardly directed proton transport.

Putative mechanism of inwardly directed proton transport

Another major difference of NsXeR from other known microbial retinal proton pumps is that it has no ionizable amino acid at the position equivalent to Asp\textsuperscript{96} in BR (in NsXeR, it is Ala\textsuperscript{71}). However, the residues His\textsuperscript{18} (10 Å from the Schiff base in the ground state) and Asp\textsuperscript{220} (12 Å), which are connected via a hydrogen bond, are located close to the expected proton acceptor position (Fig. 4B). Substitution of Asp\textsuperscript{220} with Asn completely disrupts proton pumping. His\textsuperscript{18} is a unique residue, which is not present at a similar place in other known microbial rhodopsins. Our experiments showed that substitution of His\textsuperscript{18} with any other amino acid prevents binding of retinal (all mutants are not colored), which indicated its crucial role in protein architecture. We suggest that the pair His\textsuperscript{18}-Asp\textsuperscript{220} is a proton acceptor, and the protonation processes from the Schiff base through the water molecule 2 and His\textsuperscript{18} residue, more precisely, through the pair His\textsuperscript{18}-Asp\textsuperscript{220}. Remarkably, it is exactly the same proton acceptor pair as in PRs. However, contrary to PRs in XeRs, the pair is placed at the cytoplasmic side of the protein close to the Schiff base and serves as a Schiff base proton acceptor.

![Fig. 4. NsXeR structure. (A) Comparison of NsXeR (yellow) and BR (magenta) motifs. Residues are shown as an NsXeR motif (WDSAPK) and a BR motif (RDTDDK). Two residues, H48 and D220, in NsXeR are shown as an analog of the D96 residue in BR. (B) Putative proton acceptor region in detail. The distance between the Schiff base and water molecule 2 is shown with a double-arrow red line (8.0 Å). Distances between D76 (DBS) and the Schiff base in NsXeR (BR) are 4.9 Å (3.8 Å), respectively. Cavities inside the protein calculated by HOLLOW1.2 are shown transparent pink.](http://advances.sciencemag.org/)

![Fig. 5. Putative NsXeR ion translocation pathway. Cavities (transparent pink) and putative key residues inside protein are shown. Black arrows show the putative proton path. Helices F and G are not shown. The hydrophobic membrane core boundaries were calculated using the PPM (Positioning of Proteins in Membrane) server and are shown by gray lines.](http://advances.sciencemag.org/)


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Optogenetic implications

Experiments with human embryonic kidney and neuroblastoma glioma cells

The human embryonic kidney (HEK) 293 and neuroblastoma glioma (NG) 108-15 cells were transfected with the pcDNA3.1(−) vector bearing NsXeR gene with membrane trafficking signal (17), P2A self-cleaving peptide (18), and a green fluorescent protein (GFP) variant (19) at the C terminus. Whole-cell voltage-clamped experiments were conducted, and Fig. 6A shows photocurrents generated by NsXeR in the HEK293 cell. Typical photocurrent values vary from 40 to 150 pA at −60-mV applied potential, whereas the currents normalized to the capacitance (meaning the size) of the cell are about 1.4 ± 0.5 pA/pF (measured for n = 7 cells). An additional control experiment in NG108-15 cells was performed. To exclude the transport of Cl− ions (which may account for apparent “inward” current), we replaced chloride salts in buffers with sulfate. To exclude monovalent ion transport into the cell, we replaced Na+ in the bath solution by larger molecule, N-methyl-D-glucosamine. The pH of the solutions was symmetric (pH 7.4). However, similar photocurrents were recorded in this experimental configuration (Fig. 6B), convincing us that the experiments with HEK and NG cells confirm that NsXeR is an inwardly directed proton pump.

For the measurement of the action spectra (fig. S8), ultrashort nanosecond light pulses were generated by the Opolette 355 tunable laser system (Optoprim). The pulse energies at the different wavelengths were set to values that corresponded to equal photon counts of 1019 photons/m2. To gain additional kinetic information, we recorded time-resolved photocurrents in response to ultrashort nanosecond light pulses at different membrane potentials (fig. S9). The time-resolved photocurrents are characterized by two relaxation times. At 0 mV, which corresponds to the membrane potential in the flash photolysis experiments, a bi-

exponential relaxation with τ1 = 1.1 ± 0.2 ms (n = 5) and τ2 = 11.6 ± 1.9 ms (n = 5) was found. By comparing it to the photocycle (Fig. 2), we assigned τ1 (1.1 ms versus 2 ms) to the MI/MII transition and τ2 (11.6 ms versus 27 ms) to the M2 decay. The minor difference between the time constants derived from the photocycle and the photocurrent might be due to the different environments of the protein (nanodiscs versus NG cells). At a physiological membrane potential of −60 mV, a relaxation constant of τ2 = 6.2 ± 2.8 ms (n = 5) was found for the rate-limiting step, which corresponds to a turnover rate of ~160 s−1.

Light-triggered spiking in rat hippocampal neurons

We heterologously expressed NsXeR, C-terminally fused to the Kir2.1 membrane trafficking signal (17), in rat hippocampal neurons by means of adeno-associated virus–mediated gene transfer. For the electrophysiological characterization of the transduced cells, we performed whole-cell patch-clamp experiments. Thereby, NsXeR-expressing neurons showed normal morphology and membrane properties, which indicates that heterologous expression had no detectable toxic effects. The membrane capacitance and the resting membrane potential were 32.5 ± 12.9 pF (n = 6) and −60 ± 6 mV (n = 6), respectively. The mean photocurrent at a membrane potential of −70 mV, measured upon green light illumination at saturating intensity (fig. S10), was −189 ± 80 pA (n = 6), which corresponded to a mean current density of 6.7 ± 4.4 pA/pF (n = 6).

As expected from the current densities of the photocurrents and as proven in current clamp experiments, light-triggered spiking in rat hippocampal neurons was possible (Fig. 7). NsXeR enabled a fast, neural photostimulation with a firing success rate of 100% up to a frequency of 40 Hz. Spike failures at higher stimulation frequencies can be explained by intrinsic properties of the rat hippocampal neurons because a vast

**Fig. 6. Photocurrents in HEK293 and NG108-15 cells.** Photocurrents in cells expressing NsXeR at the membrane potentials changed in 20-mV steps from −100 mV and corresponding current-voltage curves. (A) HEK293 cells with pipette solution [110 mM NaCl, 2 mM MgCl2, 10 mM EGTA, and 10 mM Hepes (pH 7.4)] and bath solution [140 mM NaCl, 2 mM MgCl2, and 10 mM Hepes (pH 7.4)]. (B) NG108-15 cells with pipette solution [110 mM Na2SO4, 4 mM MgSO4, 10 mM EGTA, and 10 mM Hepes (pH 7.4)] and bath solution [140 mM N-methyl-D-glucosamine, 4 mM MgSO4, and 10 mM Hepes (pH 7.4)] (control measurements to confirm that protons are responsible for inwardly directed current).
majority of rat hippocampal neurons have a maximal firing frequency of 40 to 60 Hz (20).

An important observation is that light-triggered spiking could be achieved with a pulse width of only 3 ms (fig. S11A), which is shorter than the turnover time of the pump (6.2 ± 2.8 ms). Hence, the extent of depolarization due to the transport of a single proton by each NsXeR is sufficient to successfully trigger action potentials. A similar behavior was observed in hippocampal neurons transduced with the inhibitory light-driven Cl− pump NpHR (21). However, a variability of the spike latencies was observed (fig. S11), which, in some cases, required longer pulse widths for the light-triggered spiking (fig. S11B). Longer spike latencies could be explained by a comparatively lower expression of NsXeR in those neurons.

CONCLUSIONS
We performed comprehensive functional studies of the representatives of the yet noncharacterized XeRs from the Nanohaloarchaea family of microbial rhodopsins and showed that they are inwardly directed proton pumps. A rigorous study of the pumping activity of NsXeR in model membrane systems, E. coli cells, HEK cells, NG cells, and rat hippocampal neuronal cells confirmed that, in all these cells, NsXeR works as an inwardly directed proton pump. Its biological function is rather obscure. The functionally similar pump PoXeR found in the marine bacterium P. oceani has been proposed to have a role in signal transduction (4), but this is highly unlikely in extremely simplified and small cells as the Nanohaloarchaea with a single rhodopsin gene in their genomes (P. oceani has three). Given that there are no extant cultures of these microbes, determining the biological function of this inwardly directed proton pump remains elusive.

We also demonstrated that the NsXeR is a powerful pump with a turnover rate of 160 s⁻¹, which is able to elicit action potentials in rat hippocampal neuronal cells up to their maximal intrinsic firing frequency. Because of its intrinsic properties as a proton pump, NsXeR is completely independent of the ion conditions, which makes this rhodopsin an attractive alternative for light-induced remote control of neurons as the well-known cation-selective channelrhodopsins.

The crystallographic structure of NsXeR reveals the ion translocation pathway that is very different from that of the known rhodopsins. The structure and our data on the function of the protein mutants allowed us to propose a mechanism of inwardly directed proton pumping.

MATERIALS AND METHODS
Phylogenetic analysis and sequence alignment
For the phylogenetic tree of microbial rhodopsin proteins, 52 rhodopsin sequences were aligned using MUSCLE. Phylogenetic reconstruction
was conducted by maximum likelihood using MEGA6 with the following parameters: Jones-Taylor-Thornton model, 100 bootstraps, and γ distribution with five discrete categories. Positions with less than 80% site coverage were eliminated. Only bootstraps greater than 50% are shown. GenBank accession numbers were written in parentheses for each protein.

**Cloning**

NsXeR (UniProt 1D: G0QG75), HrvXeR (7), and AlkXeR (8) coding DNAs were synthesized commercially (Eurofins). The nucleotide sequences were optimized for *E. coli* expression using the GeneOptimizer software (Life Technologies). The genes, together with the 5′ ribosome-binding sites and the 3′ extensions coding additional LEHHHHHHH* tags, were introduced into the pET15b expression vector (Novagen) via XbaI and BamHI restriction sites. The mutants were prepared by site-directed mutagenesis and verified by sequencing.

**E. coli expression, solubilization, and purification**

The protein was expressed as described previously (22) with modifications. *E. coli* cells of strain C41 (DE3) (Lucigen) were transformed with the expression plasmids. Transformants were grown at 37°C in shaking baffled flasks in an autodinducing medium, ZYP-5052 (23), containing ampicillin (100 mg/liter), and were induced at an OD_{600} (OD at 600 nm) of 0.6 to 0.7 with 1 mM isopropyl-β-d-thiogalactopyranoside and supplemented with 10 μM all-trans retinol. Three hours after induction, the cells were collected by centrifugation at 3000g for 30 min. The collected cells were disrupted in M-110P Lab Homogenizer (Microfluidics) at 25,000 psi in a buffer containing 20 mM tris-HCl (pH 8.0), 5% glycerol, 0.5% Triton X-100 (Sigma-Aldrich), and deoxyribonuclease I (50 mg/liter) (Sigma-Aldrich). The membrane fraction of cell lysate was isolated by ultracentrifugation at 90,000g for 1 hour at 4°C. The pellet was resuspended in a buffer containing 50 mM NaH_{2}PO_{4}/Na_{2}HPO_{4} (pH 8.0), 0.1 M NaCl, and 1% DDM (Anatrace, Affymetrix) and stirred overnight for solubilization. The insoluble fraction was removed by ultracentrifugation at 90,000g for 1 hour at 4°C. The supernatant was loaded on a Ni-NTA column (Qiagen), and XeRs were eluted in a buffer containing 50 mM NaH_{2}PO_{4}/Na_{2}HPO_{4} (pH 7.5), 0.1 M NaCl, 0.3 M imidazole, and 0.2% DDM. The eluate was dialyzed against 100 volumes of 50 mM NaH_{2}PO_{4}/Na_{2}HPO_{4} (pH 7.5) and 0.1 M NaCl buffer twice for 2 hours to dispose imidazole. Finally, proteins were concentrated to 70 mg/ml for crystallization.

**Liposome preparation**

Phospholipids (asolectin from soybean, Sigma-Aldrich) were dissolved in CHCl_{3} (choloroform ultrapure, PanReac AppliChem) and dried under vacuum. Phospholipids (asolectin from soybean, Sigma-Aldrich) were dissolved in CHCl_{3} (chloroform ultrapure, PanReac AppliChem) and dried under vacuum. The membrane fraction of cell lysate was isolated by ultracentrifugation at 90,000g for 1 hour at 4°C. The supernatant was loaded on a Ni-NTA column (Qiagen), and XeRs were eluted in a buffer containing 50 mM NaH_{2}PO_{4}/Na_{2}HPO_{4} (pH 7.5), 0.1 M NaCl, 0.3 M imidazole, and 0.2% DDM. The eluate was dialyzed against 100 volumes of 50 mM NaH_{2}PO_{4}/Na_{2}HPO_{4} (pH 7.5) and 0.1 M NaCl buffer twice for 2 hours to dispose imidazole. Finally, proteins were concentrated to 70 mg/ml for crystallization.

**Incorporation in nanodiscs**

The proteonanodiscs were assembled using standard protocol (24). DMPC (1,2-dimyristoyl-sn-glycero-3-phosphocholine) (Avanti Polar Lipids) was used as lipid. An elongated MSP1E3 version of apolipoprotein-1 was used. The molar ratio during assembly was DMPC/MSP1E3/NsXeR = 100:2:3.

**Measurements of pump activity in *E. coli* suspensions**

The protein was expressed as described above. The cells were collected by centrifugation at 3000g for 10 min and were washed three times with an unbuffered salt solution (100 mM NaCl and 10 mM MgCl_{2}), with 30-min intervals between the washes to allow exchange of the ions inside the cells with the bulk. After that, the cells were resuspended in 100 mM NaCl solution and adjusted to an OD_{600} of 8.5. The measurements were performed in 3-ml aliquots of stirred cell suspension kept at 1°C. The cells were illuminated for 5 min using a halogen lamp (Intralux 5000-1, Volpi), and the light-induced pH changes were monitored with a pH meter (Lab 850, SCHOTT Instruments). Measurements were repeated under the same conditions after the addition of 30 μM CCCP.

**Measurement of pump activity in the liposomes**

The measurements were performed on 2 ml of stirred proteoliposome suspension at 0°C. Proteoliposomes were illuminated for 18 min using a halogen lamp (Intralux 5000-1, Volpi) and then were kept in the dark for another 18 min. Changes in pH were monitored using a pH meter (Lab 850, SCHOTT Instruments). Measurements were repeated for different starting pH and in the presence of 40 μM CCCP under the same conditions.

**Spectroscopic characterization and time-resolved absorption spectroscopy**

The absorption spectra were recorded using the Shimadzu UV-2401PC spectrophotometer. The laser flash photolysis setup was similar to that described by Chizhov and co-workers (25). The excitation/detection systems were composed as such: a Surelite II-10 Nd:YAG laser (Continuum Inc.) was used, providing pulses of 5-ns duration at 532-nm wavelength and an energy of 3 mJ per pulse. Samples (5 × 5-mm spectroscopic quartz cuvette; Hellma GmbH & Co.) were placed in a thermostated house between two collimated and mechanically coupled monochromators (1/8 m model 77250, Oriel Corp.). The probing light (xenon arc lamp, 75 W, Osram) passed the first monochromator sample and arrived after a second monochromator at a photomultiplier tube (PMT) detector (R3896, Hamamatsu). The current-to-voltage converter of the PMT determines the time resolution of the measurement system of ca. 50 ns (measured as an apparent pulse width of the 5-ns laser pulse). Two digital oscilloscopes (LeCroy 9361 and 9400A, 25 and 32 kilobytes of buffer memory per channel, respectively) were used to record the traces of transient transmission changes in two overlapping time windows. The maximal digitizing rate was 10 ns per data point. Transient absorption changes were recorded from 10 ns after the laser pulses until full completion of the phototransformation. At each wavelength, 25 laser pulses were averaged to improve the signal-to-noise ratio. The logarithmic data compression reduced the initial number of data points per trace (~50,000) to ~600 points evenly distributed in a log time scale giving ~100 points per time decade. The wavelengths were varied from 300 to 730 nm in steps of 2 nm (altogether, 216 spectral points) using a computer-controlled step motor. Absorption spectra of the samples were measured before and after each experiment on a standard spectrophotometer (DU-800, Beckman Coulter). Here, we report results of the analysis of two data sets: the XeR protein reconstituted in nanodiscs and in liposomes.
Data treatment and global fit analysis
Each data set was independently analyzed using the global multieponential nonlinear least-squares fitting program MEXFIT (25). The number of exponential components was incremented until the SD of weighted residuals did not further improve. After establishing the apparent rate constants and their assignment to the internal irreversible transitions of a single chain of relaxation processes, the amplitude spectra of exponents were transformed to the difference spectra of the corresponding intermediates in respect to the spectrum of the final state. Subsequently, the absolute absorption spectra of states were determined by adding the difference spectra divided by the fraction of converted molecules to the spectra of the final states. Criteria for the determination of the fraction value were the absence of negative absorbencies and contributions from the initial state to the calculated spectra of final state. For further details of the methods, see the study by Chizhov et al. (25).

Retinal extraction
Retinal extraction was performed on samples that have been dark-adapted for 16 hours or prior to photostimulation with a light from a 75-W halogen light longpass-filtered at 480 nm for 1 min. The conditions were similar to those in the study by Inoue et al. (4). Briefly, 500 mM hydroxyglutamine was added to the samples just before denaturation with ice-cold methanol. Retinal oximes were extracted with hexane and loaded on a ProntoSIL-OH 120–3 column. The flow rate was 1 ml/min of 12% (v/v) ethyl acetate and 0.12% (v/v) in hexane at room temperature.

Crystallization
The crystals were grown using the in meso approach (13), similar to that used in our previous work (26). The solubilized protein in the crystallization buffer was mixed with monodecenoic acid (Nu-Chek Prep) (pre-melted at 50°C) in a 1:1 ratio to form a lipidic mesophase. Aliquots (150 nl) of a protein-mesophase mixture were spotted on a 96-well lipidic cubic phase glass sandwich plate (Marienfeld) and overlaid with 600 nl of precipitant solution by means of the NT8 crystallization robot (Formulatrix). The best crystals were obtained with a protein concentration of 30 mg/ml and 2.8 to 3.4 M sodium malonate (pH 8.0) (Hampton Research). The crystals were grown at 22°C and appeared in 1 to 4 weeks. Note that the mesophase mixture was spotted for crystallization directly after preparation, because the XeR protein embedded into the bilayer of the mesophase (at 22°C) and not overlaid with precipitant solution was losing its purple color (significantly within several hours) likely because of denaturation processes and loss of retinal.

Data collection
X-ray diffraction data (wavelengths, 0.969 and 0.972 Å) were collected at ID23-1, ID29, and ID30B beamlines of the European Synchrotron Radiation Facility at 100 K using a PILATUS 6M detector. Diffraction images were processed with XDS software (27). The reflection intensities were scaled with Scala from the CCP4 suite (28). The crystallographic data statistics are shown in table S1.

Structure refinement
Reference model (archaeorhodopsin-2, PDB 2E14) for molecular replacement was chosen with the MoRDa pipeline (29). Initial phases were successfully obtained in the P2_12_1 space group by an Automated Model Building and Rebuilding using AutoBuild (30). The initial model was iteratively refined using REFMAC5 (31), PHENIX, and Coot (32).
References and Notes

Fig. S5. Overall architecture of XeR.

Fig. S3. Photocycles of the XeR.

Table S1. Crystallographic data collection and refinement statistics.

Table S2. List of mutations to XeR and their implications on proton pumping.

Supplementary Materials

Supplementary material for this article is available at http://advances.sciencemag.org/cgi/content/full/3/9/ea1603187/DC1

Fig. S11. Variability of spike latency.

Table S5. Crystallographic data collection and refinement statistics.

Fig. 3. Overall architecture of XeR.

Fig. S6. Comparison of the XeR structure with structures of other microbial rhodopsins.

Fig. S7. Details of the XeR proton-translocation pathway.

Fig. S8. Action spectrum of photocurrents in N1618-15 cells expressing XeR (black) and XeR absorption spectrum (red).

Fig. S9. Ns photocurrents in response to ultrashort light pulses.

Fig. S10. Light intensity dependence of XeR.

Fig. S11. Variability of spike latency.

Table S1. Crystallographic data collection and refinement statistics.

Table S2. List of mutations to XeR and their implications on proton pumping.

References and Notes


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