The AAA+ ATPase RavA and its binding partner ViaA modulate E. coli aminoglycoside sensitivity through interaction with the inner membrane

Enteric bacteria have to adapt to environmental stresses in the human gastrointestinal tract such as acid and nutrient stress, oxygen limitation and exposure to antibiotics. Membrane lipid composition has recently emerged as a key factor for stress adaptation. The E. coli ravA-viaA operon is essential for aminoglycoside bactericidal activity under anaerobiosis but its mechanism of action is unclear. Here we characterise the VWA domain-protein ViaA and its interaction with the AAA+ ATPase RavA, and find that both proteins localise at the inner cell membrane. We demonstrate that RavA and ViaA target specific phospholipids and subsequently identify their lipid-binding sites. We further show that mutations abolishing interaction with lipids restore induced changes in cell membrane morphology and lipid composition. Finally we reveal that these mutations render E. coli gentamicin-resistant under fumarate respiration conditions. Our work thus uncovers a ravA-viaA-based pathway which is mobilised in response to aminoglycosides under anaerobiosis and engaged in cell membrane regulation.
that both RavA and ViaA interact with specific membrane components and modify cellular lipid homeostasis. We further reveal that RavA and ViaA localise to the inner membrane, affect membrane morphology and show that, when overexpressed inside cells, both proteins normalise to the inner membrane, affect membrane interaction with RavA, and demonstrate that their mutations abolish lipid binding in vitro and strongly attenuates the effect on lipid homeostasis in vivo. Moreover, we introduce these mutations into the E. coli ravA-viaA operon on the AG sensitisation. Altogether, this work reveals a possible scenario for the function of ViaA in bacterial physiology in general, and in AGs sensitisation remains scarce, and binding to its potential interaction partners has only been shown indirectly\cite{12}. Initial attempts to purify a His-tagged ViaA protein using Immobilized Metal Affinity Chromatography (IMAC) and size-exclusion chromatography (SEC) (Methods) resulted in prohibitively low amounts of purified ViaA protein. However, addition of an N-terminal AviTag to the C-terminally His-tagged ViaA (hereafter named AviTag-ViaA-His) stabilised the protein and enabled its high yield purification for characterisation by multi-angle laser light scattering (MALLS) and small-angle X-ray scattering (SAXS) (Fig. 1b–d, Methods). MALLS experiments with purified AviTag-ViaA-His sample showed a monodisperse peak and yielded a molecular weight (MW) of 123 kDa, corresponding to roughly two times the theoretical MW of the AviTag-ViaA-His construct (60.4 kDa). SAXS studies confirmed the dimeric state of AviTag-ViaA-His in solution and resulted in predicted MWS of 130 and 117 kDa using SAXSMoW\cite{17} and ScÅtter\cite{16} respectively. Moreover, the distance distribution function calculated from the SAXS data suggests an elongated particle, while the Kratky plot reveals a degree of flexibility, and corresponds to a Kratky plot expected for a multidomain protein with flexible linker (Fig. 1c, d). Although the dimeric character of the purified AviTag-ViaA-His construct was verified by both MALLS and SAXS, we cannot exclude the possibility that non-tagged ViaA may harbor a different protein (Fig. 1a, residues 1–319). The C-terminal part (C-Terminal domain of ViaA, CTV), starting from residue 320, is predicted to be a WWA domain and contains the characteristic MIDAS motif (Fig. 1a). While studies of the potential role of E. coli ViaA in the maturation of Nuo and Frd have been initiated\cite{12}, no protocols for the preparative purification of ViaA are available. Its biochemical/biophysical characterisation remains scarce, and binding to its potential interaction partners has only been shown indirectly\cite{12}. Initial attempts to purify a His-tagged ViaA construct using Immobilized Metal Affinity Chromatography (IMAC) and size-exclusion chromatography (SEC) (Methods) resulted in prohibitively low amounts of purified ViaA protein. However, addition of an N-terminal AviTag to the C-terminally His-tagged ViaA (hereafter named AviTag-ViaA-His) stabilised the protein and enabled its high yield purification for characterisation by multi-angle laser light scattering (MALLS) and small-angle X-ray scattering (SAXS) (Fig. 1b–d, Methods). MALLS experiments with purified AviTag-ViaA-His sample showed a monodisperse peak and yielded a molecular weight (MW) of 123 kDa, corresponding to roughly two times the theoretical MW of the AviTag-ViaA-His construct (60.4 kDa). SAXS studies confirmed the dimeric state of AviTag-ViaA-His in solution and resulted in predicted MWS of 130 and 117 kDa using SAXSMoW\cite{17} and ScÅtter\cite{16} respectively. Moreover, the distance distribution function calculated from the SAXS data suggests an elongated particle, while the Kratky plot reveals a degree of flexibility, and corresponds to a Kratky plot expected for a multidomain protein with flexible linker (Fig. 1c, d). Although the dimeric character of the purified AviTag-ViaA-His construct was verified by both MALLS and SAXS, we cannot exclude the possibility that non-tagged ViaA may harbor a different...
stoichiometry in solution. Furthermore, we note that the elongated character and apparent flexibility of ViaA might be accentuated by the presence of non-cleaved tags.

The strength and kinetics of the RavA-ViaA interaction are nucleotide-dependent

While a previous observation that ViaA or NTV slightly enhance the ATPase activity of RavA suggested a physical interaction between the two proteins via the N-terminal part of ViaA, direct measurements of the RavA-ViaA interaction are unavailable. Pull-down assays using SPA-tagged RavA did not bring down ViaA, and vice versa, pointing to a rather weak or transient interaction. The advantage of AviTag-containing constructs is that they can be biotinylated in vitro and coupled to Streptavidin (SA)-biosensors for binding studies using Bio-Layer Interferometry (BLI). To address potential effects of the protein orientation on the biosensor, either N- or C-terminally tagged constructs (Methods) were immobilised and transferred to wells containing a concentration series of purified RavA in the absence or presence of ADP or ATP (Fig. 2a, b). The affinity of the apo-RavA to immobilised His-ViaA-AviTag and AviTag-ViaA-His could be described by dissociation constants ($K_D$) of 11.0 µM and 18.9 µM respectively, showing that the location of the AviTag does not have a major influence and validating the weak nature of the RavA-ViaA interaction. ADP binding to RavA increased the strength of the RavA-ViaA interaction to ~2.2 µM, whereas the presence of ATP altered the shape of the BLI curves that could only be reliably fitted using a 2:1 heterogeneous ligand binding model, resulting in $K_D$ values of 30.3/1.0 µM and 37.5/0.5 µM for His-ViaA-AviTag and AviTag-ViaA-His respectively. The latter may point to the presence of a mixture of RavA conformations after addition of ATP, with different ViaA binding affinities. Taken together, these BLI binding studies revealed that ViaA directly interacts with RavA, and that the strength of this interaction is dependent on the nucleotide-bound state of RavA. ViaA most likely solely interacts with hexameric RavA, in accordance with other characterized AAA+ ATPase and VWA domain-containing protein pairs. Since RavA is present as a functional hexamer after incubation with ADP or ATP, but has the propensity to partially fall apart into monomers in the absence of ADP/ATP, this provides a possible explanation for the notably lower affinity of ViaA for apo-RavA.

Fig. 2 | Characterization of the ViaA-RavA interaction by Bio-Layer Interferometry (BLI) binding studies. a & b BLI measurements of His-ViaA-AviTag (a) or AviTag-ViaA-His (b) coupled on BLI biosensors and RavA, with or without added ADP/ATP. The blue curves correspond to the measured signal while the red curves correspond to the calculated fit using a 1:1 (no nucleotide, ADP) or 2:1 heterogeneous ligand binding (ATP) interaction model. c BLI measurements of AviTag-ViaA-His coupled on BLI biosensors and either NuoEF (blue curve), NuoEFG (green curve) or FrdA (red curve). SDS-PAGE gels of purified NuoEF, NuoEFG and FrdA are shown on the right. BLI experiments were performed in triplicate, and one representative experiment is shown. Source data are provided as a Source Data file.
Both RavA and ViaA show membrane localisation in E. coli cells

Complementary BLI studies using His-NTV-AviTag demonstrated similar RavA binding kinetics as the full-length ViaA despite the monomericity of the NTV construct (Supplementary Fig. 1), confirming that NTV is sufficient for RavA binding. In addition, the absence of the LARA domain of RavA responsible for the LdcI-RavA cage formation did not affect the binding of RavA to ViaA (Supplementary Fig. 1), indicating that the LARA domain is not involved in the RavA-ViaA interaction.

Previous observation that upon cell fractionation RavA was mostly present in the cytoplasmic fraction whereas the majority of ViaA partitioned into the inner membrane fraction, led the authors to hypothesise that the presence of ViaA binding to purified NuoEFG and FrdA did not result in any discernible interaction with either His-ViaA-AviTag or AvisM-ViaA-His (Fig. 2c).

RavA accumulates under the inner membrane whereas ViaA modifies membrane morphology of E. coli cells

In parallel to imaging the RavA-OE and ViaA-OE bacteria by epifluorescence and super-resolution microscopy, bacteria overexpressing His-RavA, His-ViaA and AvisM-ViaA-His were subjected to high pressure freezing and freeze substitution followed by ultrathin cell sectioning, and their ultrastructure examined by transmission electron microscopy (TEM). A dark layer of matter, supposedly corresponding to the bacterial inner membrane, in line with the fluorescence microscopy observations (Fig. 3b). Most strikingly, arrays of ectopic intracellular membrane tubes were discovered to underlie the inner membrane of the ViaA-OE bacteria (Fig. 3b). Interestingly, overexpression of few membrane proteins with particular topologies has previously been noticed to induce formation of tubular membrane networks of reminiscent hexagonal phase morphologies. Such cardiolipin (CL)-enriched neo-membranes are proposed to form in order to accommodate the highly overproduced membrane protein, thereby relieving the inner cellular membrane from the associated stress. Thus, on the one side we have biochemically and biophysically characterised a soluble form of ViaA in vitro, and on the other side our morphological cellular EM
Both RavA and ViaA bind specific anionic phospholipids in vitro

The inner membranes of *E. coli* consist of three major anionic phospholipids: 70-80% phosphatidylethanolamine (PE), 20-25% phosphatidylglycerol (PG) and ~5% cardiolipin (CL). For ViaA bound via RavA or RavA bound via ViaA: Lipid binding was first allowed for RavA and subsequently ViaA was added, or vice versa. For ‘LdcI-RavA-complex’, proteins were mixed before incubation on the membrane (see also Method). b Quantification of cardiolipin (CL) levels by TLC and GC-FID/MS in wild-type (WT) MG1655 *E. coli* cells and MG1655 *E. coli* cells overexpressing His-RavA, His-RavA ΔLARA, AviTag-ViaA-His, AviTag-ViaA476E,479E-His and AviTag-ViaA472-His, visualized by a Tukey representation showing all points within a box indicating the median, 25th and 75th percentiles and whiskers down to the minimum and up to the maximum value. Each point represents a biological repeat, with *p*-value = 0.0357 for ViaAΔLARA andViaAΔ472+E479E or ** for *p*-value < 0.01 (*p*-value = 0.0025). The # indicates a significant difference (*p*-value = 0.0167) with ViaA-OE. Source data are provided as a Source Data file.

observations agree with and corroborate our optical imaging data that show localisation of ViaA and RavA at the inner membrane of the bacterial cell. This raises two immediate questions: (i) are ViaA and RavA capable of directly binding to lipids, and (ii) do they modulate cellular lipid homeostasis, and in particular, does ViaA overexpression increase the cellular amounts of CL? In this respect, it is interesting to note that the conical shape of CL is known to favor its clustering in negative curvature regions such as cell poles and the division septum[12,13], which would agree with the localization of the overexpressed ViaA and RavA.

Both RavA and ViaA bind specific anionic phospholipids in vitro

The inner membranes of *E. coli* consist of three major anionic phospholipids: 70-80% phosphatidylethanolamine (PE), 20-25% phosphatidylglycerol (PG) and ~5% cardiolipin (CL), the exact content of the latter being culture condition and growth phase-dependent[14,15]. The universal precursor of these phospholipids is phosphatidic acid (PA), present in extremely low amount in the *E. coli* membrane. To investigate whether ViaA and RavA are capable of directly binding to lipids, we employed dot-blot assays using PE, PG, CL, PA as well as phosphatidylcholine (PC) and phosphatidylserine (PS) (see Methods). While dot-blot assays are a semiquantitative method, and no direct comparison can be made between intensities of individual dots, they are nonetheless indicative of the relative propensity of a protein to interact with a particular lipid immobilised on a nitrocellulose membrane[16]. Our dot-blots revealed that purified RavA specifically binds PG, whereas ViaA specifically binds PA and to a noticeably lesser extent CL (Fig. 4a, Supplementary Fig. 3). RavA interactions with ViaA and PG are mutually exclusive; likewise, inside the LdcI-RavA complex, RavA is no longer able to interact with PG. In contrast, lipid-bound ViaA is still capable of interacting with RavA (Fig. 4a, Supplementary Fig. 3). Surprisingly, RavAΔLARA loses the PG binding capacity (Supplementary Fig. 3), which shows that the LARA domain is implicated not only in the interaction with LdcI but also in the interaction with lipids. In this light, and since the LARA domain is involved in lipid binding but not in ViaA binding (Supplementary Fig. 1), the observation that RavA cannot simultaneously interact with ViaA and PG suggests that binding to PG may induce a conformational change in the RavA molecule, making it inapt for ViaA binding.

The observation that ViaA can simultaneously interact with RavA and with lipids is consistent with ViaA being a two-domain protein, with the NTV binding to RavA and the CTV binding to lipids. Since the 3D structure of ViaA is unknown, we examined its primary sequence and the 2D structure prediction of the CTV provided by AlphaFold[17,18] and RoseTTAFold[19] (Fig. 5) for hints to possible positions of a lipid binding site. The C-terminal end of ViaA is highly positively charged, with eight arginines, six of which are situated in the predicted α-helix at the C-terminal extremity (Fig. 5a). Compelled by the amphipatic nature of this helix (Fig. 5b) and its high conservation among enterobacterial ViaA proteins (Fig. 5c), we reasoned that the C-terminus of ViaA might be involved in electrostatic interactions with the negatively charged head groups of PA and CL. In particular, R476 and R479 are predicted to be situated on the same side of the α-helix and seem to form a positive patch (Fig. 5b). To evaluate this hypothesis, we designed the three following mutants: ViaA472Δ, devoid of the entire C-terminus, ViaA476E479E and ViaA472ΔE476E479E. As shown in Supplementary Fig. 3, mutations of R476 and R479 into alanines notably attenuate interaction with lipids, whereas the removal of the C-terminus and the R-to-E double mutation result in the abrogation of the lipid-binding propensity. Altogether, combined with the membrane distribution and effects on membrane morphology, ViaA unexpectedly joins the list of peripheral membrane proteins tethered to the inner *E. coli* membrane through an amphipathic helix displaying affinity for anionic lipids and in particular CL, which also includes proteins such as the cell division site selection ATPase MinC[20,21] and the cell shape-determining actin homolog MrEB[22]. Strikingly, although ViaA is a peripheral membrane protein, its membrane-targeting C-terminal sequence contains all the key features of a high-affinity CL-binding site on bacterial integral membrane proteins, recently identified by molecular dynamics simulations: three or two adjacent basic residues, at least one polar, a neighbouring aromatic and a glycine proposed to confer a higher affinity for the CL head group.

Finally, to further validate the proposed lipid binding sites of RavA and ViaA, we examined the morphology of RavAΔLARA OE, ViaA476E479E OE and ViaA472Δ OE cells by EM and compared it to the observations presented in Fig. 3b. Remarkably, these mutants formed soluble cytosolic bodies inside the bacterial cells (Supplementary Fig. 4), although the overexpression levels remained very similar to those of the lipid binding-competent counterparts (Supplementary Fig. 5). Thus, the inner membrane localisation and the morphological changes observed with RavA-OE and ViaA-OE are unequivocally related to their propensity to target specific phospholipids.

ViaA modifies cellular lipid homeostasis in vivo

We then investigated the effect of RavA or ViaA overexpression on the membrane lipid composition (Fig. 4b, Supplementary Fig. 6). To this...
end, lipids were extracted from different cellular samples, and analysed by gas chromatography, thin layer chromatography and mass spectrometry (see Methods). As shown in Supplementary Fig. 6, RavA-ΔLARA-OE, RavAΔLARA-OE, ViaAR476E/R479E-OE and ViaA1-472-OE bacteria contained slightly but statistically significantly fewer lipids, quantified by their fatty acids, than the wild type (WT) MG1655 cells, whereas the total fatty acid content in ViaA-OE remained roughly similar to the WT. A similar behaviour was observed for the relative proportion of PG among the total lipids, whereas the relative proportion of PE remained unchanged. As anticipated from the electron microscopy observations, the most striking changes were observed with CL, the proportion of which was 6 to 10-fold increased in the ViaA-OE cells, whereas overexpression of the other constructs led to a much milder (but still statistically significant) CL increase in comparison to the WT bacteria (Fig. 4b). One should keep in mind that as observed for some rare membrane proteins, an inner membrane stress due to its saturation resulting from the ViaA overexpression may be relieved by induction of the CL-enriched neo-membranes that enclose the excess of ViaA. At physiological concentrations of ViaA however, the CL content of the inner membrane may not be significantly higher than in the absence of ViaA, and a massive membrane tubulation as observed in Fig. 3b is, at any rate, not to be expected. The low native expression level of ViaA precludes conclusive quantitative assessments of the potential subtle difference in the lipid metabolism between the WT and the MG1655-ΔravA-ΔviaA strains under anaerobic conditions favoring expression of the ravA-viaA operon.

Lipid binding-deficient chromosomal mutants of RavA and ViaA impair RavA and ViaA function in gentamicin sensitisation

Having recently shown that ravA-viaA sensitise E. coli to gentamicin (Gm) in fumarate respiratory condition, we decided to check if lipid binding-deficient chromosomal MG1655 mutants ViaA1-472, ViaAΔLARA, ViaAR476E/R479E and RavAΔLARA are still capable of Gm sensitisation. To this end, we performed a time-dependent killing experiment, using a Gm concentration equivalent to twice the minimum inhibitory concentration. As shown in Fig. 6, all mutants exhibited increased resistance to Gm compared to the WT strain. This result demonstrates that RavA and ViaA mutants, designed to be unable to bind lipids, prevent Gm toxicity under fumarate respiratory conditions.

**Fig. 5 | Structure and sequence-based prediction of the ViaA lipid binding site.** a Cartoon presentation of Alphafold (left, light grey) and RoseTTAFold (right, light grey) structural predictions for the ViaA VWA domain (residues 320-483). The MIDAS motif (green) as well as Arginine residues in the C-terminal helix (dark blue) are annotated and shown as sticks. The Alphafold and RoseTTAFold models are shown superimposed on the right in dark and light grey respectively. The Alphafold prediction of E. coli ViaA can be found at https://alphafold.ebi.ac.uk/entry/A0A828TYA7. The majority of the C-terminal VWA domain (155 out of 163 residues, 95.1%), including most of the C-terminal α-helix, is predicted with a Model Confidence level of ‘confident’ (90 > pLDDT > 70) to ‘very high’ (pLDDT > 90). b Helical wheel diagram of the C-terminal helix of ViaA (residues 471-483), with annotated and color-coded residues. c Multiple sequence alignment of the C-terminal helix of different enterobacterial ViaA orthologues. Residues are color-coded and level of conservation is annotated with ‘*’ (perfect alignment), ‘.’ (strong similarity) and ‘.’ (weak similarity).
An attractive hypothesis could be that ViaA, eventually with the help of RavA, would sensitise E. coli to Gm by directly binding to the membrane and modifying its permeability. To address this possibility, we performed planar lipid bilayer experiments (Supplementary Fig. 7) but did not detect formation of membrane pores that would facilitate AG transport. Therefore, we concluded that RavA and ViaA target phospholipids without perforating the lipid bilayer such as to directly enable Gm uptake into the bacterial cell.

Finally, we took additional advantage of our time-dependent killing assay to demonstrate that the PamCherry tag does not affect the properties of ViaA. Indeed, a complementation assay with over-expressed PamCherry-ViaA and ViaA-PamCherry (Supplementary Fig. 8) showed that either of the constructs could efficiently restore the impaired Gm toxicity for the MG1655ΔravAΔviaA mutant strain.

Discussion
Since AGs are notoriously inefficient under the anaerobic and acidic conditions of the human gastrointestinal tract, insights into the mechanism of the ravA-viaA function in E. coli sensitisation to AGs should improve our understanding and fight against the global threat of antibiotic resistance. The E. coli MoxR AAA+ ATPase RavA has long been known to tightly bind one of the main enterobacterial acid stress response proteins, the acid stress-inducible lysine decarboxylase Ldc, thereby preventing its inhibition by the nutrient stress response alarmone ppGpp59. However, a characteristic of the MoxR AAA+ ATPases is also the close co-occurrence of their genes with genes encoding VWA domain-containing proteins, with which they are functionally linked60. The ravA-viaA operon, shown to be controlled by the anaerobic transcriptional regulator Fnr61, sensitises E. coli to AGs in respiratory conditions when fumarate is used as electron acceptor instead of O259,62. Thus, we decided to focus this work on a thorough characterisation of ViaA and the RavA-ViaA interaction, and investigated their molecular functions beyond the Ldc-RavA interaction.

We now provide extensive in vitro and in vivo biochemical, biophysical, optical imaging and morphological evidence that RavA and ViaA do not only interact in a nucleotide-dependent fashion and bind specific phospholipids in vitro, but also localise at the bacterial inner membrane and modulate membrane lipid composition upon overexpression in vivo. In particular, we demonstrate specific RavA-PG and ViaA-PA/CL interaction, and reveal a prominent effect of ViaA overexpression on the CL-enrichment of the E. coli inner membrane. A possible explanation of the effect of ViaA-OE on CL can be proposed based on our finding that ViaA interacts with PA (Fig. 4a). Indeed, PA, PG and CL are tightly interconnected: PA, only present in tiny amounts in E. coli cells, is a metabolic hub for PG synthesis, whereas two PG molecules are necessary to produce CL63. The synthesis of CL in bacteria requires that a first PG receives a phosphatidyl group from a second PG by a transsterification reaction catalysed by cardiolipin synthase Cls64. E. coli contains three Cls isoforms65, with ClsA being the major contributor to CL synthesis during exponential growth. Interestingly, PA was shown to strongly inhibit ClsA activity64. Consequently, the association of ViaA-PA with PA at the inner membrane level could trap PA, thereby preventing Cls inhibition and eventually favouring CL synthesis, leading to a modification in the lipid homeostasis. Independently of the particular mechanism and considering the physiologically low amount of ViaA inside the E. coli cell, one may anticipate that by binding to cone-shaped anionic phospholipids such as PA and CL, natively expressed ViaA may locally act on the inner membrane curvature, affect its permeability or influence some other local membrane properties60.

Importantly, we show that the RavA and ViaA lipid-binding propensity is directly linked to their effect on the AG bactericidal activity under anaerobiosis, because mutations abolishing interaction with lipids preclude Gm toxicity under conditions of fumarate respiration. Our finding that RavA and ViaA do not permeabilise the lipid bilayer, and the independent observations by us and by others that anaerobic RavA-ViaA-mediated AG sensitivity is dependent on the proton motive force (pmf)59,64, suggest that they may positively act on Frd or other respiratory complexes, thereby enhancing the pmf required for efficient AG uptake. Taking into account the absence of a direct interaction with purified FrdA and NuoEFG in a BLI setup as described above, as well as the in vitro lipid binding and the in vivo membrane remodelling activity of overexpressed RavA and ViaA revealed in the present study, we speculate that under physiological respiration conditions, RavA and ViaA might chaperone certain respiratory complexes by acting on lipid microdomains in which these complexes are inserted. This hypothesis aligns with our recent observation of a patchy peripheral distribution of Ldc66, which we tentatively attributed to an attraction of this proton-consuming acid stress response enzyme to CL-enriched lipid microdomains forming proton sinks67 that compartmentalise oxidative phosphorylation complexes68,69. Thus, this work sets the stage for future investigations of an unprecedented molecular network that links the Ldc-RavA-ViaA triad with bacterial stress adaptation, membrane homeostasis, respiratory complexes and aminoglycoside bactericidal activity.

Methods
Bacterial strains and plasmids construction
Constructs used for experiments presented in each of the main and supplementary figures are summarised in Supplementary Table 1. The original plasmids used for creation of new constructs used in this study
are listed in Supplementary Table 2. All novel plasmids, primers, recombinant strains and cloning strategies are summarised in Supplementary Table 3. The *ravA* and *viaA* genes were PCR amplified from *Escherichia coli* K-12 MG1655 genomic DNA using Phusion polymerase (Biolabs). All PCR products were purified by DNA cleanup kit (Qiagen). Gibson assemblies were performed using 0.4 U T5 exonuclease, 2.5 U Phusion polymerase, and 400 U Taq ligase (New England Biolabs) in 1 x ISO buffer consisting of 100 mM Tris-HCl pH 7.5, 10 mM MgCl2, 0.8 mM dNTP mix, 10 mM dithiothreitol (DTT), 50 mg polyethylene glycol (PEG) – 8000, 1 mM nicotinamide adenine dinucleotide (NAD). A total of 7.5 μL of the Gibson Master Mix was mixed with 2.5 μL DNA, containing ~100 ng of vector. The mix was incubated for 60 min at 50 °C. Transformations were performed in Top10 competent bacteria (One Shot TOPO10 chemically competent *E. coli*, Invitrogen) and selected using 100 μg/mL ampicillin and 34 μg/mL chloramphenicol (Euromedex). Agarose gel purification and DNA plasmid extractions were performed using a QIAquick Gel extraction kit (QIAGEN). Restriction enzyme digests were performed according to manufacturer recommendations (Biolabs). Bacteria were made electrocompetent by growing cells to an OD600 of around 0.7. Cells were then placed on ice and washed three times with ice-cold, sterile water. Electroporation using the MicroPulser (BioRad) was followed by 1 h growth on LB-ampicillin.

Mutant strains of K-12 substring MG1655 (ATCC 47076) were generated by recombining following the protocols of earlier publications24,25 and using the recombineering constructs summarised in Supplementary Table 4. Briefly, the pKD46 plasmid was used to express the three proteins Gam, Exo, and Beta, that mediate homologous recombination (HR) and that are originally derived from the bacteriophage lambda. On pKD46, the expression of those genes is controlled by the *araBAD* promoter. pKD46 has an ampicillin resistance gene and a temperature-sensitive origin of replication (ORI), hence cells with pKD46 were grown at 30 °C with ampicillin. Recombineering requires DNA substrates with regions homologous to the target genome. Those substrates were produced by PCR using specifically designed pKD3-plasmids serving as PCR-template. pKD3 encodes the gene *CATT* allowing selection of engineered bacteria using chloramphenicol. The *CATT* cassette is flanked by FRT sites and can be removed using FLP recombinase. FLP is expressed from the pCP20 plasmid. pCP20 has a temperature-sensitive ORI and encodes the ampicillin resistance gene *ampR*, hence cells were grown at 30 °C with ampicillin to keep the plasmid. To induce expression of FLP and to lose the pKD46 plasmid, cells were harvested by centrifuging the cultures at 4,000 g for 45 min.

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centrifugation at 4,000 g for 10 min. The cell pellet was resuspended in 50 mM MES, 50 mM NaCl, pH 6.6, 10 µg/mL DNase and 10X Complete tablet and disrupted by one passage through a Homogeniser at 18,000 psi. Cell debris was removed by centrifugation for 1 h at 250,000 g. The supernatant was filtered using a 0.2 µm filter and flown over a 5 ml Streptactin-Sepharose column (GE Healthcare) equilibrated with buffer A (50 mM MES, 50 mM NaCl, pH 6.6). The column was washed with buffer A, and the NuoEF and EFG fragments were eluted with buffer A supplemented with 2.5 mM D-desthiobiotin. The eluted NuoEF and NuoEF mixture appeared reddish/brown, and was further purified using a SD200 10/300 increase column (GE Healthcare) equilibrated with 50 mM MES, 500 mM NaCl, pH 6.6, resulting in two separated peaks containing NuoEF and NuoEF respectively. Fractions containing NuoEF and NuOE, verified by SDS-PAGE, were concentrated separately, flash frozen and stored at −80 °C.

Expression of soluble FrdA was based on the protocol by Léger et al.25 Chemically competent E. coli BL21 (DE3) cells with a knock-out in FrdB were transformed with N-terminal His-tagged FrdA in the pET-His_3C vector, gently obtained by Dr. Christophe Romier, Strasbourg. The resulting transformants were used to inoculate 200 mL of LB medium with 50 µg/mL Ampicillin in a 1 L flask and the culture was grown at 37 °C with vigorous aeration (250 rpm) ON. The pre-culture was used to inoculate 0.5 mL LB medium with 500 µg/mL Ampicillin. The resulting culture was grown at 37 °C until the OD reached 0.6. Gene expression was induced with 0.5 mM IPTG. After + 18 h of expression at 18 °C, cells were pelleted by centrifugation at 4000 g for 45 min. The cell pellet was resuspended in 30 mL Buffer A (50 mM KH₂PO₄, pH 7.0, 500 mM NaCl, 1% glycerol) supplemented with 1X Complete tablet and 0.5 µL benzonase. Cells were opened by sonication, and cell debris was removed by centrifugation for 1 h at 20,000 g. The supernatant was filtered using a 0.2 µm filter and flown over a 5 ml NINTA IMAC column (GE Healthcare) equilibrated with buffer A (50 mM KH₂PO₄, pH 7.0, 500 mM NaCl, 1% glycerol). Bound FrdA was washed with 5% buffer B (50 mM KH₂PO₄, pH 7.0, 500 mM NaCl, 1% glycerol, 500 mM imidazole), followed by elution using a gradient from 5–100% buffer B. Eluted FrdA fractions appeared bright yellow due to the present FAD cofactor. The eluted FrdA fraction was subsequently concentrated and injected onto a SD200 10/300 increase column (GE Healthcare) equilibrated with 20 mM HEPES pH 7.5, 300 mM NaCl, 10% glycerol, 1 mM DTT. Purified FrdA fractions were flash-frozen and stored at −80 °C for later use.

Multi-angle laser light scattering (MALLS)
Prior to conducting MALLS experiments, flash-frozen purified AviTag-ViaA-His and His-NTV-Avi samples were thawed and centrifuged at 20,000 g for 30 min. SEC-MALLS experiments were conducted at 4 °C on a high-performance liquid chromatography (HPLC) system (Sichardz, Kyoto, Japan) consisting of a DGU-20 AD degasser, an LC-20 AD pump, a SIL20-ACTR autosampler, a C180-A communication interface, an SPD-M20A UV-Vis detector, a FRC-10A fraction collector, an X-L-Therm column oven (WynSep, Sainte Foy d’Aigrefeuille, France) and static light scattering miniDawn Treos, dynamic light scattering DynaPro NANOSTAR and refractive index Optilab rEX detectors (Wyatt, Santa-Barbara, USA).

Purified AviTag-ViaA-His (80 µL at 3 mg/mL) or His-NTV-AviTag (80 µL at 2 mg/mL) were injected on a Superdex 200 increase 10/300 GL column (GE Healthcare), equilibrated at 4 °C with a buffer containing 25 mM HEPES pH 7.5, 300 mM NaCl, 10 mM MgCl₂ and 10% Glycerol, at a flow rate of 0.5 mL/min. Bovine serum albumin (BSA) at 2 mg/mL in phosphate-buffered saline (PBS) buffer was injected as a control. Data was analyzed using the ASTRA software package (Wyatt, Santa-Barbara, USA). The extinction coefficient and refractive index increments for the proteins were calculated from the amino acid sequences using the SEDFIT software.

Small Angle X-Ray Scattering (SAXS)
SAXS data were collected on the BM-29 BIOSAXS beamline at the ESRF (Grenoble, France)44, equipped with a Pilatus3 2M detector operated at a wavelength of 0.9919 Å and using a sample-detector distance 2.867 m, resulting in a scattering moment transfer range of 0.003 Å⁻¹ to 0.494 Å⁻¹. Purified AviTag-ViaA-His was measured at a concentration of 3 mg/mL in a buffer containing 25 mM HEPES pH 7.5, 300 mM NaCl, 10 mM MgCl₂ and 10% Glycerol. Measurements were performed at 20 °C, and 10 frames with an individual exposure time of 0.5 s were taken per sample. Initial data integration, averaging and background subtraction were performed using PRIMUS-QT from the ATSAS software package.

The forward scattering (I₀) and radius of gyration (r_g) were determined by PRIMUS-QT using Guinier approximation. The Porod volume estimate (V_P) was evaluated using Autoporod. The maximum particle dimension (D_max) and distance distribution function P(r) were evaluated using ScAtter. The molecular mass of the His-ViaA-AviTag sample was calculated using the online SAXSMoW 2.0 program and the ScAtter software package.

Bio-Layer Interferometry (BLI)
For BLI binding studies, biotinylated AviTag-ViaA-His, His-ViaA-Avi and His-NTV-Avi samples were expressed and purified as described earlier, but with the addition of 50 µM D-biotin to the LB medium during expression overnight at 18 °C. Binding studies were performed with C-terminally His-tagged RavA and RavΔLARA proteins purified as described. BLI experiments were performed in HBS kinetics buffer, containing 25 mM HEPES pH 7.5, 300 mM NaCl, 10 mM MgCl₂, 10% Glycerol, 0.1% w/v BSA and 0.02% v/v Tween 20, using an Octet RED96 instrument (FortëBio) operated at 293 K. Streptavidin-coated biosensors (FortëBio) were functionalised with biotinylated AviTag-ViaA-His, His-ViaA-AviTag or His-NTV-AviTag to a maximum signal of 1 nm, subsequently quenched with 10 µg mL⁻¹ biocytin, and transferred to wells containing 5 different concentrations of ligand. When RavA or RavΔLARA was used as a ligand, 1 mM ADP was added to the HBS kinetics buffer and RavA or RavΔLARA samples were incubated with 1 mM ADP for 10 min prior to conducting measurements. Buffer subtraction was performed using a functionalized biosensor measuring running buffer. To check for nonspecific binding during the experiments, non-functionalized biosensors were used to measure the signal from the highest ligand concentration as well as running buffer. All data were fitted with the FortëBio Data Analysis 9.0 software using a 1:1 interaction model. All binding experiments were performed in triplicate (technical triplicates), and calculated K_D, K_D and K_D values represent the averages of these triplicate experiments.

Nanobody production and labelling
The anti-RavA-Nb and anti-ViaA-Nb were obtained from the nanobody generation platform of the AFMB laboratory (Marseille, France) as described. The anti-BC2-Nb was kindly provided by Ulrich Rothbauer. Nanobodies were labelled as described.

Overexpression of recombinant RavA and ViaA constructs for fluorescence imaging, cellular EM observations, and lipid extraction and analysis
MGI655 cells were transformed with a low-copy auxiliary pT7 pol26 plasmid that codes for T7 RNA polymerase under the control of a lac promoter. The resulting MGI655/pT7 pol26 (Kar) strain was then transformed with a plasmid (Amp) carrying a gene coding for a desired RavA or ViaA construct under the control of the T7 promoter. The cells were cultured at 37 °C until the OD₆₀₀ reached 0.6, and then RavA-OE or ViaA-OE was induced with 40 µM IPTG for 12 h, at 18 °C, under aerobic conditions. For STORM imaging of RavA-OE shown in Fig. 3A, His-BC2-RavA and RavA-BC2-His constructs were used. PALM imaging of ViaA-OE, NTV-OE and CTV-OE shown in Fig. 3A and
Supplementary Figure 2A was performed with His-PamCherry-ViaA, His-ViaA-PamCherry, NT-ViaA-PamCherry-His and His-PamCherry-CTV. For wide-field images of RaV-A-OE and ViaA-OE, His-RaV-A, His-ViaA and AviTag-ViaA-His constructs were used (Supplementary Figure 2B), and in parallel, an aliquot of each of the cultures was used for cellular EM observations (Fig. 3B). Experiments dedicated to lipid extraction and quantification as well as the assessment of the lipid binding site (Fig. 4B, Supplementary Figure 4, Supplementary Figure 5 and Supplementary Figure 6) were all performed with the same RavA-OE and ViaA-OE constructs, namely His-RavA, His-RavAΔΔ, His-ViaA and AviTag-ViaA-His (identical results obtained with His-ViaA), AviTag-ViaA472-His or AviTag-ViaA474E/479E-His. See Supplementary Table 3 for summary.

Fluorescence imaging

For immunofluorescence staining cells were harvested, fixed and permeabilised as described. For epifluorescence imaging of fluorescent protein fusion constructs the procedure was the same except that the fixation was performed with 1% formaldehyde solution in PBS, and that no permeabilisation was necessary.

Wide field imaging

For each sample, 2 μL of cells in suspension were mounted between a glass slide and a 1% gel coverslip, and observed using an inverted IX81 microscope, with the UPLFLN 100× oil immersion objective from Olympus (numerical aperture 1.3), using a fibered Xite™ Metal-Halide excitation lamp in conjunction with the appropriate excitation filters, dichroic mirrors, and emission filters specific for DAPI/Hoechst, AF488, mCherry or AF647 (4X4MB set, Semrock). Acquisitions were performed with Volocity software (Quorum Technologies) using a sCMOS 2048 × 2048 camera (Hamamatsu ORCA Flash 4, 16 bits/pixel) achieving a final magnification of 64 nm per pixel.

STORM and PALM imaging

Super-resolution single molecule localization microscopy was performed using STORM (after nanobody labeling) and PALM (PamCherry fusion proteins) approaches. For STORM imaging, cells labeled as mentioned above, were transferred to a glucose buffer containing 50 mM NaCl, 150 mM Tris (pH 8.0), 10% glucose, 100 mM MEA (mercaptoethanol) and 1X Glox solution from a 10x stock containing 50 mM NaCl, 150 mM Tris (pH 8.0), 10% glucose, 100 mM MEA (mercaptoethanol) and 1X Glox solution from a 10x stock containing 1 μM catalase and 2.3 μM glucose oxidase. For PALM, cells expressing the ViaA fused constructs with PamCherry, were resuspended in PBS. In each case, 2 μL of the cells in suspension were mounted as specified. Mounted samples were imaged on an IX81 microscope (Olympus) by focusing the excitation lasers to the back focal plane of an oil immersion UAPONIO0X (N.A. 1.49) objective. Acquisitions were performed using an Evolve 512 camera with a gain set to 200 (electron-multiplying charge-coupled device EMCCD, 16 bits/pixel, Photometrics) using Metamorph (Molecular Devices). Excitation lasers power was controlled by an Acousto-Optical Tunable Filter (OATF, Quanta Tech). SMLM datasets of about 30,000 frames were generated using a FEI Tecnai12 120 kV LaB6 microscope with an Orius SC1000 CCD camera (Gatan).

Lipid extraction

Lipids were extracted from freeze-dried cells. First, cells were harvested by centrifugation and then immediately frozen in liquid nitrogen. Once freeze-dried, the pellet was suspended in 4 ml of boiling ethanol for 5 min to prevent lipid degradation and lipids were extracted according to Folch et al. by addition of 2 ml of methanol and 8 ml of chloroform. The mixture was saturated with argon and stirred for 1 h at room temperature. After filtration through glass wool, cell remains were rinsed with 3 ml of chloroform/methanol 23: v/v and 5 ml of NaCl 1% were added to initiate biphasic formation. The chloroform phase was dried under argon and the lipid extract was stored at −20 °C.

TLC and GC-FID/MS phospholipid quantification

Total phospholipids were quantified from their fatty acids. The lipid extract was solubilised in pure chloroform and 5 μg of C21:0 (internal standard) were added in an aliquot fraction. Fatty acids were converted to methyl esters (FAME) by a 1-h incubation in 3 ml 2.5% H2SO4 in pure methanol at 100 °C. The reaction was stopped by addition of 3 ml water and 3 ml hexane. The hexane phase was analyzed by gas chromatography coupled to flame ionisation detector (FID) and quadrupole mass spectrometer (full scan acquisition from 50 to 450 m/z) with an electronic impact source (Clarus 680 SQST MS, Perkin Elmer) on a BX70 (SGE) column. FAMES were identified by comparison of their retention times with those of standards (Bacterial Acid Methyl Ester (BAMES) Mix, SigmaAldrich) and by their mass fragmentation spectra compared to the NIST (National Institute of Standards and Technology) database v4.2. They were quantified using C21:0 for calibration. To quantify each class of phospholipid, 300 μg of lipids were separated by two-dimensional thin layer chromatography (TLC) onto glass-backed silica gel plates (Merck). The first solvent was chloroform/methanol/water (65:25:4, v/v) and the second one chloroform:aceton/methanol/acetic acid (50:20:10:5, v/v/v). Lipids were sprayed with 2% 8-anilino-1-naphthalenesulfonic acid in methanol, then visualised under UV light and scraped off the plate. Lipids in the scraped silica were quantified by methanolysis and GC-FID/MS as described above. The total amount of PA in the E. coli membranes being extremely low, PA could not be detected in these experiments, meaning that in the conditions of this study PA represented less than 0.1% of the total membrane phospholipids.

Dot blot assay (protein-lipid overlay assay)

All phospholipids were purchased from Avanti Lipids (Sigma). 2 μL of chlorofom solutions (5, 0.5 and 0.05 mg/mL) of 1-palmitoyl-2-oleoyl-glycerol-3-phosphocholine (16:0-18:1 PC), 1-palmitoyl-2-oleoyl-sn-glycero-3-phospho-L-serine (16:0-18:1 PS), 1-palmitoyl-2-oleoyl-sn-glycerol-3-phosphoethanolamine (PE 16:0-18:1 PE), 1-palmitoyl-2-oleoyl-sn-glycerol-3-phospho-L(-'rac-glycerol) (16:0-18:1 PG), 1-palmitoyl-2-oleoyl-sn-glycerol-3-phosphate (16:0-18:1 PA) and 1,3-bis[1-palmitoyl-2-oleoyl-sn-glycerol-3-phospho-
glycerol (16:0:18:1 Cardiolipin) were spotted using a Hamilton syringe onto a nitrocellulose membrane (Biorad trans-blot turbo RTA Midi 0.2 μm) to yield 10. 1 and 0.1 µg of the lipid per spot. The membranes were blocked using a Tris-buffered saline (TBS) solution (pH 7.4) supplemented with 10% (v/v) non-fat milk powder at room temperature for 1h before incubated with 10 µg/mL of the purified proteins (His-Rava, AviTag-ViaA-His, LdcI-His) or protein complex (LdcI-Rava) in TBS containing 0.05% (v/v) Tween-20 (TBS). LdcI was purified as previously described. After overnight incubation at 4 °C, the membranes were washed with TBS (3 x 15 min) and probed either with a rat polyclonal antibody raised against the purified ViaA (Qalam-antibody) or a rabbit polyclonal antibody raised against the purified Rava or LdcI proteins (Qalam-antibody), diluted 1:10.000 in TBS, at room temperature for 1h. The membranes were washed with TBS (3 x 15 min) and further incubated with either anti-mouse or anti-rabbit IgG secondary antibody conjugated with horseradish peroxidase (Merck), diluted 1:10.000 in TBS, at room temperature for 1h. After washing with TBS (3 x 15 min), the chemiluminescence signal was developed using a Pierce ECL Western blotting substrate (Thermo Fisher Scientific, USA) and recorded using a ChemiDoc XR+ System (Bio Rad, USA).

For Rava bound to ViaA, the milk-blocked membrane was incubated with TBS alone (Rava only) or with 10 µg/mL AviTag-ViaA-His overnight at 4 °C, washed three times with TBS buffer and incubated with 10 µg/mL His-Rava for 2h at room temperature. The chemiluminescent signal was developed after the incubation of the membranes with anti-Rava serum followed by incubation with the HRP-conjugated secondary antibody. Likewise, for ViaA bound via Rava, the membrane was incubated with 10 µg/mL His-Rava overnight before incubation with 10 µg/mL AviTag-ViaA-His. The LdcI-Rava complex was prepared by mixing the purified LdcI and His-Rava proteins in molar ratio of 1:2.25 (LdcI-Rava) before incubating for 30 min at room temperature. The milk-blocked membranes were incubated with His-Rava (10 µg/mL) or LdcI (6.5 µg/mL) alone or with the LdcI-Rava complex (corresponding to the final concentration of LdcI and Rava proteins of 6.5 µg/mL and 10 µg/mL, respectively) diluted in TBS supplemented with 10 mM MgCl2 and 2 mM ADP. After overnight incubation at 4 °C, the membranes were washed and the chemiluminescent signal was developed after incubation of the membranes with anti-Rava or anti-LdcI sera followed by incubation with the HRP-conjugated secondary antibody (both diluted also in TBS-Mg-ADP buffer).

**Time-dependent killing assay**

This experiment was performed as previously described. Briefly, overnight cultures were diluted (1/100) and grown anaerobically at 37 °C to an OD600 of 0.2 in LB medium supplemented with 10 mM fumarate. At this point (T0), Gm was added to the cells at 16 µg/mL. After 0, 1.5 and 3h, 100 µL of cells were diluted in sterile phosphate buffer saline solution (PBS buffer), spotted on LB agar and incubated at 37 °C for 48h. Cell survival was determined by counting CFU/mL and normalized relative to T0. This assay was performed in an anaerobic chamber (Jacomex, France).

**Planar lipid bilayer experiments**

Planar lipid bilayer measurements were performed at 25 °C using a home-made Teflon cells separated by a diaphragm with a circular hole with the diameter of 0.5 mm. The membrane was formed by a painting method using a mixture of lipids composed of PA:PG:PE (10:45:45) dissolved in n-decane and 3% asolectin dissolved in n-decane:butanol (9:1) for ViaA and Rava proteins and the β, pertussis pore-forming CyaA toxin, respectively. The membrane current was recorded by Theta Ag/AgCl electrodes after addition of 2 mM AviTag-ViaA-His, His-RavaA or 250 pM CyaA in 10 mM TRIS-HCl (pH 7.4), 0.15 M KCl and 2 mM CaCl2 using applied potential of ~50 and ~50 mV. The signal was amplified by an LCA-200-100G Ultra-Low-Noise Current Amplifier (Femto, Germany) and digitised by a Keithley KPCI-3108 PCI Bus Data Acquisition Boards card. The signal was analysed using QuB (https://qub.mandelics.com) and processed using a 10-Hz filter.

**Reporting summary**

Further information on research design is available in the Nature Research Reporting Summary linked to this article.

**Data availability**

The data that support this study are available from the corresponding authors upon reasonable request. The source data underlying Figs. 1, 2, 4, 6, and Supplementary Figures 1, 5, 6, 7 and 8 are provided as a Source Data file. Source data are provided with this paper.

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Competing interests

The authors declare no competing interests.

Additional information

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