Chapter 6

Membrane Protein Production in Lactococcus lactis for Functional Studies

Daphne Seigneurin-Berny, Martin S. King, Emiline Sautron, Lucas Moyet, Patrice Catty, François André, Norbert Rolland, Edmund R.S. Kunji, and Annie Frelet-Barrand

Abstract

Due to their unique properties, expression and study of membrane proteins in heterologous systems remains difficult. Among the bacterial systems available, the Gram-positive lactic bacterium, *Lactococcus lactis*, traditionally used in food fermentations, is nowadays widely used for large-scale production and functional characterization of bacterial and eukaryotic membrane proteins. The aim of this chapter is to describe the different possibilities for the functional characterization of peripheral or intrinsic membrane proteins expressed in *Lactococcus lactis*.

Key words Lactococcus lactis, Membrane proteins, Expression, Transport assays

1 Introduction

In the past decades, Lactococcus lactis, a Gram-positive bacterium traditionally used in food fermentations, has emerged as a useful system for functional expression of prokaryotic and eukaryotic membrane proteins (MPs) [1]. L. lactis is an attractive alternative host for Escherichia coli, especially for eukaryotic MPs, because of (1) its moderate proteolytic activity, (2) the absence of inclusion body formation and endotoxin production [2, 3], (3) the efficient targeting of MPs into a single glycolipid cytoplasmic membrane [2, 4, 5], and (4) its ability to express MPs in their oligomeric state [2, 6]. This facultative anaerobe-aerobe lactic acid bacterium (LAB) grows at 30 °C with a doubling time of 35–60 min [7]; it is easy and inexpensive to grow and genetic methods and vector systems are well developed [8]. In addition to the classical cloning techniques, different strategies have been developed to obtain a larger number of recombinant clones [9, 10].

Isabelle Mus-Veteau (ed.), Heterologous Expression of Membrane Proteins: Methods and Protocols, Methods in Molecular Biology, vol. 1432, DOI 10.1007/978-1-4939-3637-3_6, © Springer Science+Business Media New York 2016

The expression of heterologous proteins in L. lactis has been facilitated both by advances in genetic methods and by new developments in molecular biology techniques. Using these tools, various vectors containing either constitutive or inducible promoters have been developed to obtain increased levels of proteins and to control their production. They currently constitute the basis of all expression systems in L. lactis [11]. The tightly regulated nisincontrolled gene expression (NICE) system is the most commonly used [12]. This promising and powerful expression system is based on genes involved in the biosynthesis and regulation of the antimicrobial peptide, nisin. When a gene of interest is placed upstream of the inducible promoter PnisA on a plasmid, its expression can be induced by the addition of subinhibitory amounts of nisin (0.1-5)ng/mL) to the culture medium [13]. The NICE system has proved to be highly versatile and is widely used in pharmaceutical, medical, and bio- and food-technology applications [14]. This wellcharacterized system is nowadays widely used for functional studies of homologously and heterologously expressed soluble and membrane proteins from diverse origins (prokaryotic or eukaryotic), topologies, and sizes (for reviews, see [1] and [14]). Moreover, in the last years, three structures have been obtained after expression of MPs using the NICE system [15-17] as well as several domain structures of human membrane proteins [18, 19].

In this chapter, we will give some examples of eukaryotic MPs for which functional analysis has been carried out after their expression in *L. lactis* using the NICE system. These functional characterizations can be performed on: (1) whole-cell bacteria, (2) membrane extracts, (3) fused membrane vesicles, (4) proteoliposomes after reconstitution of the MPs in phospholipids, using radioactive substrates, or (5) directly solubilized and purified membrane proteins [2, 3, 10, 12, 18, 19].

2 Materials

2.1 Growth of Recombinant Bacteria and Expression of the Proteins of Interest

- 1. Lactococcus lactis NZ9000 and nisin-producing NZ9700 strains (NIZO; see Notes 1 and 2).
- 2. M171GChl medium: M17 broth, 1% [w/v] glucose, 10 μg mL⁻¹ chloramphenicol (*see* Note 3).
- 3. Laboratory glassware bottles (Schott bottles).
- 4. Incubator for cell growth.
- 5. Appropriate buffers for bacterial resuspension (see Note 4).
- 2.2 Isolation
 of Lactococcal
 Membranes
 with the Cell Disruptor
- 1. One Shot (Constant Cell Disruption Systems, Northants, UK) (see Note 5).
- 2. Appropriate buffers for protein resuspension (see Note 4).

2.3 SDS-PAGE and Detection of Recombinant Protein

- 1. Acrylamide-bis ready-to-use solution, 30% [w/v] (37.5:1).
- 2. 8× Laemmli resolving gel buffer: 3 M Tris–HCl pH 8.8 (60.6 g Tris–HCl resuspended in Milli-Q water; adjust to pH 8.8 at 25 °C with 12 N HCl. Store at room temperature).
- 3. 4× Laemmli stacking gel buffer: 0.5 M Tris–HCl pH 6.8 (363 g Tris–HCl resuspended in Milli-Q water; adjust to pH 6.8 at 25 °C with 12 N HCl. Store at room temperature).
- 4. Aqueous solution 20% [w/v] sodium dodecyl sulfate (SDS).
- 5. Ammonium persulfate: Prepare 10% [w/v] solution in water and immediately freeze in single-use (200 μ L) aliquots at -20 °C.
- 6. Tetramethylethylenediamine (TEMED).
- 7. Resolving gels (10% acrylamide): 3.3 mL of 30% [w/v] acrylamide solution, 1.25 mL of 8x Laemmli resolving gel buffer, 50 μ L of 20% [w/v] SDS, 5.3 mL of water, 10 μ L of TEMED, and 100 μ L of 10% [w/v] ammonium persulfate (see Note 6).
- 8. Stacking gels (5% [w/v] acrylamide): 2.8 mL of 30% [w/v] acrylamide solution, 1.25 mL of 4× Laemmli stacking gel buffer, 25 μ L of SDS 20% [w/v], 2.8 mL of water, 5 μ L of TEMED, and 50 μ L of 10% [w/v] ammonium persulfate.
- 9. Lacmmli running buffer (10×): For 1 L, 144.2 g of glycine (192 mM), 30.3 g of Tris–HCl (25 mM); add 50 mL of 20% [w/v] SDS (0.1% final concentration) and Milli-Q water. Store at room temperature.
- 10. Molecular weight marker.
- 11. Reducing sample buffer (4×): 0.08 M Tris–HCl, pH 6.8, 40% [v/v] glycerol, 1% [w/v] SDS, 0.1 mM bromophenol blue, 10 mM dithiothreitol. Store at -20 °C.
- 12. Sample buffer: 100 mL reducing buffer and 20 mL of 20% [w/v] SDS.
- 13. Control protein: Recombinant *Strep*-tag II fusion protein, MW about 28 kDa (0.1 mg mL⁻¹) (IBA, Goettingen, Germany).
- 14. System for protein transfer to nitrocellulose membranes (central core assembly, holder cassette, nitrocellulose filter paper, fibber pads, and cooling unit).
- 15. Protein transfer buffer: dilute running buffer $1 \times$ with ethanol to a final concentration of 20% [v/v]. Store at 4 °C.
- 16. Nitrocellulose or polyvinylidene difluoride (PVDF) membranes.
- 17. 3 MM paper from Whatman.
- 18. Protein-specific antibody or conjugate specific to the affinity tag (see Note 7).
- 19. Bio-Safe Coomassie (Biorad).
- 20. Electrochemiluminescence (ECL) detection kit.

2.4 Functional Characterization of Membrane Proteins Expressed in L. lactis

2.4.1 Dehydrogenase Assay on Purified Protein (ceQORH)

- 1. Solubilization buffer: 50 mM MOPS pH 7.8 containing 0.5 or 1 M NaCl.
- 2. 10 mM Tris-HCl pH 8.0.
- 3. Ni-NTA resin (Qiagen).
- 4. Binding buffer: 5 mM imidazole, 0.5 M NaCl, 20 mM Tris-HCl pH 7.9.
- 5. Wash buffer: 60 mM imidazole, 0.5 M NaCl, 20 mM Tris-HCl pH 7.9.
- 6. Elution buffer: 0.5 M imidazole, 0.25 M NaCl, 10 mM Tris-HCl pH 7.9.
- 7. Dehydrogenase reaction buffer: 100 μ M NADPH, 100 μ M nitroblue tetrazolium (NBT), 10 mM Tris-HCl pH 8.0.
- 8. PD10 column (GE Healthcare).
- 9. Eppendorf centrifuge.
- 10. Lipids (P3644, Sigma).
- 11. Spectrophotometer.

2.4.2 Phosphorylation Assays with AtHMA6 and AtHMA8 Using L. lactis Membranes

- 1. ATP phosphorylation buffer: 20 mM Hepes pH 7.0, 100 mM KCl, 5 mM MgCl₂, 300 mM sucrose (*see* **Note 8**).
- 2. Pi phosphorylation buffer: 20 mM Hepes pH 6.0, 10 mM MgCl₂, 20% [v/v] DMSO (see Note 9).
- 3. Metal solutions: prepare solutions at concentration ranging from 1 to 100 μ M in phosphorylation buffer or water (see Note 10).
- 4. 1 mM 32 Pi (10–100 μ Ci nmol $^{-1}$, Perkin Elmer, 7 μ L): Add 1 mL of 1 mM 32 Po (prepared in 100 mM Hepes pH 5.6) directly in the tube containing the isotope 32 Pi. Filter the solution through a 0.2 μ m membrane. To avoid loss of the solution in the filter, push the volume of the solution stayed in the filter using an empty syringe. Use 10 μ L/reaction. Store at 4 $^{\circ}$ C.
- 5. $10~\mu M~[\gamma^{-32}P]ATP~(50-500~\mu Ci~nmol^{-1}, Perkin~Elmer, 7~\mu L)$: for 10~reactions, add $1~\mu L~of~[\gamma^{-32}P]ATP~to~110~\mu L~of~a~solution~of~10~\mu M~ATP~(see~Note~11)$. Prepare a stock solution of 400 mM ATP in H_2O , aliquot in small volumes, and store at $-20~^{\circ}C$. $10~\mu M~ATP$ is prepared freshly from one stored aliquot of 400 mM ATP.
- 6. Stop buffer: 1 mM KH₂PO₄ in 7% [v/v] trichloroacetic acid (TCA). Store at 4 °C.
- 7. Denaturing buffer: 5 mM Tris-PO₄ pH 5.0, 6.7 mM urea, 400 mM DTT, 5% [w/v] SDS, 0.004% [w/v] orange G (see Note 12).
- 8. Chelator mix: 1 mM bicinchoninic acid (BCA) and 100 μM bathocuproine disulfonate (BCS) (see Note 13).

- 9. Resolving gel: 6 mL of Acrylamide/Bis 24/0.8% [w/v] solution (see Note 14), 4.5 mL of 4× resolving gel buffer (260 mM Tris-H₃PO₄ pH 6.5, 0.4% SDS), 7.4 mL of H₂O, 18 μL of TEMED, and 100 μL of 10% [w/v] ammonium persulfate.
- 10. Stacking gel: 1.2 mL of Acrylamide/Bis 24/0.8% [v/v] solution, 2 mL of 4× stacking gel buffer (260 mM Tris- H_3PO_4 pH 5.5, 0.4% SDS), 4.64 mL of H_2O , 7.5 μ L of TEMED, and 160 μ L of 10% [w/v] ammonium persulfate.
- 11. Running buffer: 0.17 mM MOPS (pH 6.0 adjusted with 2 M Tris), 0.1% [w/v] SDS. Store at 4 °C before use (do not store for more than 1 week) (*see* Note 15).
- 12. Acetic acid 15% [v/v].
- 13. Gel staining medium: acetic acid/isopropanol/water, 10/25/65 [v/v/v], supplemented with 2.5 g.L⁻¹ of Coomassie Brilliant Blue R250.
- 14. Gel destaining medium: 30% [v/v] ethanol.
- 15. Eppendorf centrifuge.
- 16. Gel electrophoresis apparatus (Bio-Rad Protean 3 or equivalent), with the various accessories needed for protein separation by electrophoresis (combs, plates, and casting apparatus).
- 17. Phosphorimaging device (see Note 16).

2.4.3 Transport Assays with Whole Cells Expressing AtAATP1/NTT1

- 1. 50 mM potassium phosphate buffer pH 7.0.
- 2. 3.33 nM [α - 32 P]ATP (3000 mCi mmol $^{-1}$, Perkin Elmer). Add 1 μ L to 50 mM potassium phosphate buffer pH 7.0 containing 1.5 mM cold ATP (A9062; Sigma) to obtain a 50 μ M solution. Store on ice until use.
- 3. Filter membranes 0.45 µm (HAWP02500; Millipore).
- 4. Scintillation vials.
- 5. d.d. water.
- 6. Polymeric Vacuum Filter Holder (1225 Sampling Manifold; Millipore).
- 7. Multi-Purpose Scintillation Counter.
- 1. E. coli polar lipid extract (Avanti Polar Lipids).
- 2. Egg yolk phosphatidylcholine (Avanti Polar Lipids).
- 3. Nitrogen.
- 4. Diethyl ether.
- 5. Substrate/inhibitor, 10×stock (see Note 17).
 - ADP to give a final concentration of 5 mM
 - Carboxyatractyloside (CATR; Sigma) to give a final concentration of 2 μM
- 2.4.4 Transport Assays with Whole Cells and Fused Membrane Vesicles Expressing Mitochondrial Carriers

- Bongkrekic acid (BKA; Sigma) to give a final concentration of 2 μM
- 6. Extruder Set (Avanti Polar Lipids).
- 7. I μm polycarbonate filter (Whatman); filter supports (Whatman).
- 8. PD-10 column (GE Healthcare).
- 9. 2 mL Eppendorf tubes.
- 10. Hamilton robot (with vacuum manifold).
- 11. 96-well MultiScreenHTS-Hi Flow-FB opaque, Barex plastic plates (pore size = 1 µm; Millipore).
- 12. 96-well MultiScreenHTS-HA opaque, Barex plastic plates (pore size = 0.45 μm; Millipore).
- 13. 1.5 μM [¹⁴C]-ADP (60 mCi mmol⁻¹ = 2.22 GBq mmol⁻¹; Perkin Elmer) prepared in PIPES buffer to start the transport assays with mitochondrial carriers.
- 14. BackSeal black backing paper (Perkin Elmer).
- 15. MicroScint-20 (Perkin Elmer).
- 16. MultiScreen sealing tape, clear backing paper (Perkin Elmer).
- 17. TopCount (Perkin Elmer).

3 Methods

3.1 Growth
of Recombinant
Bacteria
and Expression
of the Proteins
of Interest

The gene(s) of protein(s) of interest have to be cloned first into an expression vector containing nisin-inducible promoter either through classical cloning methods [2] or other strategies developed in the last years to facilitate cloning [9, 10]. First trials could be performed following protocols already described [2, 10, 20–22]. Here we present protocols that can be optimized for each protein of interest.

- 1. Inoculate M17G1Chl precultures with concentrated glycerol stocks or frozen cell stocks of recombinant bacteria carrying the gene of protein of interest and bacteria carrying the empty vector as negative control.
- 2. Incubate overnight at 30 °C without shaking (see Notes 18 and 19).
- 3. Inoculate M17G1Chl with 1/40° precultures (see Note 20).
- 4. Incubate cultures at 30 °C; measure OD_{600nm} every 45 min to construct growth curve (doubling roughly every 45 min).
- Induce protein expression by addition of homemade nisin (see Note 21) at OD_{600nm} from 0.5 to 0.8 depending on proteins of interest (see Note 22).

- 6. Swirl immediately to prevent cell lysis; return the flasks to the 30 °C incubator for further 2.5–4 h (*see* Note 23).
- 7. Depending on functional tests, bacteria are either centrifuged, resuspended with an appropriate buffer (see Note 4) and centrifuged again before storage at -20 °C (see Subheading 3.2), or directly used (see Subheading 3.4.1) or snap-frozen and stored in liquid nitrogen (see Subheading 3.4.4).

3.2 Isolation of Lactococcal Membranes with the Cell Disruptor

- 1. Resuspend the bacteria into the appropriate buffer (see Note 4).
- 2. Disrupt the bacteria by twofold passages through a One Shot at 35,000 p.s.i. (2.3 kbars).
- 3. Centrifuge $100,000 \times g$, 15 min, 4 °C and transfer the supernatant into ultracentrifuge tubes.
- 4. Centrifuge 100,000 × g, 1 h, 4 °C; resuspend the pellet and homogenize into the appropriate buffer (see Note 4).
- 5. Snap-freeze and store at -80 °C or in liquid nitrogen until use.

3.3 Detection of the Recombinant Protein Produced

- 1. Prior to the experiment, prepare acrylamide gels for protein electrophoresis, the gel apparatus according to the manufacturer's specifications, and the different gel solutions (stacking gel, acrylamide separating gel; see Note 6).
- 2. Heat the protein samples at 95 °C for 5 min to solubilize the proteins (*see* **Note 24**). Load protein samples, one molecular weight marker, and positive controls in defined quantities.
- 3. Run gels for 1 h at room temperature at 150 V with constant voltage (see Note 25).
- 4. After electrophoresis, perform the transfer for 1 h 30 min at 100 V in protein transfer medium prior to Western blotting analysis.
- 5. Recover the nitrocellulose membrane and rinse the membrane with water. The following incubation and washing steps require agitation on a rocking plate at room temperature.
- 6. Perform Western blotting analysis and/or Coomassie blue staining using protocols already established or given by manufacturers.
- 7. Perform ECL detection (Figs. 1 and 2)

3.4 Functional Characterization of Membrane Proteins

3.4.1 Dehydrogenase Assay on Purified Protein (ceQORH) The chloroplast envelope Quinone OxidoReductase Homologue (ceQORH) protein from *Arabidopsis thaliana* is a peripheral protein associated with the chloroplast envelope through electrostatic interactions [24]. This nuclear-encoded protein is devoid of a classical and cleavable transit peptide and uses an alternative targeting pathway for its import into the chloroplast [25, 26]. The ceQORH protein is structurally related to bacterial, fungal, and animal proteins with known quinone oxidoreductase function. In an earlier

- 12. Follow the formation of Formazan at 560 nm using a Spectrophotometer.
- 13. Deduce the enzymatic activities from the OD measurement using the molar absorption coefficient (see Note 30, Fig. 3c).

3.4.2 Phosphorylation Assays with AtHMA6 and AtHMA8 Using L. lactis Membranes

P_{IB}-ATPases (reviewed in [28]) belong to the large family of P-type ATPases that are transmembrane proteins responsible for the transport of ions and phospholipids across plasma and organelle membranes using the energy provided by ATP hydrolysis. Like all P-type ATPases, PIB-ATPases (or HMA for Heavy Metal ATPase) are composed of a transmembrane domain M containing the transport site and determining ion selectivity, and of three cytosolic loops constituting the catalytic domain. P_{IR}-ATPases have six to eight predicted transmembrane helices and have been classified into several subgroups according to their ionic specificity [29]. Recently, the crystal structure of a prokaryotic P_{IB}-ATPase, LpCopA, has been solved providing new topological information on these enzymes [30]. In Arabidopsis species, AtHMA6 and AtHMA8 are two chloroplastic ATPases of the PIB-1 subgroup involved in Cu transport across the chloroplast envelope and the thylakoid respectively [31, 32]. The enzymatic properties of these two transmembrane proteins could be assessed using in vitro biochemical assays [23, 33] after their successful and efficient expression in Lactococcus lactis. Phosphorylation assays performed on lactococcal membranes expressing these exogenous PIB-ATPases (see Note 31) could provide information about (1) the kinetic parameters of the enzyme using phosphorylation from ATP (see Fig. 4a-c), and (2) the apparent affinity for the translocated metal using phosphorylation from Pi (Fig. 4b). These phosphorylation assays can be performed on all P_{IB}-ATPases whatever their ionic specificity to assess their enzymatic properties.

Phosphorylation from ATP:

- 1. Prepare a mix containing 0.5 mg mL $^{-1}$ of *L. lactis* membranes, with metals or chelators at the desired concentration (*see* **Note 32**) and complete with ATP phosphorylation buffer to a final volume of 90 μ L.
- 2. Start the reaction by addition of 10 μ L of 10 μ M [γ -³²P]ATP (1 μ M final). Vortex the suspension.
- 3. Stop the reaction 30 s later (*see* **Note 33**) by addition of 1 mL ice-cold Stop buffer. Vortex the suspension and incubate 30 min on ice.
- 4. Centrifuge for 15 min, at 15,000 × g, 4 °C and keep the pellet (see Note 34).
- 5. Wash the pellet with 1 mL of ice-cold Stop buffer and centrifuge for 15 min, at 10,000 × g, 4 °C.

Phosphorylation assays from Pi:

- 1. Prepare a mix containing 1 mg mL⁻¹ of *L. lactis* membranes, metals, or chelators (*see* **Note 32**) in Pi phosphorylation buffer to a final volume of 90 μL.
- 2. Incubate the mix 5 min at 30 °C.
- 3. Start the reaction by addition of 10 μ L of 1 mM ^{32}Pi (100 μ M final). Vortex the suspension and incubate the reaction mix at 30 °C for 10 min.
- 4. Stop the reaction by addition of 1 mL ice-cold stop buffer. Vortex the suspension and incubate 30 min on ice.
- 5. Then proceed as described in steps 4–12 for phosphorylation assays from ATP (Fig.4b).

3.4.3 Transport Assays with Whole Cells Expressing AtAATP1/NTT1 The nucleotide transporter I, AtAATP1/NTT1, a highly hydrophobic membrane protein with 12 predicted transmembrane domains [34], is localized within the inner membrane of the chloroplast envelope [35]. This translocator imports ATP in exchange of ADP and Pi [36] in contrast to mitochondrial ATP/ADP translocators [37]. It supplies energy to chloroplasts used by storage plastids required for starch synthesis and to allow nocturnal anabolic reactions in chloroplasts [38].

- 1. Centrifuge $4350 \times g$, 10 min twice and resuspend recombinant bacteria into 30 mL to a final concentration of 100 mg mL⁻¹ (3 mg/30 μ L) in ice-cold 50 mM potassium phosphate buffer pH 7.0.
- 2. Add 50 μ M [α - 32 P]ATP (3000 mCi mmol $^{-1}$; Perkin Elmer) diluted in ice-cold 50 mM potassium phosphate buffer pH 7.0 to each sample (*see* Note 36).
- 3. Incubate at 25 °C for planned time periods and stop nucleotide uptake by addition of 1 mL of ice-cold potassium phosphate buffer.
- 4. Filtrate the cells through a 0.45 μm filter under vacuum.
- 5. Wash three times with 1 mL of ice-cold potassium phosphate buffer.
- 6. Transfer filter to a scintillation vial and add 3.5 mL of d.d. water
- 7. Measure the radioactivity retained on the filters in a scintillation counter.
- 8. Generate graphs using the KaleidaGraph version 4.02 (Synergy Software) and fit experimental data with the appropriate curve (i.e., single exponential) (Fig. 5).

3.4.4 High-Throughput Transport Assays of Mitochondrial Carriers Mitochondrial carriers link the biochemical pathways of the cytosol and the mitochondrion matrix by transporting metabolites, nucleotides, inorganic ions, and cofactors across the mitochondrial inner High-throughput transport assays can be carried out using a Hamilton MicroLab Star robot. The first five steps are programmed to be carried out by the robot in 96-well format, allowing eight different uptake experiments to be performed simultaneously.

- 1. Pipet 100 μ L bacteria (OD_{600nm} = 25) into the wells of a 96-well MultiScreen_{HTS}-Hi Flow-FB plate (pore size = I μ m) or fused membrane vesicles (5 μ g) into a 96-well MultiScreen_{HTS}-HA plate (pore size = 0.45 μ m), while the plate is placed on a vacuum manifold.
- 2. Initiate transport with the addition of 100 μ L PIPES buffer containing 1.5 μ M of ¹⁴C-labeled nucleotide.
- 3. Incubate at room temperature for planned time periods, the longer time points being added first.
- 4. Stop transport by filtration followed immediately by the addition of 200 μ L of ice-cold PIPES buffer to all wells.
- 5. Wash wells two times with 200 μL ice-cold PIPES buffer.
- 6. Leave the plates to dry overnight.
- 7. Stick black backing paper on the underside of the filter plate.
- 8. Add 200 µL of MicroScint-20 to each well using the robot.
- 9. Stick clear backing paper on the topside of the filter plate; stand for at least 4 h to allow filter dissolution.
- 10. Load the plates into the TopCount Scintillation Counter. Initial rates are determined from the linear part of the uptake curves (first 60 s) (see Fig. 6).

4 Notes

- 1. Nisin can be either commercial or produced by the nisinproducing strain NZ9700. We have noticed that homemade nisin gave rise to higher amounts of proteins compared to commercial one [21].
- Recombinant bacteria are generated through transformation with an expression vector containing the gene of interest; in our studies, we use pNZ8148.
- 3. The concentration of antibiotic (chloramphenicol) could vary from 5 to $10~\mu g~mL^{-1}$.
- 4. The buffers for bacterial and protein resuspension have to be adjusted to the protein of interest (50 mM Tris-HCl pH 8.0 for ceQORH [10] and 20 mM HEPES pH 6.0 for AtHMA6 and AtHMA8 [33] containing 6 or 20% glycerol for protein resuspension respectively; 50 mM potassium phosphate buffer pH 7.0 for AtNTT1 [10]; 10 mM PIPES pH 7.0, 50 mM NaCl for mitochondrial carriers [3]).

- 37. Quickly thawing the pellets is vital for transport activity.
- 38. The syringes are not airtight at 4 °C for prolonged periods of time and will leak.

Acknowledgments

This study received financial support from the Commissariat à l'Energie Atomique et aux Energies Alternatives (CEA), the Centre National de la Recherche Scientifique (CNRS), the French National Institute for Agricultural Research (INRA), the University Joseph Fourier (Grenoble), and the Medical Research Council UK. E.S. was funded by a joint grant from the GRAL Labex (Grenoble Alliance for Integrated Structural Cell Biology: ANR-10-LABEX-04) and the CEA.

References

- Bakari S, André F, Seigneurin-Berny D, Delaforge M, Rolland N, Frelet-Barrand A (2014) Lactococcus lactis, recent developments in functional expression of membrane proteins. In: Mus-Veteau I (ed) Membrane proteins production for structural analysis. Springer, New-York, USA, pp 107–132, Chapter 5
- 2. Kunji ERS, Slotboom DJ, Poolman B (2003) Lactococcus lactis as host for overproduction of functional membrane proteins. Biochim Biophys Acta 1610:97–108
- 3. Kunji ERS, Chan KW, Slotboom DJ, Floyd S, O'Connor R, Monné M (2005) Eukaryotic membrane protein overproduction in Lactococcus lactis. Curr Opin Biotechnol 16:546–551
- Monné M, Chan KW, Slotboom DJ, Kunji ERS (2005) Functional expression of eukaryotic membrane proteins in Lactococcus lactis. Protein Sci 14:3048–3056
- Bernaudat F, Frelet-Barrand A, Pochon N, Dementin S, Hivin P, Boutigny S, Rioux JB, Salvi D, Seigneurin-Berny D, Richaud P, Joyard J, Pignol D, Sabaty M, Desnos T, Pebay-Peyroula E, Darrouzet E, Vernet T, Rolland N (2011) Heterologous expression of membrane proteins: choosing the appropriate host. PLoS One 6, e29191
- Herzig S, Raemy E, Montessuit S, Veuthey JL, Zamboni N, Westermann B, Kunji ERS, Martinou JC (2012) Identification and functional expression of the mitochondrial pyruvate carrier. Science 337:93–96

- Gasson MJ, de Vos WM (eds) (1994) Genetics and biotechnology of lactic acid bacteria. Blackie Academic and Professional, London, United Kingdom
- Morello E, Bermúdez-Humarán LG, Llull D, Solé V, Miraglio N, Langella P, Poquet I (2008) Lactococcus lactis, an efficient cell factory for recombinant protein production and secretion. J Mol Microbiol Biotechnol 14:48–58
- Geertsma ER, Poolman B (2007) Highthroughput cloning and expression in recalcitrant bacteria. Nat Methods 4:705–707
- Frelet-Barrand A, Boutigny S, Moyet L, Deniaud A, Seigneurin-Berny D, Salvi D, Bernaudat F, Richaud P, Pebay-Peyroula E, Joyard J, Rolland N (2010) Lactococcus lactis, an alternative system for functional expression of peripheral and intrinsic Arabidopsis membrane proteins. PLoS One 5, e8746
- 11. Pontes DS, de Azevedo MS, Chatel JM, Langella P, Azevedo V, Miyoshi A (2011) Lactococcus lactis as a live vector: heterologous protein production and DNA delivery systems. Protein Expr Purif 79:165–175
- Micrau I, Kleerebezem M (2005) 10 years of the nisin-controlled gene expression system (NICE) in Lactococcus lactis. Appl Microbiol Biotechnol 68:705–717
- de Ruyter PG, Kuipers OP, de Vos WM (1996) Controlled gene expression systems for Lactococcus lactis with the food-grade inducer nisin. Appl Environ Microbiol 62: 3662–3667

- Zhou XX, Li WF, Ma GX, Pan YJ (2006) The nisin-controlled gene expression system: construction, application and improvements. Biotechnol Adv 24:285–295
- 15. Erkens GB, Berntsson RP, Fulyani F, Majsnerowska M, Vujičić-Žagar A, Ter Beck J, Poolman B, Slotboom DJ (2011) The structural basis of modularity in ECF-type ABC transporters. Nat Struct Mol Biol 18:755–760
- Berntsson RP, ter Beek J, Majsnerowska M, Duurkens RH, Puri P, Poolman B, Slotboom DJ (2012) Structural divergence of paralogous S components from ECF-type ABC transporters. Proc Natl Acad Sci U S A 109:13990–13995
- Malinauskaite L, Quick M, Reinhard L, Lyons JA, Yano H, Javitch JA, Nissen P (2014) A mechanism for intracellular release of Na+ by neurotransmitter/sodium symporters. Nat Struct Mol Biol 21:1006–1012
- 18. Thangaratnarajah C, Ruprecht JJ, Kunji ERS (2014) Calcium-induced conformational changes of the regulatory domain of human mitochondrial aspartate/glutamate carriers. Nat Commun 5:5491
- Harborne SP, Ruprecht JJ, Kunji ERS (2015)
 Calcium-induced conformational changes in the regulatory domain of the human mitochondrial ATP-Mg/Pi carrier. Biochim Biophys Acta 1847:1245–1253
- Frelct-Barrand A, Boutigny S, Kunji ER, Rolland N (2010) Membrane protein expression in Lactococcus lactis. Methods Mol Biol 601:67–85
- Boutigny S, Sautron E, Frelet-Barrand A, Moyet L, Salvi D, Rolland N, Seigneurin-Berny D (2015) Functional expression of plant membrane proteins in Lactococcus lactis. Methods Mol Biol 1258:147–165
- King MS, Boes C, Kunji ERS (2015) Membrane protein expression in Lactococcus lactis. Methods Enzymol 556:77–97
- 23. Sautron E, Mayerhofer H, Giustini C, Pro D, Crouzy S, Ravaud S, Pebay-Peyroula E, Rolland N, Catty P, Seigneurin-Berny D (2015) HMA6 and HMA8 are two chloroplast Cu+-ATPases with different enzymatic properties. Biosci Rep 35(3): pii:e00201
- Miras S, Salvi D, Ferro M, Grunwald D, Garin J, Joyard J, Rolland N (2002) Non-canonical transit peptide for import into the chloroplast. J Biol Chem 277:47770–47778
- 25. Miras S, Salvi D, Piette L, Seigneurin-Berny D, Grunwald D, Reinbothe C, Joyard J, Reinbothe S, Rolland N (2007) Toc159- and Toc75-independent import of a transit sequence-less precursor into the inner envelope of chloroplasts. J Biol Chem 282:29482–29492

- Chang W, Soll J, Bolter B (2014) A new member of the psToc159 family contributes to distinct protein targeting pathways in pea chloroplasts. Front Plant Sci 5:239
- 27. Jager-Vottero P, Dorne AJ, Jordanov J, Douce R, Joyard J (1997) Redox chains in chloroplast envelope membranes: spectroscopic evidence for the presence of electron carriers, including iron-sulfur centers. Proc Natl Acad Sci U S A 94:1597–1602
- Rosenzweig AC, Arguello JM (2012) Toward a molecular understanding of metal transport by P(1B)-type ATPases. Curr Top Membr 69: 113–136
- Arguello JM (2003) Identification of ionselectivity determinants in heavy-metal transport P1B-type ATPases. J Membr Biol 195: 93–108
- Gourdon P, Liu XY, Skjorringe T, Morth JP, Moller LB, Pedersen BP, Nissen P (2011) Crystal structure of a copper-transporting PIBtype ATPase. Nature 475:59–64
- Shikanai T, Muller-Moule P, Munekage Y, Niyogi KK, Pilon M (2003) PAA1, a P-type ATPase of Arabidopsis, functions in copper transport in chloroplasts. Plant Cell 15: 1333–1346
- Abdel-Ghany SE, Muller-Moule P, Niyogi KK, Pilon M, Shikanai T (2005) Two P-type ATPases are required for copper delivery in Arabidopsis thaliana chloroplasts. Plant Cell 17:1233–1251
- 33. Catty P, Boutigny S, Miras R, Joyard J, Rolland N, Seigneurin-Berny D (2011) Biochemical characterization of AtHMA6/PAA1, a chloroplast envelope Cu(I)-ATPase. J Biol Chem 286:36188–36197
- 34. Kampfenkel K, Möhlmann T, Batz O, Van Montagu M, Inze D, Neuhaus HE (1995) Molecular characterization of an Arabidopsis thaliana cDNA encoding a novel putative adenylate translocator of higher plants. FEBS Lett 374:351–355
- 35. Neuhaus HE, Thom E, Möhlmann T, Steup M, Kampfenkel K (1997) Characterization of a novel eukaryotic ATP/ADP translocator located in the plastid envelope of Arabidopsis thaliana L. Plant J 11:73–82
- Trentmann O, Jung B, Neuhaus HE, Haferkamp I (2008) Nonmitochondrial ATP/ ADP transporters accept phosphate as third substrate. J Biol Chem 283:36486–36493
- Haferkamp I, Fernie AR, Neuhaus HE (2011)
 Adenine nucleotide transport in plants: much more than a mitochondrial issue. Trends Plant Sci 16:507–515
- 38. Tjaden J, Mohlmann T, Kampfenkel K, Henrichs G, Neuhaus HE (1998) Altered plas-

- tidic ATP/ADP-transporter activity influences potato (Solanum tuberosum L.) tuber morphology, yield and composition of tuber starch. Plant J 16:531–540
- 39. Kunji ERS (2012) Structural and mechanistic aspects of mitochondrial transport proteins. In: Ferguson S (eds), Comprehensive Biophysics, Elsevier. pp 174–205
- 40. Palmieri F (2014) Mitochondrial transporters of the SLC25 family and associated diseases: a review. J Inherit Metab Dis 37:565–575
- 41. Pebay-Peyroula E, Dahout-Gonzalez C, Kahn R, Trezeguet V, Lauquin GJ, Brandolin G (2003) Structure of mitochondrial ADP/ATP carrier in complex with carboxyatractyloside. Nature 426:39–44
- 42. Kunji ERS, Crichton PG (2010) Mitochondrial carriers function as monomers. Biochim Biophys Acta 1797:817–831
- Robinson AJ, Kunji ERS (2006) Mitochondrial carriers in the cytoplasmic state have a common substrate binding site. Proc Natl Acad Sci U S A 103:2617–2622
- 44. Robinson AJ, Overy C, Kunji ERS (2008) The mechanism of transport by mitochondrial

- carriers based on analysis of symmetry. Proc Natl Acad Sci U S A 105:17766–17771
- 45. Ruprecht JJ, Hellawell AM, Harding M, Crichton PG, Mccoy AJ, Kunji ERS (2014) Structures of yeast mitochondrial ADP/ATP carriers support a domain-based alternatingaccess transport mechanism. Proc Natl Acad Sci U S A 111:E426–E434
- 46. Klingenberg M (2008) The ADP and ATP transport in mitochondria and its carrier. Biochim Biophys Acta 1778:1978–2021
- 47. Mierau I, Leij P, van Swam I, Blommestein B, Floris E, Mond J, Smid EJ (2005) Industrial-scale production and purification of a heterologous protein in Lactococcus lactis using the nisin controlled gene expression system NICE: the case of lysostaphin. Microb Cell Fact 4:15
- 48. Hillar A, Loewen PC (1995) Comparison of isoniazid oxidation catalyzed by bacterial catalase-peroxidases and horseradish peroxidase. Arch Biochem Biophys 323:438–446
- Kuhlbrandt W (2004) Biology, structure and mechanism of P-type ATPases. Nat Rev Mol Cell Biol 5:282–295