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Minimal metabolic pathways for ATP and generation of a proton motive force in synthetic cells

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Summary, Appendix and References

Summary

This thesis describes the development of new metabolic routes for synthetic cells. A pathway is presented that generates a proton motive force, as well as a pathway that provides the cell with energy in the form of ATP. Alongside, methods are presented to monitor these pathways with sensors and external methods.

Chapter 1 introduces the concept of a synthetic cell. Moreover, it considers how much energy in the form of ATP is required for a synthetic cell to maintain itself and to reproduce. To generate this amount of energy, several methods are discussed to yield ATP and energy in the form of electrochemical gradients. As a result of the small size of these vesicles, monitoring of these pathways is challenging. Therefore, a list is provided with several protein sensors and chemical probes that enable the measurement of several parameters inside a synthetic cell.

Chapter 2 describes the development of an enzymatic pathway that generates a proton motive force in proteoliposomes. It consists of a membrane transporter, which transports the substrate L-malate to the inside of the vesicles, and an internal enzyme which converts it into lactate which subsequently can leave the vesicles either by passive diffusion or transport by the membrane transporter. This process consumes a proton, thereby increasing the internal pH. We show that the import of L-malate versus the export of lactate is electrogenic. This generates the second component of the proton motive force, a membrane potential with a negative charge on the inside of the vesicles. The electrical potential that is achieved is approximately -30 mV, which is lower than the membrane potential of some bacteria (like *E. coli*), but could be sufficient for the generation of ATP via the F₁F₀-ATPsynthetase.

In **Chapter 3** two methods for the measurement of amino acids are compared. While amino acids are routinely quantified by many labs, the basic amino acids L-arginine, L-citrulline and L-ornithine proved to be difficult to measure. We have tried GC-MS, which is commonly used for amino acids. This method requires volatile compounds, therefore derivatization of the amino acids is necessary. This proved to be troublesome, as the yields for arginine, citrulline and ornithine are low. Moreover, upon derivatization, arginine can convert into citrulline, making quantification nearly impossible. Reversed phase HPLC proves to be a much better method with simple and fast derivatization. Despite the structural similarities between L-arginine and L-citrulline, separation is sufficient and interpretation of the data is straightforward. As a bonus, this method enables the measurement of NH₃, which makes HPLC the method of choice.

In **chapter 4** a pathway is presented that is able to provide ATP for synthetic cells. It consists of a membrane transporter and three internal enzymes. The pathway is

started by adding L-arginine to the outside of the vesicles. L-arginine is imported by the membrane transporter and converted into L-citrulline and subsequently L-ornithine plus carbamoyl phosphate. L-ornithine is subsequently exported by the transporter. In the last step of the pathway, the phosphate group of carbamoyl phosphate is transferred to ADP, yielding ATP. As L-arginine import and L-ornithine export is coupled in a 1-to-1 ratio, there is no build-up of waste products inside of the synthetic cells and the pathway can run for extended amounts of time. We monitor both the ATP to ADP ratio and pH inside the vesicles, as well as the total amount of L-arginine, L-citrulline, L-ornithine and ammonia. Additionally, we show that the generated ATP can be utilized to import glycine betaine from the external medium by introduction of another membrane transporter. When our vesicles are hyperosmotically challenged, import of glycine betaine appears to stabilize the ATP-to-ADP ratio over longer periods of time.

A method to monitor the membrane potential of vesicles is presented in **chapter 5**. Electrical probes cannot be used on the scale of our liposomes. Instead, fluorescent molecules are used. These so-called Nernstian probes are notoriously difficult to work with as they readily stick to surfaces and are sensitive to temperature and the lipid-to-dye ratio. We present a protocol that provides a solid basis for experiments and we were able to calibrate the signal of the probe to negative inside membrane potentials ranging from 0 to -162 mV.

For the monitoring of the ATP concentration inside synthetic cells, multiple sensors were evaluated. The ATeam ATP sensors were tested and the results can be found in the **Appendix**. These are interesting sensors, but they were found to be unsuitable for use in artificial cells.

Samenvatting

Dit proefschrift beschrijft de ontwikkeling van nieuwe metabolische routes voor synthetische cellen. De eerste route die beschreven wordt genereert een proton motive force, oftewel een elektrisch membraan potentiaal en een verschil in pH aan beide kanten van het membraan. De tweede route voorziet de synthetische cel van energie in de vorm van ATP, de universele energiedrager die in alle levende cellen, dus ook in ons lichaam, een grote rol speelt in vele metabolisme processen. Tegelijkertijd worden ook werklijnen beschreven om deze routes te monitoren met (eiwit) sensoren en andere externe methodes.

Hoofdstuk 1 introduceert het concept van een synthetische cel. Deze begint bij een lege cel, oftewel een klein blaasje afgesloten door een membraan. Aan dit blaasje worden eiwitten toegevoegd, zowel binnenin de cel als in het membraan. Met deze eiwitten worden functies toegevoegd en met elke functie lijkt de synthetische cel steeds meer op een echte (bacteriële) cel. In dit hoofdstuk wordt ook beschreven hoeveel energie zo'n cel uiteindelijk nodig zal hebben om zichzelf in stand te kunnen blijven houden en zich te kunnen vermenigvuldigen. Deze energie kan op verschillende manier gegenereerd worden, bijvoorbeeld in de vorm van ATP en elektrochemische gradiënten. Het kleine formaat van een synthetische cel maakt het moeilijk om de processen binnenin cel te volgen. Om dit makkelijker te maken hebben we een lijst opgesteld van chemische en eiwitsensoren die daarbij van pas kunnen komen en de verschillende parameters kunnen monitoren.

In **hoofdstuk 2** wordt een enzymatische route beschreven die een proton motive force kan opwekken in liposomen. Deze route bestaat uit een membraaneiwit dat L-malaat (appelzuur) van buiten de cel naar binnen kan transporteren en een intern eiwit dat het getransporteerde L-malaat omzet naar lactaat (melkzuur). Lactaat kan de cel weer verlaten door zelf passief over het membraan te diffunderen of met behulp van het membraaneiwit. Bij de omzetting van L-malaat naar lactaat wordt een proton opgenomen. Dit zorgt er voor dat de pH aan de binnenkant stijgt. Daarnaast laten we ook zien dat het transport van L-malaat over het membraan elektrogeen is, er wordt een elektrisch potentiaal over het membraan gegenereerd (de binnenkant wordt negatief geladen). Het potentiaalverschil dat opgewekt wordt is ongeveer -30 mV. Dit is lager dan bijvoorbeeld het membraanpotentiaal dat *E. coli* heeft, maar kan onder omstandigheden genoeg energie leveren om bijvoorbeeld ATP te genereren via het F₁F₀-ATPsynthetase membraaneiwit.

Hoofdstuk 3 gaat over methodes om de concentraties van aminozuren te meten. Hoewel dit voor menig lab routinewerk is, blijken de basische aminozuren arginine, citrulline en ornithine lastig te meten. Als eerste hebben we gaschromatografie

gekoppeld aan massaspectrometrie geprobeerd. Voor deze methoden moeten de moleculen vluchtig zijn. Om de aminozuren vluchtig te maken worden de moleculen eerst chemisch aangepast. Voor vele aminozuren is dit eenvoudig, maar dit proces loopt zeer slecht bij arginine, citrulline en ornithine. Daar komt bij dat arginine na deze stap uiteen kan vallen in citrulline, wat de kwantificatie praktisch onmogelijk maakt. Een tweede methode, vloeistofchromatografie met omgekeerde polariteit, zorgt voor betere resultaten. Ook hier moeten de aminozuren chemisch worden aangepast, maar deze stap is snel en eenvoudig. Ondanks dat arginine en citrulline erg op elkaar lijken weet deze methode ze te scheiden en de concentraties te meten. Samen met het feit dat ook ammonia met deze methode gemeten kan worden, maakt dat vloeistofchromatografie de voorkeur krijgt.

Hoofdstuk 4 gaat over een metabolische route die ATP kan genereren in synthetische cellen. Deze route bestaat uit een membraantransporter en drie intracellulaire eiwitten. De productie van ATP start met het toevoegen van L-arginine aan de buitenkant van de cellen, waarna het door de membraantransporter naar binnen wordt gebracht. L-arginine wordt omgezet in L-citrulline en vervolgens in L-ornithine plus carbamoyl fosfaat. L-ornithine is een restproduct en wordt weer naar buiten gebracht door het membraaneiwit. In de laatste stap van de keten wordt de fosfaat groep van carbamoyl fosfaat overgezet op ADP, met als eindproduct ATP. Doordat de import van L-arginine en de export van L-ornithine gekoppeld zijn met een 1 op 1 ratio is er geen ophoping van het restproduct en kan de productie van ATP voor langere tijd door blijven gaan. In het proces meten we de ATP tot ADP ratio, de interne pH, de concentraties van L-arginine, L-citrulline, L-ornithine en als laatste ammoniak. Daarbij kunnen we ook aantonen dat de gegenereerde ATP daadwerkelijk gebruikt kan worden voor het importeren van glycine betaine door een tweede membraan transporter. Deze import van glycine betaine kan zelfs de cellen stabiliseren als we ze resuspenderen in een oplossing met een hoog zoutgehalte.

In **hoofdstuk 5** wordt een methode gepresenteerd om een membraanpotentiaal te meten. In grote cellen kan dit gedaan worden met elektrodes, maar dit is niet mogelijk in onze synthetische cellen omdat ze te klein zijn. Om het membraanpotentiaal te meten maken we gebruik van fluorescente moleculen, in dit geval zogenoemde Nernstian probes. Het werken met deze moleculen is niet eenvoudig aangezien ze snel blijven plakken aan oppervlakken en zeer gevoelig zijn voor de temperatuur en de ratio tussen membraanlipiden en de fluorescente moleculen zelf. Met deze methode kunnen we membraanpotentialen meten tussen 0 en -162 mV (de negatieve lading zit aan de binnenkant van de cellen) en is daarmee een goede basis voor toekomstige experimenten.

Om ATP concentraties binnen synthetische cellen zijn meerdere eiwitsensoren getest. In hoofdstuk 4 hebben we PercevalHR gebruikt, maar ook de ATeam sensoren zijn interessant. De resultaten van de drie ATeam sensoren zijn te vinden in de **Appendix**.

Appendix

ATeam ATP sensor evaluation

The ATeam sensors were among the first fluorescent probes for detecting ATP⁸⁶. Three versions are available: ATeam 1.03, which utilizes the ϵ subunit of the F₀F₁ ATP synthase from *Bacillus subtilis* to bind ATP. This ATP binding domain is replaced by the ϵ subunit of the F₀F₁ ATP synthase from *Bacillus* sp. PS3 in ATeam 3.10, which resulted in a much higher affinity of the sensor for ATP. Lastly, DTeam is identical to ATeam 1.03 but has two mutations, which abolishes its capacity to bind ATP.

The ATeam sensors are FRET-based sensors and exploit the fluorescent proteins CFP and mVenus. The ϵ subunit adopts a compact conformation when bound to ATP, which draws the two FPs closer together. This results in an increased FRET efficiency. As a readout, the emission intensities of CFP and mVenus are recorded at 475 and 527 nm, respectively, upon excitation of CFP at 435 nm.

These sensors were evaluated for their use in vesicles containing the arginine breakdown pathway (see chapter 4). The experiments were conducted with the sensors in solution and revealed that ATeam 1.03 has a K_D for Mg-ATP of 1 mM. The 3.10 variant has an affinity for Mg-ATP of 1 μ M that is approximately a 1000-fold higher. However, this sensor is also sensitive towards ADP and AMP, albeit with lower affinities (K_D values of 57 μ M and 1 mM for ADP and AMP, respectively). As anticipated, DTeam does not bind ADP and AMP in the concentration range from 0.1 μ M to 10 mM.

The effect of NaCl on the binding of Mg-ATP to the Ateam sensors was also studied. The affinity towards ATP of ATeam 3.10 was decreased at higher salt concentrations (Fig. 2). At a concentration of 1 M NaCl, the K_D was an order of magnitude higher than without added salt. The salt effect was not observed with ATeam 1.03, as its affinity to ATP was virtually unaffected by NaCl.

The design of the ATeam sensors is similar to that of the crowding sensors published by Boersma *et al.*¹⁰², except that the ϵ subunit is replaced by a flexible domain composed of two α -helices. To test whether the ATeam sensors are sensitive to macromolecular crowding, we conducted an experiment using Ficoll PM70 to simulate a high degree of excluded volume (Fig. 3). All three sensors behaved similar towards crowding by Ficoll PM70. The FRET ratio increased with Ficoll concentration, implying that the sensors are not solely responding to ATP.

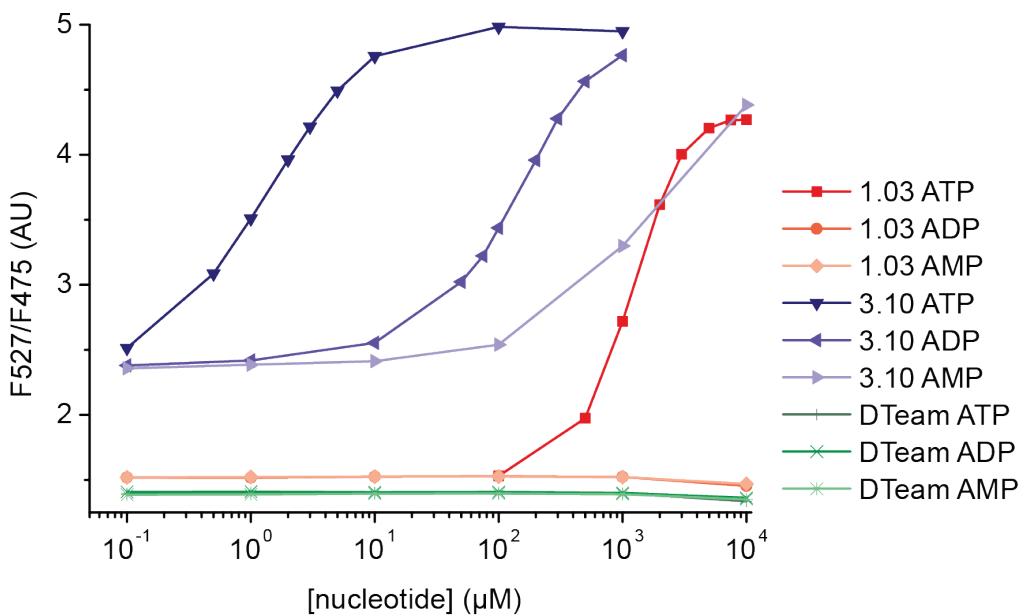


Figure 1. Changes in the fluorescent ratios of the ATeam sensors upon addition of nucleotides in 50 mM KPi pH 7.4, 150 mM NaCl plus 0.2 % BSA. All nucleotides were added with equimolar amounts of MgCl₂.

Based on the data presented in Figure 1, ATeam 3.10 is not suitable for the use in vesicles containing the arginine deiminase pathway. This sensor has the highest affinity towards ATP and should theoretically be able to report the production of even tiny amounts of ATP. In reality it will already be fully saturated at the start of an experiment, as the ADP concentration inside the vesicles is ten times higher than the K_D for ADP. Ateam 1.03 does not have this problem and could be used to measure ATP inside of vesicles. The linear range is however limited (approximately from 0.1 to 2 mM of ATP), which may lead to an on or off behaviour in liposomes. This impedes the quantification of ATP inside vesicles. Moreover, the effect on ionic strength and crowding of osmotically shocking vesicles as shown in Chapter 4, Figure 5 will further hamper the usefulness ATeam sensors inside proteoliposomes.

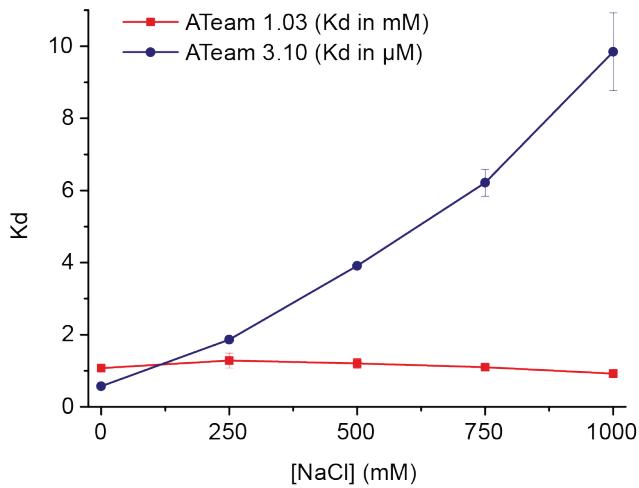


Figure 2. Sensitivity of the ATeam sensors to NaCl in 50 mM KPi pH 7.4. The K_D of ATeam 1.03 and 3.10 as a function of NaCl concentration.

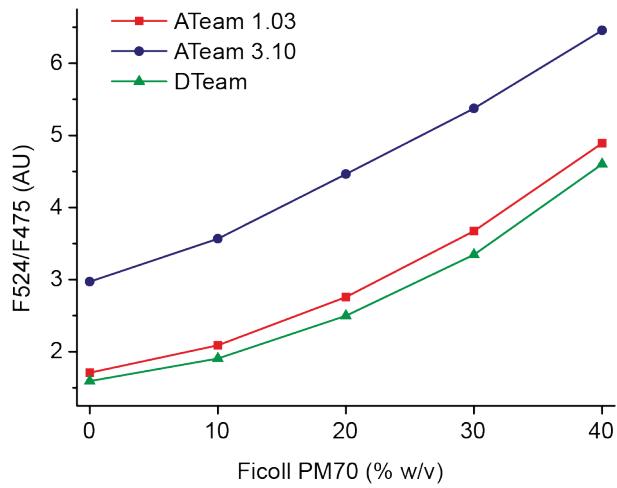


Figure 3. The effect of macromolecular crowding on the ATeam 1.03 (red), ATeam 3.10 (blue) and DTeam (green) in 50 mM KPi pH 7.4. Ficoll PM70 was used as crowding agent.

Methods

E. coli BL21-DE3 cells containing either pRset_A1.03, pRset_A3.10 or pRset_DTeam were grown in lysogeny broth with 100 µg ml⁻¹ ampicillin. 0.5L cultures were grown at 30 °C, 200 rpm to an OD₆₀₀ of 0.6, after which they were cooled to 20 °C. 100 µg of IPTG was added to start the transcription of the sensor gene from the plasmid. The cultures were incubated for 24 hours at 20 °C, 200 rpm before being harvested by centrifugation (6000 x g, 4 °C, 15 min) and washed with 600 ml of 50 mM NaPi pH 7.4, 100 mM NaCl. After centrifugation (6000 x g, 4 °C, 15 min), the cells were resuspended in approximately 30 ml of 20 mM NaPi PH 7.4, 100 mM NaCl and stored at -20 °C. After thawing 100 µg mL⁻¹ of DNase was added and the cells were lysed by high-pressure disruption in a single passage at 25 kpsi and 4 °C. Directly after lysis 0.1 mM of PMSF was added. The suspension was spun at 145.000 x g for 60 minutes at 4 °C to remove cell debris. The supernatant was flash frozen in LN₂ and stored at -80 °C.

All purification steps were performed at 4 °C or on ice, unless specified otherwise. Ni²⁺-sepharose resin was pre-equilibrated with wash buffer (50 mM NaPi pH 8, 200 mM NaCl) supplemented with 10 mM imidazole. Cell lysate was thawed on ice, added to the equilibrated resin and nutated for 1h. The mixture was transferred to a polyprep column (Bio-Rad Laboratories, Inc.) and washed with 20 column volumes of wash buffer supplemented with 25 mM Imidazole. The protein was eluted with a maximum of 3 column volumes of was buffer supplemented with 250 mM Imidazole. Subsequently, the elution fractions were run on a Superdex 200 Increase 10/300 GL size-exclusion column (GE Healthcare) in 10 mM NaPi pH 7.4, 150 mM NaCl. Fractions with sensor were aliquoted in volumes of 50 µl, flash frozen in LN₂ and stored at -80 °C.

To measure the fluorescence of the ATeam sensors in solution, sensor was diluted to a concentration of 5 µg mL⁻¹ in 50 mM KPi pH 7.4, 150 mM NaCl and 0.2 % (w/v) of BSA in 105.250-QS cuvettes (Hellma Analytics). The spectrum of the ATeam sensors was measured by a Jasco FP-8300 spectrofluorometer at 37 °C. Excitation was set at 435 ±5 nm, emission was captured from 460 ±5 nm to 560 ±5 nm.

References

1. Gibson DG, Glass JI, Lartigue C, et al. Creation of a bacterial cell controlled by a chemically synthesized genome. *Science*. 2010;329(5987):52-56. doi:10.1126/science.1190719
2. Hutchison CA, Chuang RY, Noskov VN, et al. Design and synthesis of a minimal bacterial genome. *Science*. 2016;351(6280):aad6253. doi:10.1126/science.aad6253
3. Porcar M, Danchin A, de Lorenzo V, et al. The ten grand challenges of synthetic life. *Syst Synth Biol*. 2011;5(1-2):1-9. doi:10.1007/s11693-011-9084-5
4. Opgenorth PH, Korman TP, Iancu L, Bowie JU. A molecular rheostat maintains ATP levels to drive a synthetic biochemistry system. *Nat Chem Biol*. 2017;13(9):938-942. doi:10.1038/nchembio.2418
5. Bhattacharya A, Brea RJ, Niederholtmeyer H, Devaraj NK. A minimal biochemical route towards *de novo* formation of synthetic phospholipid membranes. *Nat Commun*. 2019;10(1):300. doi:10.1038/s41467-018-08174-x
6. Noireaux V, Maeda YT, Libchaber A. Development of an artificial cell, from self-organization to computation and self-reproduction. *Proc Natl Acad Sci U S A*. 2011;108(9):3473-3480. doi:10.1073/pnas.1017075108
7. Caschera F, Noireaux V. Integration of biological parts toward the synthesis of a minimal cell. *Curr Opin Chem Biol*. 2014;22:85-91. doi:10.1016/j.cbpa.2014.09.028
8. Lee KY, Park SJ, Lee KA, et al. Photosynthetic artificial organelles sustain and control ATP-dependent reactions in a protocellular system. *Nat Biotechnol*. 2018;36(6):530-535. doi:10.1038/nbt.4140
9. Loose M, Mitchison TJ. The bacterial cell division proteins FtsA and FtsZ self-organize into dynamic cytoskeletal patterns. *Nat Cell Biol*. 2014;16(1):38-46. doi:10.1038/ncb2885
10. Matsuura T, Hosoda K, Kazuta Y, Ichihashi N, Suzuki H, Yomo T. Effects of compartment size on the kinetics of intracompartimental multimeric protein synthesis. *ACS Synth Biol*. 2012;1(9):431-437. doi:10.1021/sb300041z
11. Ledford H. Beyond CRISPR: A guide to the many other ways to edit a genome. *Nature*. 2016;536(7615):136-137. doi:10.1038/536136b

12. Mohanraju P, Makarova KS, Zetsche B, Zhang F, Koonin E V, van der Oost J. Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems. *Science*. 2016;353(6299):aad5147. doi:10.1126/science.aad5147
13. Moran NA, Bennett GM. The tiniest tiny genomes. *Annu Rev Microbiol*. 2014;68(1):195-215. doi:10.1146/annurev-micro-091213-112901
14. Pérez-Brocal V, Gil R, Ramos S, et al. A small microbial genome: the end of a long symbiotic relationship? *Science*. 2006;314(5797):312-313. doi:10.1126/science.1130441
15. Ferguson SJ. ATP synthase: from sequence to ring size to the P/O ratio. *Proc Natl Acad Sci U S A*. 2010;107(39):16755-16756. doi:10.1073/pnas.1012260107
16. Watt IN, Montgomery MG, Runswick MJ, Leslie AGW, Walker JE. Bioenergetic cost of making an adenosine triphosphate molecule in animal mitochondria. *Proc Natl Acad Sci U S A*. 2010;107(39):16823-16827. doi:10.1073/pnas.1011099107
17. Pogoryelov D, Yu J, Meier T, Vonck J, Dimroth P, Muller DJ. The c15 ring of the Spirulina platensis F-ATP synthase: F1/F0 symmetry mismatch is not obligatory. *EMBO Rep*. 2005;6(11):1040-1044. doi:10.1038/sj.embo.7400517
18. Junge W, Nelson N. ATP Synthase. *Annu Rev Biochem*. 2015;84(1):631-657. doi:10.1146/annurev-biochem-060614-034124
19. Gibbons C, Montgomery MG, Leslie AG, Walker JE. The structure of the central stalk in bovine F(1)-ATPase at 2.4 Å resolution. *Nat Struct Biol*. 2000;7(11):1055-1061. doi:10.1038/80981
20. Rodgers AJ, Wilce MC. Structure of the gamma-epsilon complex of ATP synthase. *Nat Struct Biol*. 2000;7(11):1051-1054. doi:10.1038/80975
21. Tsunoda SP, Rodgers AJ, Aggeler R, Wilce MC, Yoshida M, Capaldi RA. Large conformational changes of the epsilon subunit in the bacterial F1F0 ATP synthase provide a ratchet action to regulate this rotary motor enzyme. *Proc Natl Acad Sci U S A*. 2001;98(12):6560-6564. doi:10.1073/pnas.111128098
22. Meyrat A, von Ballmoos C. ATP synthesis at physiological nucleotide concentrations. *Sci Rep*. 2019;9(1):3070. doi:10.1038/s41598-019-38564-0

23. Driessens AJ, Poolman B, Kiewiet R, Konings W. Arginine transport in *Streptococcus lactis* is catalyzed by a cationic exchanger. *Proc Natl Acad Sci U S A.* 1987;84(17):6093-6097. doi:10.1073/pnas.84.17.6093
24. Pols T, Sikkema HR, Gaastra BF, et al. A synthetic metabolic network for physicochemical homeostasis. *Nat Commun.* 2019;10(1):4239. doi:10.1038/s41467-019-12287-2
25. Dimroth P, Schink B. Energy conservation in the decarboxylation of dicarboxylic acids by fermenting bacteria. *Arch Microbiol.* 1998;170(2):69-77.
26. Dimroth P. The generation of an electrochemical gradient of sodium ions upon decarboxylation of oxaloacetate by the membrane-bound and Na⁺-activated oxaloacetate decarboxylase from *Klebsiella aerogenes*. *Eur J Biochem.* 1982;121(2):443-449.
27. Poolman B, Molenaar D, Smid EJ, et al. Malolactic fermentation: electrogenic malate uptake and malate/lactate antiport generate metabolic energy. *J Bacteriol.* 1991;173(19):6030-6037. doi:10.1128/jb.173.19.6030-6037.1991
28. Anantharam V, Allison MJ, Maloney PC. Oxalate:formate exchange. The basis for energy coupling in *Oxalobacter*. *J Biol Chem.* 1989;264(13):7244-7250. <http://www.ncbi.nlm.nih.gov/pubmed/2708365>
29. Gabba M, Frallicciardi J, van 't Klooster J, et al. Weak Acid Permeation in Synthetic Lipid Vesicles and Across the Yeast Plasma Membrane. *Biophys J.* 2020;118(2):422-434. doi:10.1016/j.bpj.2019.11.3384
30. Berg M, Hilbi H, Dimroth P. Sequence of a gene cluster from *Malonomonas rubra* encoding components of the malonate decarboxylase Na⁺ pump and evidence for their function. *Eur J Biochem.* 1997;245(1):103-115. doi:10.1111/j.1432-1033.1997.00103.x
31. Hilpert W, Schink B, Dimroth P. Life by a new decarboxylation-dependent energy conservation mechanism with Na as coupling ion. *EMBO J.* 1984;3(8):1665-1670. <http://www.ncbi.nlm.nih.gov/pubmed/16453537>
32. Hirai T, Heymann JAW, Shi D, Sarker R, Maloney PC, Subramaniam S. Three-dimensional structure of a bacterial oxalate transporter. *Nat Struct Biol.* 2002;9(8):597-600. doi:10.1038/nsb821
33. Salema M, Poolman B, Lolkema JS, Dias MCL, Konings WN. Uniport of Monoanionic L-malate in Membrane Vesicles from *Leuconostoc Oenos*. *Eur J Biochem.* 1994;225(1):289-295. doi:10.1111/j.1432-1033.1994.00289.x

34. Salema M, Capucho I, Poolman B, San Romão M V, Dias MC. In vitro reassembly of the malolactic fermentation pathway of *Leuconostoc oenos* (*Oenococcus oeni*). *J Bacteriol.* 1996;178(18):5537-5539. doi:10.1128/jb.178.18.5537-5539.1996
35. Ilgū H, Jeckelmann JM, Gapsys V, Ucurum Z, de Groot BL, Fotiadis D. Insights into the molecular basis for substrate binding and specificity of the wild-type L-arginine/agmatine antiporter AdiC. *Proc Natl Acad Sci U S A.* 2016;113(37):10358-10363. doi:10.1073/pnas.1605442113
36. Chisholm RL, Firtel R a. Insights into morphogenesis from a simple developmental system. *Nat Rev Mol Cell Biol.* 2004;5(7):531-541. doi:10.1038/nrm1427
37. Ma D, Lu P, Yan C, et al. Structure and mechanism of a glutamate-GABA antiporter. *Nature.* 2012;483(7391):632-636. doi:10.1038/nature10917
38. Molenaar D, Bosscher JS, ten Brink B, Driessens AJ, Konings WN. Generation of a proton motive force by histidine decarboxylation and electrogenic histidine/histamine antiport in *Lactobacillus buchneri*. *J Bacteriol.* 1993;175(10):2864-2870. doi:10.1128/jb.175.10.2864-2870.1993
39. Romano A, Trip H, Lolkema JS, Lucas PM. Three-component lysine/ornithine decarboxylation system in *Lactobacillus saerimneri* 30a. *J Bacteriol.* 2013;195(6):1249-1254. doi:10.1128/JB.02070-12
40. Coton M, Fernández M, Trip H, et al. Characterization of the tyramine-producing pathway in *Sporolactobacillus* sp. P3J. *Microbiology (Reading).* 2011;157(Pt 6):1841-1849. doi:10.1099/mic.0.046367-0
41. Berhanu S, Ueda T, Kuruma Y. Artificial photosynthetic cell producing energy for protein synthesis. *Nat Commun.* 2019;10(1):1325. doi:10.1038/s41467-019-09147-4
42. Spitzer J, Poolman B. The role of biomacromolecular crowding, ionic strength, and physicochemical gradients in the complexities of life's emergence. *Microbiol Mol Biol Rev.* 2009;73(2):371-388. doi:10.1128/MMBR.00010-09
43. Gebicki JM, Hicks M. Ufasomes are stable particles surrounded by unsaturated fatty acid membranes. *Nature.* 1973;243(5404):232-234.
44. Budin I, Debnath A, Szostak JW. Concentration-driven growth of model protocell membranes. *J Am Chem Soc.* 2012;134(51):20812-20819. doi:10.1021/ja310382d

45. Henrich C, Szostak JW. Controlled growth of filamentous fatty acid vesicles under flow. *Langmuir*. 2014;30(49):14916-14925. doi:10.1021/la503933x
46. Jin L, Kamat NP, Jena S, Szostak JW. Fatty Acid/Phospholipid Blended Membranes: A Potential Intermediate State in Protocellular Evolution. *Small*. 2018;14(15):e1704077. doi:10.1002/smll.201704077
47. Puiggallí-Jou A, Del Valle LJ, Alemán C. Biomimetic hybrid membranes: incorporation of transport proteins/peptides into polymer supports. *Soft Matter*. 2019;15(13):2722-2736. doi:10.1039/c8sm02513d
48. Beales PA, Khan S, Muench SP, Jeuken LJC. Durable vesicles for reconstitution of membrane proteins in biotechnology. *Biochem Soc Trans*. 2017;45(1):15-26. doi:10.1042/BST20160019
49. Seneviratne R, Khan S, Moscrop E, et al. A reconstitution method for integral membrane proteins in hybrid lipid-polymer vesicles for enhanced functional durability. *Methods*. 2018;147:142-149. doi:10.1016/j.ymeth.2018.01.021
50. Geertsma ER, Nik Mahmood NABB, Schuurman-Wolters GK, Poolman B. Membrane reconstitution of ABC transporters and assays of translocator function. *Nat Protoc*. 2008;3(2):256-266. doi:10.1038/nprot.2007.519
51. Bianchi F, Klooster JS van 't, Ruiz SJ, et al. Asymmetry in inward- and outward-affinity constant of transport explain unidirectional lysine flux in *Saccharomyces cerevisiae*. *Sci Rep*. 2016;6:31443. doi:10.1038/srep31443
52. Dupuy AD, Engelman DM. Protein area occupancy at the center of the red blood cell membrane. *Proc Natl Acad Sci U S A*. 2008;105(8):2848-2852. doi:10.1073/pnas.0712379105
53. Ramadurai S, Holt A, Krasnikov V, van den Bogaart G, Killian JA, Poolman B. Lateral diffusion of membrane proteins. *J Am Chem Soc*. 2009;131(35):12650-12656. doi:10.1021/ja902853g
54. Rigaud JL, Pitard B, Levy D. Reconstitution of membrane proteins into liposomes: application to energy-transducing membrane proteins. *Biochim Biophys Acta*. 1995;1231(3):223-246. <http://www.ncbi.nlm.nih.gov/pubmed/7578213>
55. Knol J, Sjollema K, Poolman B. Detergent-mediated reconstitution of membrane proteins. *Biochemistry*. 1998;37(46):16410-16415. doi:10.1021/bi981596u

56. Seinen AB, Driessen AJM. Single-Molecule Studies on the Protein Translocon. *Annu Rev Biophys.* 2019;48:185-207. doi:10.1146/annurev-biophys-052118-115352
57. van den Bogaart G, Hermans N, Krasnikov V, Poolman B. Protein mobility and diffusive barriers in *Escherichia coli*: consequences of osmotic stress. *Mol Microbiol.* 2007;64(3):858-871. doi:10.1111/j.1365-2958.2007.05705.x
58. van den Berg J, Boersma AJ, Poolman B. Microorganisms maintain crowding homeostasis. *Nat Rev Microbiol.* Published online March 27, 2017. doi:10.1038/nrmicro.2017.17
59. van den Bogaart G, Kusters I, Velásquez J, et al. Dual-color fluorescence-burst analysis to study pore formation and protein-protein interactions. *Methods.* 2008;46(2):123-130. doi:10.1016/jymeth.2008.06.016
60. Doeven MK, Folgering JHA, Krasnikov V, Geertsma ER, van den Bogaart G, Poolman B. Distribution, lateral mobility and function of membrane proteins incorporated into giant unilamellar vesicles. *Biophys J.* 2005;88(2):1134-1142. doi:10.1529/biophysj.104.053413
61. Chen Z, Wang J, Sun W, et al. Synthetic beta cells for fusion-mediated dynamic insulin secretion. *Nat Chem Biol.* 2018;14(1):86-93. doi:10.1038/nchembio.2511
62. Bartelt SM, Steinkühler J, Dimova R, Wegner S V. Light-Guided Motility of a Minimal Synthetic Cell. *Nano Lett.* 2018;18(11):7268-7274. doi:10.1021/acs.nanolett.8b03469
63. Holms WH, Hamilton ID, Robertson AG. The rate of turnover of the adenosine triphosphate pool of *Escherichia coli* growing aerobically in simple defined media. *Arch Mikrobiol.* 1972;83(2):95-109.
64. Milo R, Phillips R. *Cell Biology by the Numbers*. Garland Science; 2016.
65. Harold FM. *The Vital Force: A Study of Bioenergetics.*; 1986.
66. Fang G, Konings WN, Poolman B. Kinetics and substrate specificity of membrane-reconstituted peptide transporter DtpT of *Lactococcus lactis*. *J Bacteriol.* 2000;182(9):2530-2535. doi:10.1128/jb.182.9.2530-2535.2000
67. Detmers FJ, Lanfermeijer FC, Abele R, et al. Combinatorial peptide libraries reveal the ligand-binding mechanism of the oligopeptide receptor OppA of

- Lactococcus lactis. *Proc Natl Acad Sci U S A.* 2000;97(23):12487-12492. doi:10.1073/pnas.220308797
68. Calhoun KA, Swartz JR. Energy systems for ATP regeneration in cell-free protein synthesis reactions. *Methods Mol Biol.* 2007;375:3-17. doi:10.1007/978-1-59745-388-2_1
69. Kim HC, Kim DM. Methods for energizing cell-free protein synthesis. *J Biosci Bioeng.* 2009;108(1):1-4. doi:10.1016/j.jbiosc.2009.02.007
70. Lynch M, Marinov GK. The bioenergetic costs of a gene. *Proc Natl Acad Sci U S A.* 2015;112(51):15690-15695. doi:10.1073/pnas.1514974112
71. Horn M, Collingro A, Schmitz-Esser S, et al. Illuminating the evolutionary history of chlamydiae. *Science.* 2004;304(5671):728-730. doi:10.1126/science.1096330
72. Haferkamp I, Schmitz-Esser S, Wagner M, Neigel N, Horn M, Neuhaus HE. Tapping the nucleotide pool of the host: novel nucleotide carrier proteins of Protochlamydia amoebophila. *Mol Microbiol.* 2006;60(6):1534-1545. doi:10.1111/j.1365-2958.2006.05193.x
73. Exterkate M, Caforio A, Stuart MCA, Driessens AJM. Growing Membranes In Vitro by Continuous Phospholipid Biosynthesis from Free Fatty Acids. *ACS Synth Biol.* 2018;7(1):153-165. doi:10.1021/acssynbio.7b00265
74. Hirabayashi Y, Nomura KH, Nomura K. The acetyl-CoA transporter family SLC33. *Mol Aspects Med.* 2013;34(2-3):586-589. doi:10.1016/j.mam.2012.05.009
75. Alvadia C, Lim NK, Clerico Mosina V, Oostergetel GT, Dutzler R, Paulino C. Cryo-EM structures and functional characterization of the murine lipid scramblase TMEM16F. *eLife.* 2019;8:e44365. doi:10.7554/eLife.44365
76. Biber J, Hernando N, Forster I. Phosphate transporters and their function. *Annu Rev Physiol.* 2013;75:535-550. doi:10.1146/annurev-physiol-030212-183748
77. Rhoads DB, Waters FB, Epstein W. Cation transport in Escherichia coli. VIII. Potassium transport mutants. *J Gen Physiol.* 1976;67(3):325-341. doi:10.1085/jgp.67.3.325
78. Diskowski M, Mehdipour AR, Wunnicke D, et al. Helical jackknives control the gates of the double-pore K⁺ uptake system KtrAB. *eLife.* 2017;6:e24303. doi:10.7554/eLife.24303

79. Feist AM, Henry CS, Reed JL, et al. A genome-scale metabolic reconstruction for *Escherichia coli* K-12 MG1655 that accounts for 1260 ORFs and thermodynamic information. *Mol Syst Biol.* 2007;3:121. doi:10.1038/msb4100155
80. Rappé MS, Connon SA, Vergin KL, Giovannoni SJ. Cultivation of the ubiquitous SAR11 marine bacterioplankton clade. *Nature.* 2002;418(6898):630-633. doi:10.1038/nature00917
81. Mateos-Gil P, Tarazona P, Vélez M. Bacterial cell division: modeling FtsZ assembly and force generation from single filament experimental data. *FEMS Microbiol Rev.* 2019;43(1):73-87. doi:10.1093/femsre/fuy039
82. Kim BH, Gadd GM. *Bacterial Physiology and Metabolism*. Cambridge University Press; 2008.
83. Tamura T, Hamachi I. Recent progress in design of protein-based fluorescent biosensors and their cellular applications. *ACS Chem Biol.* 2014;9(12):2708-2717. doi:10.1021/cb500661v
84. Bizzarri R, Serresi M, Luin S, Beltram F. Green fluorescent protein based pH indicators for in vivo use: a review. *Anal Bioanal Chem.* 2009;393(4):1107-1122. doi:10.1007/s00216-008-2515-9
85. Cranfill PJ, Sell BR, Baird MA, et al. Quantitative assessment of fluorescent proteins. *Nat Methods.* 2016;13(7):557-562. doi:10.1038/nmeth.3891
86. Imamura H, Nhat KPH, Togawa H, et al. Visualization of ATP levels inside single living cells with fluorescence resonance energy transfer-based genetically encoded indicators. *Proc Natl Acad Sci U S A.* 2009;106(37):15651-15656. doi:10.1073/pnas.0904764106
87. Nakano M, Imamura H, Nagai T, Noji H. Ca²⁺ regulation of mitochondrial ATP synthesis visualized at the single cell level. *ACS Chem Biol.* 2011;6(7):709-715. doi:10.1021/cb100313n
88. Botman D, van Heerden JH, Teusink B. An Improved ATP FRET Sensor For Yeast Shows Heterogeneity During Nutrient Transitions. *ACS Sens.* 2020;5(3):814-822. doi:10.1021/acssensors.9b02475
89. Yaginuma H, Kawai S, Tabata K V, et al. Diversity in ATP concentrations in a single bacterial cell population revealed by quantitative single-cell imaging. *Sci Rep.* 2014;4:6522. doi:10.1038/srep06522

90. Lobas MA, Tao R, Nagai J, et al. A genetically encoded single-wavelength sensor for imaging cytosolic and cell surface ATP. *Nat Commun.* 2019;10(1):711. doi:10.1038/s41467-019-08441-5
91. Tantama M, Martínez-François JR, Mongeon R, Yellen G. Imaging energy status in live cells with a fluorescent biosensor of the intracellular ATP-to-ADP ratio. *Nat Commun.* 2013;4:2550. doi:10.1038/ncomms3550
92. Kitajima N, Takikawa K, Sekiya H, et al. Real-time in vivo imaging of extracellular ATP in the brain with a hybrid-type fluorescent sensor. *eLife.* 2020;9:1-18. doi:10.7554/eLife.57544
93. Zhao Y, Jin J, Hu Q, et al. Genetically Encoded Fluorescent Sensors for Intracellular NADH Detection. *Cell Metab.* 2011;14(4):555-566. doi:10.1016/j.cmet.2011.09.004
94. Hung YP, Albeck JG, Tantama M, Yellen G. Imaging cytosolic NADH-NAD(+) redox state with a genetically encoded fluorescent biosensor. *Cell Metab.* 2011;14(4):545-554. doi:10.1016/j.cmet.2011.08.012
95. Somerville GA, Proctor RA. At the crossroads of bacterial metabolism and virulence factor synthesis in Staphylococci. *Microbiol Mol Biol Rev.* 2009;73(2):233-248. doi:10.1128/MMBR.00005-09
96. Zhao Y, Hu Q, Cheng F, et al. SoNar, a Highly Responsive NAD+/NADH Sensor, Allows High-Throughput Metabolic Screening of Anti-tumor Agents. *Cell Metab.* 2015;21(5):777-789. doi:10.1016/j.cmet.2015.04.009
97. Tao R, Zhao Y, Chu H, et al. Genetically encoded fluorescent sensors reveal dynamic regulation of NADPH metabolism. *Nat Methods.* 2017;14(7):720-728. doi:10.1038/nmeth.4306
98. Miesenböck G, De Angelis DA, Rothman JE. Visualizing secretion and synaptic transmission with pH-sensitive green fluorescent proteins. *Nature.* 1998;394(6689):192-195. doi:10.1038/28190
99. Tantama M, Hung YP, Yellen G. Imaging intracellular pH in live cells with a genetically encoded red fluorescent protein sensor. *J Am Chem Soc.* 2011;133(26):10034-10037. doi:10.1021/ja202902d
100. Kano K, Fendler JH. Pyranine as a sensitive pH probe for liposome interiors and surfaces. pH gradients across phospholipid vesicles. *Biochim Biophys Acta.* 1978;509(2):289-299. <http://www.ncbi.nlm.nih.gov/pubmed/26400>

101. James-Krake MR. Quick and accurate method to convert BCECF fluorescence to pH_i: calibration in three different types of cell preparations. *J Cell Physiol.* 1992;151(3):596-603. doi:10.1002/jcp.1041510320
102. Boersma AJ, Zuhorn IS, Poolman B. A sensor for quantification of macromolecular crowding in living cells. *Nat Methods.* 2015;12(3):227-229. doi:10.1038/nmeth.3257
103. Liu B, Åberg C, van Eerden FJ, Marrink SJ, Poolman B, Boersma AJ. Design and Properties of Genetically Encoded Probes for Sensing Macromolecular Crowding. *Biophys J.* 2017;112(9):1929-1939. doi:10.1016/j.bpj.2017.04.004
104. Gnutt D, Gao M, Brylski O, Heyden M, Ebbinghaus S. Excluded-volume effects in living cells. *Angew Chem Int Ed Engl.* 2015;54(8):2548-2551. doi:10.1002/anie.201409847
105. Liu B, Poolman B, Boersma AJ. Ionic Strength Sensing in Living Cells. *ACS Chem Biol.* 2017;12(10):2510-2514. doi:10.1021/acschembio.7b00348
106. Sims PJ, Waggoner AS, Wang CH, Hoffman JF. Studies on the mechanism by which cyanine dyes measure membrane potential in red blood cells and phosphatidylcholine vesicles. *Biochemistry.* 1974;13(16):3315-3330. doi:10.1021/bi00713a022
107. Apell HJ, Bersch B. Oxonol VI as an optical indicator for membrane potentials in lipid vesicles. *Biochim Biophys Acta.* 1987;903(3):480-494. doi:10.1016/0005-2736(87)90055-1
108. Kuimova MK. Mapping viscosity in cells using molecular rotors. *Physical Chemistry Chemical Physics.* 2012;14(37):12671-12686. doi:10.1039/c2cp41674c
109. Lee SC, Heo J, Woo HC, et al. Fluorescent Molecular Rotors for Viscosity Sensors. *Chemistry.* 2018;24(52):13706-13718. doi:10.1002/chem.201801389
110. Shen Y, Wu SY, Rancic V, et al. Genetically encoded fluorescent indicators for imaging intracellular potassium ion concentration. *Commun Biol.* 2019;2(1):1-10. doi:10.1038/s42003-018-0269-2
111. Minta A, Tsien RY. Fluorescent indicators for cytosolic sodium. *J Biol Chem.* 1989;264(32):19449-19457. doi:10.1016/s0021-9258(19)47321-3

112. Szmacinski H, Lakowicz JR. Sodium Green as a potential probe for intracellular sodium imaging based on fluorescence lifetime. *Anal Biochem*. 1997;250(2):131-138. doi:10.1006/abio.1997.2203
113. Meier SD, Kovalchuk Y, Rose CR. Properties of the new fluorescent Na⁺ indicator CoroNa Green: comparison with SBFI and confocal Na⁺ imaging. *J Neurosci Methods*. 2006;155(2):251-259. doi:10.1016/j.jneumeth.2006.01.009
114. Miyawaki A, Llopis J, Heim R, et al. Fluorescent indicators for Ca²⁺ based on green fluorescent proteins and calmodulin. *Nature*. 1997;388(6645):882-887. doi:10.1038/42264
115. Nagai T, Sawano A, Park ES, Miyawaki A. Circularly permuted green fluorescent proteins engineered to sense Ca²⁺. *Proc Natl Acad Sci U S A*. 2001;98(6):3197-3202. doi:10.1073/pnas.051636098
116. Grynkiewicz G, Poenie M, Tsien RY. A new generation of Ca²⁺ indicators with greatly improved fluorescence properties. *J Biol Chem*. 1985;260(6):3440-3450. doi:3838314
117. van der Heide T, Stuart MC, Poolman B. On the osmotic signal and osmosensing mechanism of an ABC transport system for glycine betaine. *EMBO J*. 2001;20(24):7022-7032. doi:10.1093/emboj/20.24.7022
118. Nagai T, Ibata K, Park ES, Kubota M, Mikoshiba K, Miyawaki A. A variant of yellow fluorescent protein with fast and efficient maturation for cell-biological applications. *Nat Biotechnol*. 2002;20(1):87-90. doi:10.1038/nbt0102-87
119. Shaner NC, Lin MZ, McKeown MR, et al. Improving the photostability of bright monomeric orange and red fluorescent proteins. *Nat Methods*. 2008;5(6):545-551. doi:10.1038/nmeth.1209
120. Tsutsui H, Karasawa S, Okamura Y, Miyawaki A. Improving membrane voltage measurements using FRET with new fluorescent proteins. *Nat Methods*. 2008;5(8):683-685. doi:10.1038/nmeth.1235
121. Goedhart J, von Stetten D, Noirclerc-Savoye M, et al. Structure-guided evolution of cyan fluorescent proteins towards a quantum yield of 93%. *Nat Commun*. 2012;3:751. doi:10.1038/ncomms1738
122. Shaner NC, Campbell RE, Steinbach PA, Giepmans BNG, Palmer AE, Tsien RY. Improved monomeric red, orange and yellow fluorescent proteins derived

- from *Discosoma* sp. red fluorescent protein. *Nat Biotechnol.* 2004;22(12):1567-1572. doi:10.1038/nbt1037
123. Patterson G, Day RN, Piston D. Fluorescent protein spectra. *J Cell Sci.* 2001;114(Pt 5):837-838.
124. Roberts TM, Rudolf F, Meyer A, et al. Identification and Characterisation of a pH-stable GFP. *Sci Rep.* 2016;6:28166. doi:10.1038/srep28166
125. Griesbeck O, Baird GS, Campbell RE, Zacharias DA, Tsien RY. Reducing the environmental sensitivity of yellow fluorescent protein. Mechanism and applications. *Journal of Biological Chemistry.* 2001;276(31):29188-29194. doi:10.1074/jbc.M102815200
126. Zapata-Hommer O, Griesbeck O. Efficiently folding and circularly permuted variants of the Sapphire mutant of GFP. *BMC Biotechnol.* 2003;3:5. doi:10.1186/1472-6750-3-5
127. Markwardt ML, Kremers GJ, Kraft CA, et al. An improved cerulean fluorescent protein with enhanced brightness and reduced reversible photoswitching. *PLoS One.* 2011;6(3):e17896. doi:10.1371/journal.pone.0017896
128. Lam AJ, St-Pierre F, Gong Y, et al. Improving FRET dynamic range with bright green and red fluorescent proteins. *Nat Methods.* 2012;9(10):1005-1012. doi:10.1038/nmeth.2171
129. Mitchell P. Coupling of phosphorylation to electron and hydrogen transfer by a chemi-osmotic type of mechanism. *Nature.* 1961;191:144-148. doi:10.1038/191144a0
130. Sikkema HR, Gaastra BF, Pols T, Poolman B. Cell Fuelling and Metabolic Energy Conservation in Synthetic Cells. *ChemBioChem.* Published online 2019:1-13. doi:10.1002/cbic.201900398
131. Dimroth P. Characterization of a membrane-bound biotin-containing enzyme: oxaloacetate decarboxylase from *Klebsiella aerogenes*. *Eur J Biochem.* 1981;115(2):353-358. doi:10.1111/j.1432-1033.1981.tb05245.x
132. Cox DJ, Henick-Kling T. Chemiosmotic energy from malolactic fermentation. *J Bacteriol.* 1989;171(10):5750-5752. doi:10.1128/jb.171.10.5750-5752.1989
133. Renault P, Gaillardin C, Heslot H. Role of malolactic fermentation in lactic acid bacteria. *Biochimie.* 1988;70(3):375-379. doi:10.1016/0300-9084(88)90210-6

134. Olsen EB, Russell JB, Henick-Kling T. Electrogenic L-malate transport by *Lactobacillus plantarum*: a basis for energy derivation from malolactic fermentation. *J Bacteriol.* 1991;173(19):6199-6206. doi:10.1128/jb.173.19.6199-6206.1991
135. Battermann G, Radler F. A comparative study of malolactic enzyme and malic enzyme of different lactic acid bacteria. *Can J Microbiol.* 1991;37(3):211-217. doi:10.1139/m91-032
136. Bandell M, Ansanay V, Rachidi N, Dequin S, Lolkema JS. Membrane potential-generating malate (MleP) and citrate (CitP) transporters of lactic acid bacteria are homologous proteins. Substrate specificity of the 2-hydroxycarboxylate transporter family. *J Biol Chem.* 1997;272(29):18140-18146. doi:10.1074/jbc.272.29.18140
137. Bandell M, Lolkema JS. Stereoselectivity of the membrane potential-generating citrate and malate transporters of lactic acid bacteria. *Biochemistry.* 1999;38(32):10352-10360. doi:10.1021/bi9907577
138. Bandell M, Lolkema JS. The conserved C-terminus of the citrate (CitP) and malate (MleP) transporters of lactic acid bacteria is involved in substrate recognition. *Biochemistry.* 2000;39(42):13059-13067. doi:10.1021/bi0011882
139. Wang P, Li A, Dong M, Fan M. Induction, purification and characterization of malolactic enzyme from *Oenococcus oeni* SD-2a. *European Food Research and Technology.* 2014;239(5):827-835. doi:10.1007/s00217-014-2276-y
140. Schümann C, Michlmayr H, del Hierro AM, et al. Malolactic enzyme from *Oenococcus oeni*: heterologous expression in *Escherichia coli* and biochemical characterization. *Bioengineered.* 2013;4(3):147-152. doi:10.4161/bioe.22988
141. Renault PP, Heslot H. Selection of *Streptococcus lactis* Mutants Defective in Malolactic Fermentation. *Appl Environ Microbiol.* 1987;53(2):320-324. doi:10.1128/aem.53.2.320-324.1987
142. Spettoli P, Nuti MP, Zamorani A. Properties of Malolactic Activity Purified from *Leuconostoc oenos* ML34 by Affinity Chromatography. *Appl Environ Microbiol.* 1984;48(4):900-901. doi:10.1128/aem.48.4.900-901.1984
143. Lonvaud-Funel A, de Saad AM. Purification and Properties of a Malolactic Enzyme from a Strain of *Leuconostoc mesenteroides* Isolated from Grapes. *Appl Environ Microbiol.* 1982;43(2):357-361. doi:10.1128/aem.43.2.357-361.1982

144. Geertsma ER, Poolman B. High-throughput cloning and expression in recalcitrant bacteria. *Nat Methods*. 2007;4(9):705-707. doi:10.1038/nmeth1073
145. Kuipers OP, de Ruyter PGGA, Kleerebezem M, de Vos WM. Quorum sensing-controlled gene expression in lactic acid bacteria. *J Biotechnol*. 1998;64(1):15-21. doi:10.1016/S0168-1656(98)00100-X
146. Schulz P, Garcia-Celma JJ, Fendler K. SSM-based electrophysiology. *Methods*. 2008;46(2):97-103. doi:10.1016/j.ymeth.2008.07.002
147. Pellegrini D, Onor M, Degano I, Bramanti E. Development and validation of a novel derivatization method for the determination of lactate in urine and saliva by liquid chromatography with UV and fluorescence detection. *Talanta*. 2014;130:280-287. doi:10.1016/j.talanta.2014.07.015
148. Pols T, Singh S, Deelman-Driessen C, Gaastra BF, Poolman B. Enzymology of the pathway for ATP production by arginine breakdown. *FEBS J*. Published online April 18, 2020;1-17. doi:10.1111/febs.15337
149. Biemans-Oldehinkel E, Mahmood NABN, Poolman B. A sensor for intracellular ionic strength. *Proc Natl Acad Sci U S A*. 2006;103(28):10624-10629. doi:10.1073/pnas.0603871103
150. Witkowska A, Jablonski L, Jahn R. A convenient protocol for generating giant unilamellar vesicles containing SNARE proteins using electroformation. *Sci Rep*. 2018;8(1):9422. doi:10.1038/s41598-018-27456-4
151. Bazzoni A, Barthmes M, Fendler K. *SSM-Based Electrophysiology for Transporter Research*. Vol 594. 1st ed. Elsevier Inc.; 2017. doi:10.1016/bs.mie.2017.05.008
152. Lee AG. How lipids affect the activities of integral membrane proteins. *Biochim Biophys Acta Biomembr*. 2004;1666(1-2):62-87. doi:10.1016/j.bbamem.2004.05.012
153. Konings WN. The cell membrane and the struggle for life of lactic acid bacteria. *Antonie Van Leeuwenhoek*. 2002;82(1-4):3-27. doi:10.1023/A:1020604203977
154. Kaim G, Dimroth P. ATP synthesis by F-type ATP synthase is obligatorily dependent on the transmembrane voltage. *EMBO J*. 1999;18(15):4118-4127. doi:10.1093/emboj/18.15.4118

155. Felle H, Porter JS, Slayman CL, Kaback HR. Quantitative measurements of membrane potential in *Escherichia coli*. *Biochemistry*. 1980;19(15):3585-3590. doi:10.1021/bi00556a026
156. Vacata V, Kotyk A, Sigler K. Membrane potentials in yeast cells measured by direct and indirect methods. *Biochim Biophys Acta*. 1981;643(1):265-268. doi:10.1016/0005-2736(81)90241-8
157. Stock D, Leslie AG, Walker JE. Molecular architecture of the rotary motor in ATP synthase. *Science*. 1999;286(5445):1700-1705. doi:10.1126/science.286.5445.1700
158. Vollmar M, Schlieper D, Winn M, Büchner C, Groth G. Structure of the c14 rotor ring of the proton translocating chloroplast ATP synthase. *Journal of Biological Chemistry*. 2009;284(27):18228-18235. doi:10.1074/jbc.M109.006916
159. Overath P, Keith Wright J. Lactose permease: a carrier on the move. *Trends Biochem Sci*. 1983;8(11):404-408. doi:10.1016/0968-0004(83)90305-5
160. West IC, Mitchell P. Stoichiometry of lactose-H⁺ symport across the plasma membrane of *Escherichia coli*. *Biochem J*. 1973;132(3):587-592. doi:10.1042/bj1320587
161. Gehrke CW, Nakamoto H, Zumwalt RW. Gas-liquid chromatography of protein amino acid trimethylsilyl derivatives. *J Chromatogr A*. 1969;45(1):24-51. doi:10.1016/S0021-9673(01)86179-3
162. Halket JM, Waterman D, Przyborowska AM, Patel RKP, Fraser PD, Bramley PM. Chemical derivatization and mass spectral libraries in metabolic profiling by GC/MS and LC/MS/MS. *J Exp Bot*. 2005;56(410):219-243. doi:10.1093/jxb/eri069
163. Sobolevsky TG, Revelsky AI, Miller B, Oriedo V, Chernetsova ES, Revelsky IA. Comparison of silylation and esterification/acylation procedures in GC-MS analysis of amino acids. *J Sep Sci*. 2003;26(17):1474-1478. doi:10.1002/jssc.200301492
164. Matsumura S, Kataoka H, Makita M. Capillary gas chromatographic analysis of protein amino acids as their N(O,S)-isobutoxycarbonyl methyl ester derivatives. *Biomed Chromatogr*. 1995;9(5):205-210. doi:10.1002/bmc.1130090503
165. MacKenzie SL, Tenaschuk D, Fortier G. Analysis of amino acids by gas-liquid chromatography as tert.-butyldimethylsilyl derivatives. Preparation of

- derivatives in a single reaction. *J Chromatogr.* 1987;387(C):241-253. doi:10.1016/S0021-9673(01)94528-5
166. Corso G, Esposito M, Gallo M, Russo A Dello, Antonio M. Transformation of arginine into ornithine during the preparation of its tert-butyldimethylsilyl derivative for analysis by gas chromatography/mass spectrometry. *Biol Mass Spectrom.* 1993;22(12):698-702. doi:10.1002/bms.1200221205
167. Smith PA, Villa V, King GL. Artifacts related to N-methyl-N-(tert-butyldimethylsilyl)trifluoroacetamide derivatization of citrulline revealed by gas chromatography-mass spectrometry using both electron and chemical ionization. *J Chromatogr A.* 2010;1217(33):5444-5448. doi:10.1016/j.chroma.2010.06.043
168. Takeuchi T. HPLC of Amino Acids as Dansyl and Dabsyl Derivatives. In: *Journal of Chromatography Library.* Vol 70. ; 2005:229-241. doi:10.1016/S0301-4770(05)80010-7
169. Poolman B, Driessen AJ, Konings WN. Regulation of arginine-ornithine exchange and the arginine deiminase pathway in *Streptococcus lactis*. *J Bacteriol.* 1987;169(12):5597-5604.
170. Ziegler J, Abel S. Analysis of amino acids by HPLC/electrospray negative ion tandem mass spectrometry using 9-fluorenylmethoxycarbonyl chloride (Fmoc-Cl) derivatization. *Amino Acids.* 2014;46(12):2799-2808. doi:10.1007/s00726-014-1837-5
171. Gómez-Alonso S, Hermosín-Gutiérrez I, García-Romero E. Simultaneous HPLC analysis of biogenic amines, amino acids, and ammonium ion as aminoenone derivatives in wine and beer samples. *J Agric Food Chem.* 2007;55(3):608-613. doi:10.1021/jf062820m
172. Rebane R, Oldekop ML, Herodes K. Comparison of amino acid derivatization reagents for LC-ESI-MS analysis. Introducing a novel phosphazene-based derivatization reagent. *J Chromatogr B Analyt Technol Biomed Life Sci.* 2012;904:99-106. doi:10.1016/j.jchromb.2012.07.029
173. Mawhinney TP, Robinett RS, Atalay A, Madson M a. Analysis of amino acids as their tert.-butyldimethylsilyl derivatives by gas-liquid chromatography and mass spectrometry. *J Chromatogr.* 1986;358(1):231-242. doi:10.1016/S0021-9673(01)90333-4
174. Chaves Das Neves HJ, Vasconcelos AM. Capillary gas chromatography of amino acids, including asparagine and glutamine: sensitive gas chromatographic-

- mass spectrometric and selected ion monitoring gas chromatographic-mass spectrometric detection of the N,O(S)-tert.-butyldimethylsilyl derivativ. *J Chromatogr.* 1987;392(C):249-258. doi:10.1016/s0021-9673(01)94270-0
175. Molnár-Perl I, Katona ZsF. GC-MS of amino acids as their trimethylsilyl/t-butylidemethylsilyl Derivatives: In model solutions III. *Chromatographia.* 2000;51(1):S228-S236. doi:10.1007/BF02492811
176. McGaw EA, Phinney KW, Lowenthal MS. Comparison of orthogonal liquid and gas chromatography-mass spectrometry platforms for the determination of amino acid concentrations in human plasma. *J Chromatogr A.* 2010;1217(37):5822-5831. doi:10.1016/j.chroma.2010.07.025
177. Pudlik AM, Lolkema JS. Rerouting citrate metabolism in *lactococcus lactis* to citrate-driven transamination. *Appl Environ Microbiol.* 2012;78(18):6665-6673. doi:10.1128/AEM.01811-12
178. Zamboni N, Fendt SM, Rühl M, Sauer U. ¹³C-based metabolic flux analysis. *Nat Protoc.* 2009;4(6):878-892. doi:10.1038/nprot.2009.58
179. Wood PL, Khan MA, Moskal JR. Neurochemical analysis of amino acids, polyamines and carboxylic acids: GC-MS quantitation of tBDMS derivatives using ammonia positive chemical ionization. *J Chromatogr B Analyt Technol Biomed Life Sci.* 2006;831(1-2):313-319. doi:10.1016/j.jchromb.2005.12.031
180. Blain JC, Szostak JW. Progress toward synthetic cells. *Annu Rev Biochem.* 2014;83(February):615-640. doi:10.1146/annurev-biochem-080411-124036
181. Luisi PL, Ferri F, Stano P. Approaches to semi-synthetic minimal cells: a review. *Naturwissenschaften.* 2006;93(1):1-13. doi:10.1007/s00114-005-0056-z
182. Forster AC, Church GM. Towards synthesis of a minimal cell. *Mol Syst Biol.* 2006;2. doi:10.1038/msb4100090
183. Hoshika S, Leal NA, Kim MJ, et al. Hachimoji DNA and RNA: A genetic system with eight building blocks. *Science (1979).* 2019;363(6429):884-887. doi:10.1126/science.aat0971
184. van Nies P, Westerlaken I, Blanken D, Salas M, Mencía M, Danelon C. Self-replication of DNA by its encoded proteins in liposome-based synthetic cells. *Nat Commun.* 2018;9(1):1583. doi:10.1038/s41467-018-03926-1

185. Swank Z, Laohakunakorn N, Maerkl SJ. Cell-free gene-regulatory network engineering with synthetic transcription factors. *Proc Natl Acad Sci U S A*. 2019;116(13):5892-5901. doi:10.1073/pnas.1816591116
186. Ichihashi N, Usui K, Kazuta Y, Sunami T, Matsuura T, Yomo T. Darwinian evolution in a translation-coupled RNA replication system within a cell-like compartment. *Nat Commun*. 2013;4:2494. doi:10.1038/ncomms3494
187. Kuruma Y, Stano P, Ueda T, Luisi PL. A synthetic biology approach to the construction of membrane proteins in semi-synthetic minimal cells. *Biochim Biophys Acta*. 2009;1788(2):567-574. doi:10.1016/j.bbamem.2008.10.017
188. Osawa M, Erickson HP. Liposome division by a simple bacterial division machinery. *Proc Natl Acad Sci U S A*. 2013;110(27):11000-11004. doi:10.1073/pnas.1222254110
189. Terasawa H, Nishimura K, Suzuki H, Matsuura T, Yomo T. Coupling of the fusion and budding of giant phospholipid vesicles containing macromolecules. *Proc Natl Acad Sci U S A*. 2012;109(16):5942-5947. doi:10.1073/pnas.1120327109
190. Karzbrun E, Tayar AM, Noireaux V, Bar-Ziv RH. Synthetic biology. Programmable on-chip DNA compartments as artificial cells. *Science*. 2014;345(6198):829-832. doi:10.1126/science.1255550
191. Sokolova E, Spruijt E, Hansen MMK, et al. Enhanced transcription rates in membrane-free protocells formed by coacervation of cell lysate. *Proc Natl Acad Sci U S A*. 2013;110(29):11692-11697. doi:10.1073/pnas.1222321110
192. Zepik HH, Blöchliger E, Luisi PL. A Chemical Model of Homeostasis. *Angew Chem Int Ed Engl*. 2001;40(1):199-202. doi:10.1002/1521-3773(20010105)40:1<199::AID-ANIE199>3.0.CO;2-H
193. Morrow SM, Colomer I, Fletcher SP. A chemically fuelled self-replicator. *Nat Commun*. 2019;10(1):1011. doi:10.1038/s41467-019-08885-9
194. Shimizu Y, Inoue A, Tomari Y, et al. Cell-free translation reconstituted with purified components. *Nat Biotechnol*. 2001;19(8):751-755. doi:10.1038/90802
195. Noireaux V, Libchaber A. A vesicle bioreactor as a step toward an artificial cell assembly. *Proc Natl Acad Sci U S A*. 2004;101(51):17669-17674. doi:10.1073/pnas.0408236101

196. Schwander T, Schada von Borzyskowski L, Burgener S, Cortina NS, Erb TJ. A synthetic pathway for the fixation of carbon dioxide in vitro. *Science*. 2016;354(6314):900-904. doi:10.1126/science.aah5237
197. Patel A, Malinovska L, Saha S, et al. ATP as a biological hydrotrope. *Science*. 2017;356(6339):753-756. doi:10.1126/science.aaf6846
198. Novák L, Zubáčová Z, Karnkowska A, et al. Arginine deiminase pathway enzymes: evolutionary history in metamonads and other eukaryotes. *BMC Evol Biol*. 2016;16(1):197. doi:10.1186/s12862-016-0771-4
199. Noens EEE, Kaczmarek MB, Źygo M, Lolkema JS. ArcD1 and ArcD2 Arginine/Ornithine Exchangers Encoded in the Arginine Deiminase Pathway Gene Cluster of *Lactococcus lactis*. *J Bacteriol*. 2015;197(22):3545-3553. doi:10.1128/JB.00526-15
200. Bates RG, Pinching GD. Acidic dissociation constant of ammonium ion at 0 to 50 C, and the base strength of ammonia. *J Res Natl Bur Stand* (1934). 1949;42(5):419. doi:10.6028/jres.042.037
201. Record MT, Courtenay ES, Cayley DS, Guttmann HJ. Responses of *E. coli* to osmotic stress: large changes in amounts of cytoplasmic solutes and water. *Trends Biochem Sci*. 1998;23(4):143-148. doi:10.1016/s0968-0004(98)01196-7
202. Wood JM. Bacterial osmoregulation: a paradigm for the study of cellular homeostasis. *Annu Rev Microbiol*. 2011;65(1):215-238. doi:10.1146/annurev-micro-090110-102815
203. Bourot S, Sire O, Trautwetter A, et al. Glycine betaine-assisted protein folding in a lysA mutant of *Escherichia coli*. *J Biol Chem*. 2000;275(2):1050-1056. doi:10.1074/jbc.275.2.1050
204. Stadtmiller SS, Gorensek-Benitez AH, Guseman AJ, Pielak GJ. Osmotic Shock Induced Protein Destabilization in Living Cells and Its Reversal by Glycine Betaine. *J Mol Biol*. 2017;429(8):1155-1161. doi:10.1016/j.jmb.2017.03.001
205. Berntsson RPA. *Structure and Function of Substrate-Binding Domains of ABC-Transporters*. Thesis. University of Groningen; 2010.
206. Nørholm MHH. A mutant Pfu DNA polymerase designed for advanced uracil-excision DNA engineering. *BMC Biotechnol*. 2010;10:21. doi:10.1186/1472-6750-10-21

207. Knipp M, Vasák M. A colorimetric 96-well microtiter plate assay for the determination of enzymatically formed citrulline. *Anal Biochem*. 2000;286(2):257-264. doi:10.1006/abio.2000.4805
208. Slotboom DJ, Duurkens RH, Olieman K, Erkens GB. Static light scattering to characterize membrane proteins in detergent solution. *Methods*. 2008;46(2):73-82. doi:10.1016/j.ymeth.2008.06.012
209. Stuart MCA, Boekema EJ. Two distinct mechanisms of vesicle-to-micelle and micelle-to-vesicle transition are mediated by the packing parameter of phospholipid-detergent systems. *Biochim Biophys Acta*. 2007;1768(11):2681-2689. doi:10.1016/j.bbamem.2007.06.024
210. Finkelstein A. Distinguished Lectures Series of the Society of General Physiologists. 1987;4.
211. Rath A, Glibowicka M, Nadeau VG, Chen G, Deber CM. Detergent binding explains anomalous SDS-PAGE migration of membrane proteins. *Proc Natl Acad Sci U S A*. 2009;106(6):1760-1765. doi:10.1073/pnas.0813167106
212. Okuno D, Iino R, Noji H. Rotation and structure of FoF1-ATP synthase. *J Biochem*. 2011;149(6):655-664. doi:10.1093/jb/mvr049
213. Maloney PC, Kashket ER, Wilson TH. A protonmotive force drives ATP synthesis in bacteria. *Proc Natl Acad Sci U S A*. 1974;71(10):3896-3900. doi:10.1073/pnas.71.10.3896
214. Laubinger W, Dimroth P. Characterization of the ATP synthase of Propionigenium modestum as a primary sodium pump. *Biochemistry*. 1988;27(19):7531-7537. doi:10.1021/bi00419a053
215. Lassen UV, Sten-Knudsen O. Direct measurements of membrane potential and membrane resistance of human red cells. *J Physiol*. 1968;195(3):681-696. doi:10.1113/jphysiol.1968.sp008482
216. Lolkema JS, Abbing A, Hellingwerf KJ, Konings WN. The transmembrane electrical potential in Rhodopseudomonas sphaeroides determined from the distribution of tetraphenylphosphonium after correction for its binding to cell components. *Eur J Biochem*. 1983;130(2):287-292. doi:10.1111/j.1432-1033.1983.tb07149.x
217. Lim TS, Dávila A, Wallace DC, Burke P. Assessment of mitochondrial membrane potential using an on-chip microelectrode in a microfluidic device. *Lab Chip*. 2010;10(13):1683-1688. doi:10.1039/c001818j

218. Waggoner A. Optical probes of membrane potential. *J Membr Biol.* 1976;27(4):317-334. doi:10.1007/BF01869143
219. Cohen LB, Salzberg BM. Optical measurement of membrane potential. *Rev Physiol Biochem Pharmacol.* 1978;83:35-88. doi:10.1007/3-540-08907-1_2
220. Loew LM, Simpson LL. Charge-shift probes of membrane potential: a probable electrochromic mechanism for p-aminostyrylpyridinium probes on a hemispherical lipid bilayer. *Biophys J.* 1981;34(3):353-365. doi:10.1016/S0006-3495(81)84854-0
221. Fluhler E, Burnham VG, Loew LM. Spectra, membrane binding, and potentiometric responses of new charge shift probes. *Biochemistry.* 1985;24(21):5749-5755. doi:10.1021/bi00342a010
222. Clarke RJ. Electric Field Sensitive Dyes. In: Demchenko A. (Eds) *Advanced Fluorescence Reporters in Chemistry and Biology I.*; 2010:331-344. doi:10.1007/978-3-642-04702-2_10
223. Cabrini G, Verkman AS. Potential-sensitive response mechanism of diS-C3-(5) in biological membranes. *J Membr Biol.* 1986;92(2):171-182. doi:10.1007/BF01870706
224. Guillet EG, Kimmich GA. DiO-C3-(5) and DiS-C3-(5): Interactions with RBC, ghosts and phospholipid vesicles. *J Membr Biol.* 1981;59(1):1-11. doi:10.1007/BF01870815
225. Síp M, Herman P, Plásek J, Hrouda V. Transmembrane potential measurement with carbocyanine dye dis-C3-(5): fast fluorescence decay studies. *J Photochem Photobiol B.* 1990;4(3):321-328. doi:10.1016/1011-1344(90)85037-w
226. Ivkova MN, Pechatnikov VA, Ivkov VG. Mechanism of fluorescent response of the probe diS-C3-(5) to transmembrane potential changes in a lecithin vesicle suspension. *Gen Physiol Biophys.* 1984;3(2):97-117.
227. Hladky SB, Rink TJ. Potential difference and the distribution of ions across the human red blood cell membrane; a study of the mechanism by which the fluorescent cation, diS-C3-(5) reports membrane potential. *J Physiol.* 1976;263(2):287-319. doi:10.1113/jphysiol.1976.sp011632
228. Tsien RY, Hladky SB. A quantitative resolution of the spectra of a membrane potential indicator, diS-C3-(5), bound to cell components and to red blood cells. *J Membr Biol.* 1978;38(1-2):73-97. doi:10.1007/BF01875163

229. Farrelly E, Amaral MC, Marshall L, Huang SG. A high-throughput assay for mitochondrial membrane potential in permeabilized yeast cells. *Anal Biochem*. 2001;293(2):269-276. doi:10.1006/abio.2001.5139
230. López-González I, Torres-Rodríguez P, Sánchez-Carranza O, et al. Membrane hyperpolarization during human sperm capacitation. *Mol Hum Reprod*. 2014;20(7):619-629. doi:10.1093/molehr/gau029
231. Rivett DE, Kirkpatrick A, Hewish DR, Reilly W, Werkmeister JA. Dimerization of truncated melittin analogues results in cytolytic peptides. *Biochemical Journal*. 1996;316(2):525-529. doi:10.1042/bj3160525
232. Friedhoff LT, Sonenberg M. The membrane potential of human platelets. *Blood*. 1983;61(1):180-185.
233. Omardien S, Drijfhout JW, Vaz FM, et al. Bactericidal activity of amphipathic cationic antimicrobial peptides involves altering the membrane fluidity when interacting with the phospholipid bilayer. *Biochim Biophys Acta Biomembr*. 2018;1860(11):2404-2415. doi:10.1016/j.bbamem.2018.06.004
234. Sautrey G, El Khoury M, Giro Dos Santos A, et al. Negatively charged lipids as a potential target for new amphiphilic aminoglycoside antibiotics: A biophysical study. *Journal of Biological Chemistry*. 2016;291(26):13864-13874. doi:10.1074/jbc.M115.665364
235. Morin N, Lanneluc I, Connil N, Cottenceau M, Pons AM, Sablé S. Mechanism of bactericidal activity of microcin L in *Escherichia coli* and *Salmonella enterica*. *Antimicrob Agents Chemother*. 2011;55(3):997-1007. doi:10.1128/AAC.01217-10
236. Torrent M, de la Torre BG, Nogués VM, Andreu D, Boix E. Bactericidal and membrane disruption activities of the eosinophil cationic protein are largely retained in an N-terminal fragment. *Biochem J*. 2009;421(3):425-434. doi:10.1042/BJ20082330
237. Wu M, Maier E, Benz R, Hancock REW. Mechanism of interaction of different classes of cationic antimicrobial peptides with planar bilayers and with the cytoplasmic membrane of *Escherichia coli*. *Biochemistry*. 1999;38(22):7235-7242. doi:10.1021/bi9826299
238. Strahl H, Hamoen LW. Membrane potential is important for bacterial cell division. *Proc Natl Acad Sci U S A*. 2010;107(27):12281-12286. doi:10.1073/pnas.1005485107

239. Brooijmans RJW, Poolman B, Schuurman-Wolters GK, De Vos WM, Hugenholtz J. Generation of a membrane potential by *Lactococcus lactis* through aerobic electron transport. *J Bacteriol.* 2007;189(14):5203-5209. doi:10.1128/JB.00361-07
240. Trip H, Mulder NL, Lolkema JS. Improved acid stress survival of *Lactococcus lactis* expressing the histidine decarboxylation pathway of *Streptococcus thermophilus* CHCC1524. *J Biol Chem.* 2012;287(14):11195-11204. doi:10.1074/jbc.M111.330704
241. Kumazawa T, Nomura T, Kurihara K. Liposomes as model for taste cells: receptor sites for bitter substances including N-C=S substances and mechanism of membrane potential changes. *Biochemistry.* 1988;27(4):1239-1244. doi:10.1021/bi00404a025
242. Ramos H, Valdivieso E, Gamargo M, Dagger F, Cohen BE. Amphotericin B kills unicellular leishmanias by forming aqueous pores permeable to small cations and anions. *J Membr Biol.* 1996;152(1):65-75. doi:10.1007/s002329900086
243. Fristedt U, van Der Rest M, Poolman B, Konings WN, Persson BL. Studies of cytochrome c oxidase-driven H(+) -coupled phosphate transport catalyzed by the *Saccharomyces cerevisiae* Pho84 permease in coreconstituted vesicles. *Biochemistry.* 1999;38(48):16010-16015. doi:10.1021/bi991545c
244. Markones M, Fippel A, Kaiser M, Drechsler C, Hunte C, Heerklotz H. Stairway to Asymmetry: Five Steps to Lipid-Asymmetric Proteoliposomes. *Biophys J.* 2020;118(2):294-302. doi:10.1016/j.bpj.2019.10.043
245. Alvarez-Bustamante JA, Lemeshko V V. Computational models for monitoring the trans-membrane potential with fluorescent probes: the DiSC3(5) case. *Eur Biophys J.* 2016;45(8):815-830. doi:10.1007/s00249-016-1126-1

