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Lipid discovery enabled by sequence statistics and machine learning

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eLife Assessment

This study reports **important** findings on identifying sequence motifs that predict substrate specificity in a class of lipid synthesis enzymes. It sheds light on a mechanism used by bacteria to modify the lipids in their membrane to develop antibiotic resistance. The evidence is **compelling**, with a careful application of machine learning methods, validated by mass spectrometry-based lipid analysis experiments. This interdisciplinary study will be of interest to computational biologists and to the community working on lipids and on enzymes involved in lipid synthesis or modification.

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Abstract

Bacterial membranes are complex and dynamic, arising from an array of evolutionary pressures. One enzyme that alters membrane compositions through covalent lipid modification is MprF. We recently identified that *Streptococcus agalactiae* MprF synthesizes lysyl-phosphatidylglycerol (Lys-PG) from anionic PG, and a novel cationic lipid, lysyl-glucosyl-diacylglycerol (Lys-Glc-DAG), from neutral glycolipid Glc-DAG. This unexpected result prompted us to investigate whether Lys-Glc-DAG occurs in other MprF-containing bacteria, and whether other novel MprF products exist. Here, we studied protein sequence features determining MprF substrate specificity. First, pairwise analyses identified several streptococcal MprFs synthesizing Lys-Glc-DAG. Second, a restricted Boltzmann machine-guided approach led us to discover an entirely new substrate for MprF in *Enterococcus*, diglucosyl-diacylglycerol (Glc_2-DAG), and an expanded set of organisms that modify glycolipid substrates using MprF. Overall, we combined the wealth of available sequence data with machine learning to model evolutionary constraints on MprF sequences across the bacterial domain, thereby identifying a novel cationic lipid.

1 Introduction

Lipids are ubiquitous and diverse group of amphiphathic compounds that are critical for fundamental biological processes, including the formation of cell membranes, protection, and cargo delivery; energy storage; and cell signaling pathways [1]. Chemical modifications to lipids, including changes in fatty acid tails (saturated and unsaturated) [2], modifications of head groups [3], and alterations to lipid charge [4], impact these interactions, as well as the physicochemical properties of membranes. Commonly, bacteria synthesize lipids that are negatively charged or neutral [5]. Some bacteria modify the negatively charged lipids with amino acids to make them positively charged to confer resistance to cationic antimicrobial peptides and cationic antibiotics [6, 7]. The bacterial domain is a rich source of natural lipids that are likely co-evolved for specific interactions with host tissues and other cells, yet the full extent of this chemical diversity remains unexplored. Finding bacteria that possess unique lipids can be useful for biotechnology. For example, natural lipids found in bacteria can be used for drug delivery. A study by [8] used low cytotoxic outer membrane vesicles (OMV) that contained a modified lipopolysaccharide (LPS) to deliver siRNA to targeted cancer cells. This delivery mechanism had success and demonstrates the possibility of using naturally occurring bacterial lipids for future drug delivery processes to eukaryotic cells.

One enzyme responsible for modifying lipids in bacteria is the multiple peptide resistance factor (MprF). MprF modifies lipids through the transfer of amino acids from charged tRNAs to the head group of the anionic membrane phospholipid, phosphatidylglycerol (PG) [4]. The MprF protein is comprised of two domains: an N-terminal flippase domain responsible for moving aminoacylated lipids from the inner membrane leaflet to the outer leaflet and a C-terminal synthase domain responsible for the aminoacyl transfer from tRNA to lipids [9, 10]. Recently, in *Streptococcus agalactiae* (Group B *Streptococcus*, GBS) it was found that MprF can modify two different substrates with lysine (Lys) – the glycolipid glucosyl-diacylglycerol (Glc-DAG) and the phospholipid, PG [11], generating Lys-Glc-DAG, as well as Lys-PG [11, 12] (**Figure 1**). An *S. agalactiae mprF* deletion mutant no longer synthesizes Lys-Glc-DAG or Lys-PG and expression of *S. agalactiae mprF* in the heterologous host *Streptococcus mitis* conferred Lys-Glc-DAG and Lys-PG synthesis to *S. mitis* [11]. This was the first time MprF was demonstrated to add lysine onto a neutral glycolipid (Glc-DAG).

The synthesis of Lys-Glc-DAG by *S. agalactiae* MprF illustrated a unique lipid substrate and product by the enzyme that had not been characterized before, highlighting the possibility for further exploration into unknown lipids and lipid substrates by MprF of different bacterial species. We sought to investigate the molecular determinants of enzyme specificity and identify other bacterial species that may have this novel specificity. This investigation led us from the standard methodology of BLASTp queries [13], which are based on single residue amino acid substitution frequencies, to a more modern statistical method called a Restricted Boltzmann Machine (RBM) [14], which captures global statistical patterns within natural sequence data. In this work, we develop a general strategy for combining this high-powered statistical model with lipidomic analysis to discover MprF variants with unique enzymatic activity. This process led us to the discovery of an uncharacterized lipid substrate for MprF, diglucosyl-diacylglycerol (Glc_2-DAG), which is present in several strains identified by the parameters of the statistical model. These models also provide interpretable and actionable information for use in further enzyme characterization, and we show that this application is a useful companion tool for experimental work.

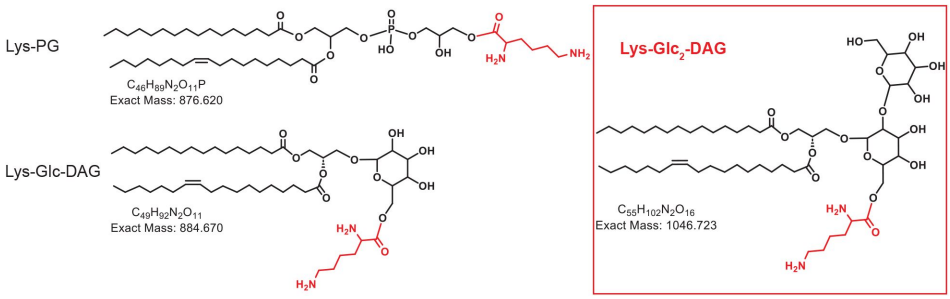


Figure 1

Chemical structures of lysine lipids. Lys-PG, lysyl-phosphatidylglycerol; Lys-Glc-DAG, lysylglucosyl-diacylglycerol; Lys-Glc_2-DAG, lysyl-diglucosyl-diacylglycerol.

2 Results

2.1 Simple pairwise sequence statistics identify streptococcal MprF enzymes that synthesize Lys-Glc-DAG

Utilizing a method based on the amino acid sequence of *S. agalactiae* MprF, we identified four streptococcal MprFs with high sequence identity to *S. agalactiae* COH1 MprF (WP 000733236.1). A BLASTp analysis found that *Streptococcus sobrinus* ATCC 27352 MprF (WP 019790557.1) had 61.4% amino acid identity to the *S. agalactiae* MprF, *Streptococcus salivarius* ATCC 7073 MprF (WP 002888893.1) had 43.09% amino acid identity, *Streptococcus ferus* MprF (WP 018030543.1) had 61.88% amino acid identity, and *Streptococcus downei* (WP 002997695.1) had 61.03% amino acid identity (**Table 1**). Plasmids were designed to express the *S. sobrinus mprF* (pSobrinus), *S. salivarius mprF* (pSalivarius), *S. ferus mprF* (pFerus), and *S. downei mprF* (pDownei) genes. The plasmids were transformed into the expression host *S. mitis* NCTC12261 (SM61). The empty vector (pABG5Δ*phoZ*, referred to as pABG5 here) was also transformed (**Figure 2a**). *S. mitis* does not natively encode *mprF* but synthesizes lipids (Glc-DAG; PG) that are substrates for *S. agalactiae* MprF [15, 16, 11], making it an appropriate heterologous host for expressing streptococcal MprFs. Previously, a plasmid expressing *S. agalactiae mprF* (pGBSMprF) [11] was generated and transformed into *S. mitis*. Lys-Glc-DAG and Lys-PG presence in SM61 was only possible with the expression of pGBSMprF (**Figure2b**) [11].

S. mitis lipids of strains expressing the plasmids pSobrinus (**Table 1**), pSalivarius (**Figure 2c**), pFerus (**Figure 2d**) and pDownei (**Table 1**) were analyzed. Lipidomic analysis found that pSobrinus, pDownei, and pFerus conferred synthesis of Lys-Glc-DAG, but not Lys-PG in *S. mitis*. Notably, pFerus confers synthesis of Lys-Glc-DAG at a similar level to *S. agalactiae* MprF (**Figures 2b, d**). In contrast, pSalivarius conferred synthesis of Lys-PG only and not Lys-Glc-DAG. Importantly, *S. salivarius* MprF also synthesized Lys-PG at a level most similar to *S. agalactiae* MprF (**Figures 2b, c**). Lysine-modified lipids synthesized by *S. mitis* strains expressing streptococcal MprFs used in this study are summarized in **Table 1**. In general, streptococcal MprF enzymes with higher amino acid percent (> 60%) to *S. agalactiae* MprF conferred Lys-Glc-DAG synthesis to *S. mitis*, but only *S. agalactiae* MprF conferred both Lys-Glc-DAG and Lys-PG synthesis in *S. mitis*.

2.2 Restricted Boltzmann Machines can provide sensitive, rational guidance for sequence classification

We set out to understand which specific MprF amino acid residues are involved in enzyme specificity for either the PG or Glc-DAG substrate. To this end, we employed a Restricted Boltzmann Machine (RBM), a probabilistic graphical model which aims to model the probability of data in a data set through statistical connections between the features of the data and a set of hidden units. [17]. This class of models is closely related to another model termed the Boltzmann Machine. The Boltzmann machine formulation is closely related to the Potts model from physics, which was successfully applied in biology to elucidate important residues in protein structure and function [18], one example being the careful tuning of enzyme specificity in bacterial two-component regulatory systems [19, 20]. The Boltzmann Machine formulation from [18], termed Direct-Coupling Analysis (DCA), stores patterns in the form of a pairwise coupling matrix and local field matrix (shown in Equation 2), which has been useful in understanding how likely pairs of residues are to interact in physical space. We hypothesize that *S. agalactiae* MprF and other MprF enzymes that utilize glycolipid substrates have unique patterns of interacting residues relative to those enzymes that use only PG as a substrate.

Table 1

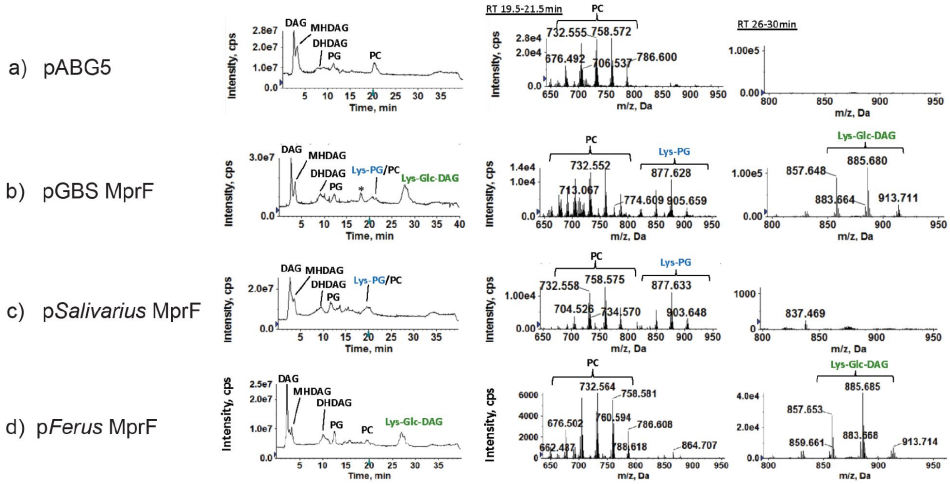
Summary of different MprF variants expressed in *S. mitis* and the lysine lipids they produce.

Percentage of amino acid identity and similarity compared to *S. agalactiae* COH1 MprF; data obtained from BLASTp. The lipids each strain synthesize are denoted by a checkmark or an x. Lys-PG, lysyl-phosphatidylglycerol; Lys-Glc-DAG, lysyl-glycosyl-diacylglycerol.

Bacteria Strains	% Amino Acid Identity (Similarity)	Lys-PG	Lys-Glc-DAG
SM61(pGBSMprF)	100.0 (100.0)	✓	✓
SM61(pFerus)	61.9 (79.0)	X	✓
SM61(pSobrinus)	61.4 (79.0)	X	✓
SM61(pDownei)	61.0 (79.0)	X	✓
SM61(pSalivarius)	43.1 (66.0)	✓	X
SM61(pABG5)	- (-)	X	X

Figure 2

Synthesis of lysine lipids (Lys-PG and Lys-Glc-DAG) in *S. mitis* expressing *mprFs* from *S. agalactiae, S. salivarus*, and *S. ferus*. (a) *S. mitis* NCTC12261 with empty vector control (pABG5) lacks lysine lipids; (b) *S. agalactiae mprF* (pGBSMprF) produces both Lys-PG and Lys-Glc-DAG; (c) *S. salivarius mprF* produces only Lys-PG; (d) *S. ferus mprF* produces only Lys-Glc-DAG. Left panels: total ion chromatograms (TIC); middle panels: mass spectra of retention time 19.5–21.5 min showing Lys-PG and PC; right panels: mass spectra of retention time 26–30 min showing Lys-Glc-DAG. Note: "*" is an extraction artifact due to chloroform used. DAG, diacylglycerol; MHDAG, monohexosyldiacylglycerol; DHDAG, dihexosyldiacylglycerol; PG, phosphatidylglycerol; Lys-PG, lysyl-phosphatidylglycerol; Lys-Glc-DAG, lysylglucosyl-diacylglycerol; PC, phosphatidylcholine.



While modeling how pairs of residues covary is powerful, many important features of enzyme function like allostery or enzyme specificity (which is the purpose of this analysis) may involve more than two residues [21], and in these situations it can be difficult to connect sets of residues using solely pairwise parameters [22]. Therefore, a more global approach is required to address our hypothesis. To this end, a RBM has recently been developed for use in the learning of protein sequence data, with special attention given to producing a model which produces sparse, interpretable, and biologically meaningful representations of these higher-order statistical couplings within the hidden units [14]. The design of this RBM can be seen in **Figure 3**, where the model architecture is represented by purple dots and green triangles. The dots are the "visible" layer, which take in input sequences and encode them into the "hidden" layer, where each triangle represents a separate hidden unit. The lines connecting the visible and hidden layers show that each hidden unit can see all the visible units (the statistics are global), but they cannot see any of the other hidden units, meaning the hidden units are mutually independent. This global model with mutually independent hidden units (see the marginal distribution form shown in **Equation 3**) allows the following useful properties: higher-order couplings between residues (sets of coupled residues instead of pairs); bimodal hidden unit outputs given the training data set (**Equation 4**); sparse, interpretable configurations of the hidden units (w_μ) (**Equation 5**) and a compositional representation of the hidden unit weights [23], where input sequences are modeled largely through combinations of hidden units instead of single, highly activating units.

The compositional representation is a critical feature of this method, allowing us to find independently coupled sets of residues which in combination describe these protein sequences, and it is achieved through the particular choices of training parameters. More details on the training parameter choices are found in *Methods and Materials*. In particular, we focus on the scoring of sequences using individual hidden units w_μ:

$$I_\mu(\mathbf{v}) = \sum_i \mathbf{w}_{i\mu}(\mathbf{v}_i) \qquad (1)$$

where **v** is an input sequence vectorized through one-hot encoding, to produce a hidden unit activation (a single number) which depends on the input sequence residues at position *i* and the value of the hidden unit weight matrix for that residue at that position.

We used this methodology to study the sequences in the family of MprF, which is a large protein composed of independent flippase and synthase domains [9, 24]. In our analysis, we restrict ourselves to the cytosolic region (see yellow box in **Figure 4a**), also known as the aminoacyl-PG synthase domain, which constituted the Pfam family DUF2156 (now renamed LPG synthase C) [25]. One hidden unit in particular is highlighted, where we find bimodal activation (**Figure 4b**) of the hidden unit (**Figure 4c**) when **Equation 1** is evaluated with the training sequences. Interpreting the sequence histograms, a positive value activation in **Figure 4b** corresponds to a sequence containing combinations of the residues listed in the positive portion of the weight diagram in **Figure 4c**, whereas a negative activation corresponds to residues in the negative portion. For display purposes, the residue weights shown in all of our hidden units correspond to the positions where the magnitude of the visible positions $w_{i\mu}$ are greater than some threshold proportional to the largest magnitude position (position 212); the hidden units has values for all possible amino acids in the entire protein length, but they are considerably smaller than this threshold and generally very low.

Two positions in particular, 152 and 212, in the positive portion of the hidden unit correspond to residues 684 and 742, which were experimentally demonstrated to be relevant for aminoacylated-PG production by the *Bacillus licheniformis* and *Pseudomonas aeruginosa* cytosolic synthase domain variants [26]; in *B. licheniformis* the residues which form a complex with the lysine from Lys-tRNA^{Lys} are shown in **Figure 4c**. We have highlighted these two aforementioned variants as well as the *S. agalactiae* variant for demonstration of sequence scoring through

Figure 3

Schematic of the RBM methodology. An aligned set of protein sequences is first used to learn a hidden unit representation that best describes the statistics of the sequence dataset given restrictions on the hidden unit representation. Then, the individual hidden units can be studied to find particular units which allow useful enzyme classification, and additionally, these weights can be meaningfully interpreted as statistically co-varying sequence configurations. Additionally, the classification can be used to create filtered datasets to train more models.

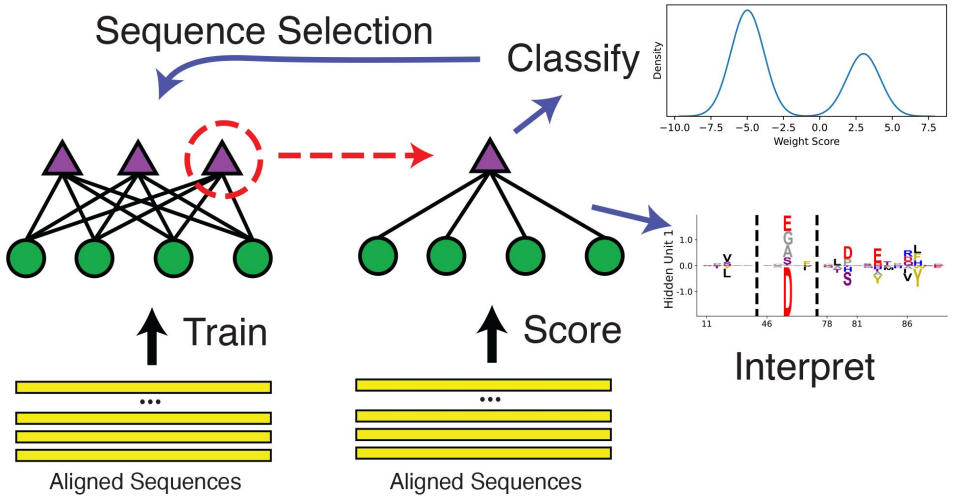
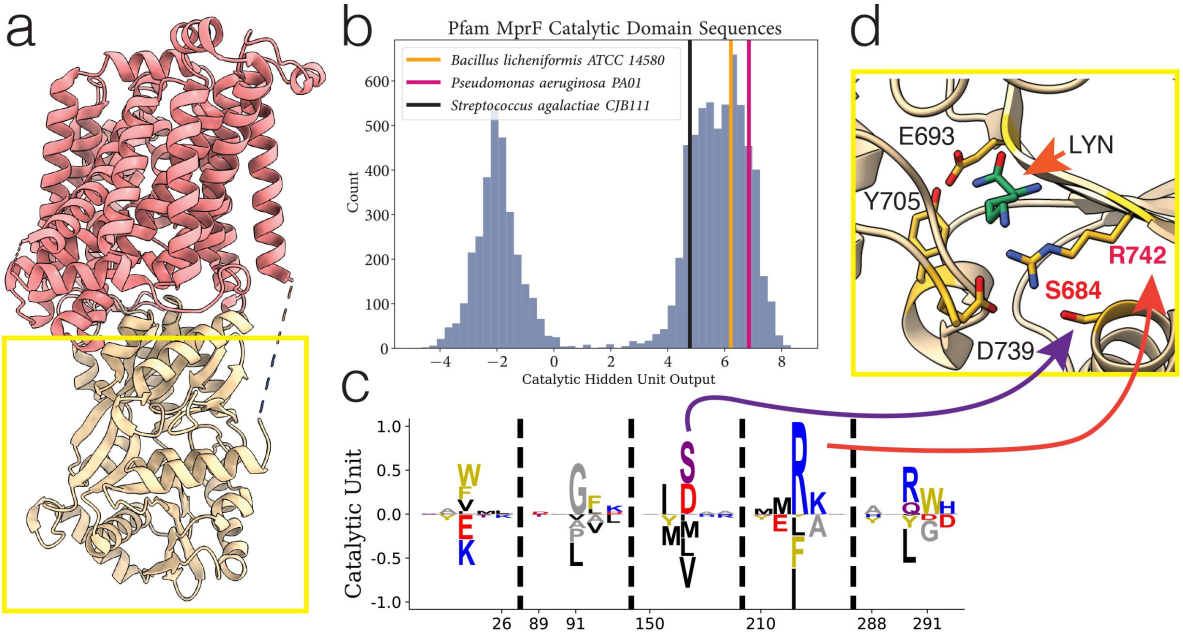


Figure 4

Example of hidden unit analysis and usage. (a) The structure of PDB:7DUW, with the red colored region being the transmembrane flippase domain and the yellow boxed region the cytosolic domain which we focus on. (b) The activations produced by inputting a sequence into a hidden unit, producing a single number as output which corresponds to a summation of negatively and positively weighted residues. Performed on entire training set (histogram in blue), highlighting sequences corresponding to predominantly positive weighted residues. (c) Hidden unit from an RBM trained on the Pfam DUF2156 domain. The MSA positions 152 and 212 correspond to residues S684 and R742, respectively. (d) Residues (in yellow) in the MprF cytosolic domain which form the binding pocket for Lys-tRNA^{Lys} (the ligand analogue L-lysine amide shown in green), from PDB:4V36. LYN, L-lysine amide.



Equation 1 in **Figure 4a**. We used this hidden unit to create a filtered data set; only sequences that contained this necessary motif were of interest to us, and we subsequently trained a new model using only sequences with a catalytic hidden unit activation greater than 2 (because it cleanly split the bimodal distribution). We outline this general workflow in **Figure 3**. We also note that the full length sequences of the sequences included in our new dataset are enriched with sequences which contain the bacterial flippase domain (shown in red in **Figure 4a**), and the sequences we removed rarely contain the flippase domain (see **Figure S2** for domain analysis).

2.3 RBM hidden units identify plausible sequence residues for functional characterization

After filtering the data set and training another model, we set out to find hidden units which could describe MprF specificity. To this end, we identify hidden units which are sparse, have high overall magnitude, and involve residues which could be plausibly linked to the lipid binding specificity (see Methods for more details). Through this search method we identified the two hidden units shown in **Figure 5a**. They both have high sparsity and high magnitude relative to the majority of other hidden units in the model, and importantly they correspond to residues localized to regions of the catalytic domain that had been previously identified through Autodock experiments using a PG molecule with side chains C5:0/C8:0 [26] (highlighted in **Figure 5a**). The scoring of the training set of sequences with these hidden units is shown in **Figure 5b**, and we see a clear separation between the cytosolic domain sequences which produces Lys-Glc-DAG (from *S. agalactiae*) and two domain variants which produce only aminoacylated-PG (from *P. aeruginosa* and *B. licheniformis*). Importantly, these output activations depend on a greatly reduced subset of the full sequence and do not correspond to clustering on total sequence identity (**Figure S1**).

Using these two hidden units as sequence classifiers with a potential link to the substrate specificity of cytosolic domain variants, we used **Figure 5b** to propose sequences in quadrant three (Q3), the quadrant occupied by the *S. agalactiae* MprF variant with this novel glycolipid-modifying function. We selected a sequence which was distant in terms of sequence identity from the *Streptococcus* genus (**Table S1**) and which has been implicated in human pathologies [27], *Enterococcus dispar* MprF. We also emphasize that the two hidden units we selected are from a set of 300 total hidden units, and that while other hidden units may differentially classify our three sequences, without the additional link to lipid binding provided by the Autodocking experiment there would be only weak justification for using their activations to make predictions.

2.4 Enterococcal MprF enzymes synthesize Lys-Glc-DAG, Lys-PG, and a novel cationic glycolipid Lys-Glc$_2$-DAG

Enterococcus dispar ATCC 51266 was identified as a possible candidate for novel lipid synthesis through the analyses described above. Remarkably, our lipidomic analysis found that *E. dispar* synthesizes a novel cationic lipid, lysyl-diglucosyl(Glc$_2$)-diacylglycerol (Lys-Glc$_2$-DAG) (**Figure 1**, **Figure 6a,b**), as well as Lys-Glc-DAG and Lys-PG (**Figure 6c**, **Figure S3**). The structural identification of Lys-Glc-$_2$-DAG was supported by exact mass measurement ($[M+H]^+$ observed at *m/z* 1047.730; calculated *m/z* 1047.731) and tandem MS (**Figure 6b**). Lys-Glc-$_2$-DAG is unusually polar and charged for a lipid; chromatographically, Lys-Glc$_2$-DAG is highly retentive on a silica-based normal phase column and elutes off the column at the very end of the gradient (**Figure S3**). The use of an amino-based HPLC column led to much improved elution profiles for Lys-Glc$_2$-DAG and other glyco- and lysine lipids (**Figure 6**).

The discovery of Lys-Glc$_2$-DAG in *Enterococcus dispar* led us to analyze other *Enterococcus* strains: *E. faecium* 1,231,410, *E. faecalis* T11 and OG1RF *E. gallinarium* EG2, *E. casseliflavus* EC10, and *E. raffinosus* Er676. All *Enterococcus* strains examined were found to synthesize Lys-PG, Lys-Glc-DAG and Lys-Glc$_2$-DAG at varying levels (**Figure 7a** and **Table 2**). MprF-dependent Lys-PG production by *E.faecalis* and *E. faecium* was previously reported [28, 29], but cationic

Figure 5

Proposed set of hidden units for classifying lipid specificity. (a) two hidden units found in an RBM trained on the filtered Pfam dataset. The hidden unit residues are highlighted in the PDB:4V34 structure, with arrows pointing to their corresponding residue sets. (b) the activations of the hidden units when scoring the sequences used in the training set and sequences from NCBI not used during training (N=23,138). *S. agalactiae* produces Lys-Glc-DAG and Lys-PG, while *B. licheniformis* and *P. aeruginosa* produces only aminoacylated-PG. Q1-Q4 are quadrant labels which we refer to throughout the paper.

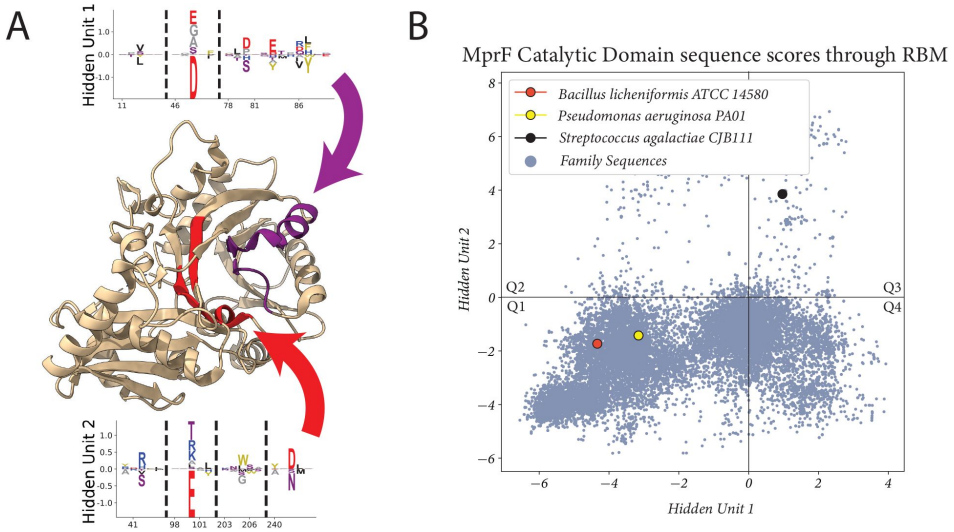
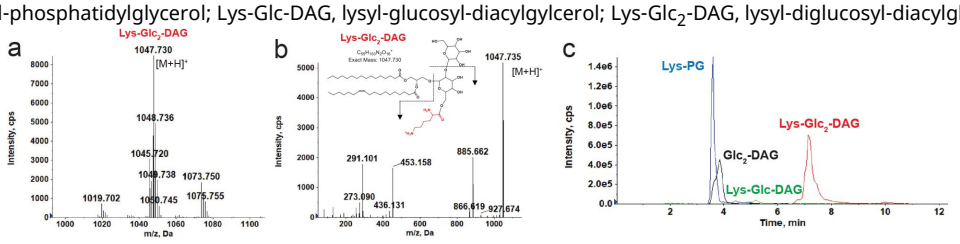


Figure 6

Identification of Lys-Glc$_2$-DAG in *E. dispar*. (a) Positive ion mass spectrum of Lys-Glc$_2$-DAG species in *E. dispar*. Major Lys-Glc$_2$-DAG species with carbon atoms (before colon) and double bonds (after colon) (b) MS/MS product ions and fragmentation scheme of the most abundant Lys-Glc$_2$-DAG ion at *m/z* 1047.73. (c) Extracted ion chromatograms of LC/MS of lysine lipids (Lys-PG, Lys-Glc-DAG, Lys-Glc$_2$-DAG) and Glc$_2$-DAG separated on an amino HPLC column. Glc$_2$-DAG, diglucosyl-diacylglycerol; Lys-PG, lysyl-phosphatidylglycerol; Lys-Glc-DAG, lysyl-glucosyl-diacylgylcerol; Lys-Glc$_2$-DAG, lysyl-diglucosyl-diacylglycerol.



glycolipids production has not been previously reported. *E. gallinarium* EG2 and *E. casseliflavus* EC10 encode a single copy of *mprF* gene, while the other enterococci we tested encode two distinct *mprF* genes (*mprF*1 and *mprF*2) [28, 29]. When these MprF sequence variants are plotted using our chosen RBM hidden units, we see that the two single copy strains plot in quadrant two (Q2), while for the two copy sequences, each MprF variant maps to separate coordinates (**Figure S4**). Both *E. raffinosus* Er676 MprF variants plot to quadrant two (with the lowest Weight 2 value being 0.34). The *E. faecium* and *E. faecalis* variants have copies plotting directly in quadrant one and variants plotting farther out from the sequence cluster; we note that the two displaced variants are both lacking the characteristic aspartic acid and glutamic acid amino acids at positions 100 and 48 in the hidden units (**Figure 5a**), which are the dominant contributions for determining quadrant one occupancy.

To clarify which variants were determinants of the novel cationic lipid production, lipidomic analysis on an *E. faecalis* OG1RF mini-mariner (EfaMarTn) transposon mutant [30] with a transposon insertion within OG1RF_10760 *mprF* (referred to as *mprF* 2 in previous studies [28]; OG1RF_10760::Tn) revealed that Lys-PG, Lys-Glc-DAG and the newly identified Lys-Glc$_2$-DAG were absent when the synthase domain of the gene was disrupted (**Figure 7b**, **Table S1**). This led us to the conclusion that *E. faecalis mprF* 2 is necessary for the synthesis of the three Lys-lipids in *E. faecalis*. When the empty vector (pABG5) was transformed into OG1RF_10760::Tn, no Lys-lipids synthesis was observed as expected (**Figure 7c**). This phenotype was complemented by expression of *E. faecalis mprF* 2 from a plasmid (pOGMprF2) (**Figure 7d**). Additionally, expression of *E. faecium mprF1* (EFTG_00601) (pEfMprF1) restored Lys-PG and Lys-Glc$_2$-DAG synthesis to the *E. faecalis* OG1RF_10760::Tn strain (**Figure 7e**), while *E. faecium mprF2* (EFTG_02430) did not rescue Lys-lipid synthesis (**Figure 7f**). Taken together, these data indicate that *E. faecalis* MprF2 (OG1RF_10760) and *E. faecium* MprF1 (EFTG_00601), like *S. agalactiae* MprF, act on both phospholipid and glycolipids substrates, additionally synthesizing the novel cationic glycolipid, Lys-Glc$_2$-DAG.

2.5 Hidden unit 2 is correlated with Glc$_N$-DAG substrate activity in MprF

When we started our RBM analysis, we had substrate specificity information for only the quadrants one and three, and through identifying the novel substrate in *E. dispar* we expanded our testing to quadrant two by testing *Enterococcus* strains. To expand our RBM analysis, we tested specific sequences which were found in quadrant four (Q4). We conducted lipid analysis on *Ligilactobacillus salivarius* ATCC 11741, *Levilactobacillus brevis* ATCC 14869, *Lacticaseibacillus rhamnosus* ATCC 7469, *Lactobacillus casei* ATCC 393, and *Lacticaseibacillus paracasei* ATCC 25302. All strains tested synthesize Lys-PG (**Table 2**). Only *Levilactobacillus brevis* and *Lacticaseibacillus paracasei* synthesized Lys-Glc$_2$-DAG, *L. paracasei* synthesized low levels of Lys-Glc$_2$-DAG. An additional quadrant one (Q1) strain *Exiguobacterium acetylicum* UTDF19-27C, was analyzed by lipidomics. It was found to synthesize only Lys-PG. This MprF falls near *Staphylococcus aureus* RN4220 and *Bacillus subtilis* 168 in our plot, both of which synthesize only Lys-PG [31, 24] (and experimentally confirmed in this study). This further supports that strains located in quadrant one of **Figure 8** are capable of Lys-PG synthesis.

Summaries of all functional species/variants tested and the Lys-lipids they produced are shown in **Table 2**, and plotted in the two RBM hidden units in **Figure 8**. We list for each MprF variant which of the three tested lipids it acts on, and in **Figure 8** we indicate whether a variant has only PG as a substrate or if it operates on Glc$_N$-DAG as a substrate irrespective of its PG activity. With this plot, we can see that sequences which plot with positive activations in hidden unit 2 are more likely to have Glc$_N$-DAG as a substrate (8/9), and sequences with negative values predominantly use PG (7/11), with a Fisher's exact test p-value of 0.028 (**Table S2**). Hidden unit

Table 2

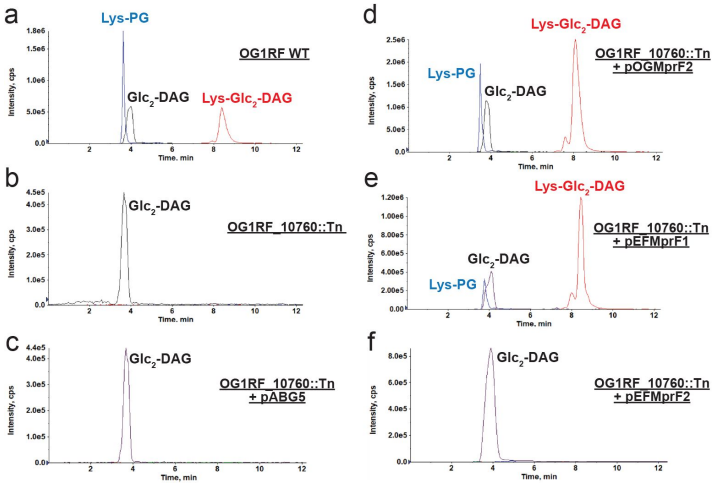
Table of all strains studied, the quadrant they occupy, and the lipids they synthesize.

** trace amounts Lys-Glc-DAG present in lipid extractions. * indicates heterologous expression of *mprF* in *Streptococcus mitis*. Lys-Glc-DAG, lysyl-glucosyl-diacylglycerol; Lys-Glc$_2$-DAG, lysyl-diglucosyl-diacylglycerol; Lys-PG, lysyl-phosphatidylglycerol.

	Bacterial Strains	Lys-Glc-DAG	Lys-Glc$_2$-DAG	Lys-PG
Q1	*Bacillus subtilis* 168	X	X	✓
	Bacillus licheniformis ATCC 14580	X	X	✓
	Staphylococcus aureus RN4220	X	X	✓
	Exiguobacterium acetylicum UTDF19-27C	X	X	✓
	Enterococcus faecalis T11/OG1RF**	✓	✓	✓
	Enterococcus faecium 1,231,410	✓	✓	✓
Q2	*Enterococcus raffinosus* Er676	✓	✓	✓
	Enterococcus gallinarum EG2	✓	✓	✓
	Enterococcus casseliflavus EC10	✓	✓	✓
Q3	*Streptococcus salivarius** ATCC 7073	X	X	✓
	Enterococcus dispar ATCC 51266	✓	✓	✓
	Streptococcus agalactiae CJB111/COH1	✓	X	✓
	*Streptococcus sobrinus** ATCC 27352	✓	X	X
	*Streptococcus downei** (WP_002997695.1)	✓	X	X
	*Streptococcus ferus** (WP_018030543.1)	✓	X	X
Q4	*Ligilactobacillus salivarius* ATCC 11741	X	X	✓
	Lacticaseibacillus rhamnosus ATCC 7469	X	X	✓
	Lactobacillus casei ATCC 393	X	X	✓
	Levilactobacillus brevis ATCC 14869	X	✓	✓
	Lacticaseibacillus paracasei ATCC 25302	X	✓	✓

Figure 7

E. faecalis MprF2 and *E. faecium* MprF1 confer Lys-Glc$_2$-DAG synthesis. (a) OG1RF-WT; (b) OG1RF_10760::Tn lacks lysine lipids; (c) OG1RF_10760::Tn + pABG5 lacks lysine lipids; (d) OG1RF_10760::Tn + pOGMprF2 restores lysine lipids; (e) OG1RF_10760::Tn + pEFMprF1 restores lysine lipids; (f) OG1RF_10760::Tn + pEFMprF2 lacks lysine lipids. Expression of OGMprF2 and EFMprF1 in OG1RF_10760 Tn mutant restore Lys-Glc$_2$-DAG synthesis. Shown are the extracted ion chromatograms of lysine lipids (Lys-PG, Lys-Glc$_2$-DAG) and Glc$_2$-DAG separated on an amino HPLC column. Note: Lys-Glc-DAG was found in trace amounts or missing from lipid extractions. Glc$_2$-DAG, diglucosyl-diacylglycerol; Lys-PG, lysyl-phosphatidylglycerol; Lys-Glc$_2$-DAG, lysyl-diglucosyl-diacylglycerol.



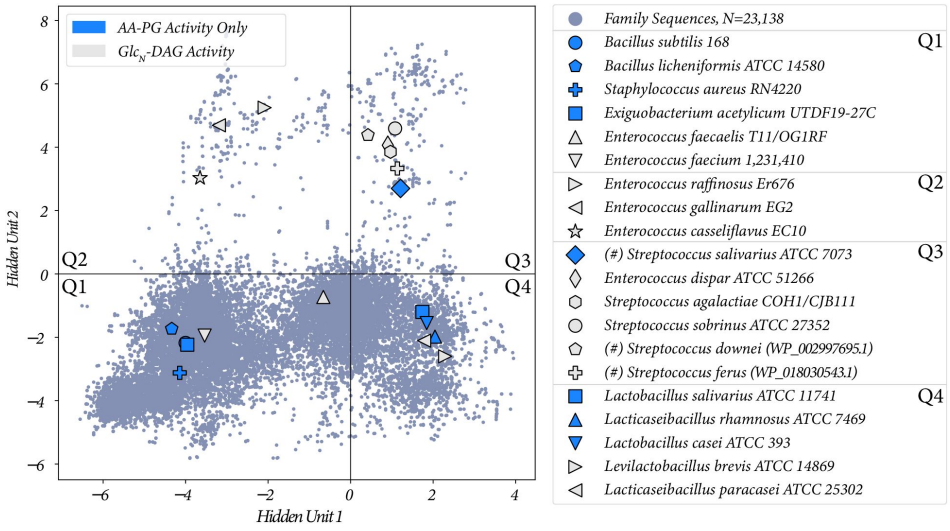


Figure 8

The two proposed hidden unit activations with all of the sequences from **Table 2** labeled. Protein ID of highlighted sequences are listed in **Table S1**. (#) indicates the lipid activity was confirmed through heterologous expression.

1, however, is not correlated with Glc_N-DAG specificity, with a Fisher's exact p-value of 0.67. Therefore we conclude that hidden unit 2, and thus the high magnitude sequence positions identified by it, are correlated with Glc_N-DAG specificity.

3 Discussion

The utilization of the *S. agalactiae* MprF amino acid sequence as a query for BLASTp was a simple method to identify various streptococcal MprFs and further our understanding of MprF specificity. This allowed us to identify three MprFs that can synthesize the highly cationic Lys-Glc-DAG. Importantly, although highly similar to *S. agalactiae* MprF, this method did not identify other streptococcal MprFs capable of lysine addition to both glycolipid and phospholipid substrates (generating Lys-Glc-DAG and Lys-PG) nor did it lead to the identification of a novel cationic glycolipid found in *Enterococcus*. Sequence logos [32] may identify important sequence features, but largely in instances where amino acids are highly conserved. When amino acids must interact to produce a specific function, yet the exact identity of those amino acids is not a requirement, methods which model the strength of amino acid coevolution in sequence sets can find important signals which in the sequence logo might appear to be negligible. For this reason we used the Restricted Boltzmann Machines (RBM) method [14], which can model statistical connectivity of residues at multiple sites in the protein sequence.

The RBM can be used in a number of ways to study sequence data. Firstly, it allowed us to filter the sequence data using hidden units (**Figure 4**); the two hidden units which formed the basis of our specificity analysis were not found in models trained on the Pfam dataset when it was initially pulled from Pfam, and this was potentially due to the presence of sequences without relevant catalytic function adding noise to the dataset. The most prominent feature for our purposes is the ability to use the hidden units learned through RBM training to classify sequences. The bimodal nature of this particular model provides a relatively simple interpretation which is straightforward to use for prediction. We show in **Figure 5** that the combination of clustering and interpretable hidden unit structure allows us to identify a small subset of residues within a structure, grounding our statistical clustering in MprF's structural features. The combination of experimental evidence and evolutionary information provided a strong rationale for selecting organisms for further study, ultimately leading to the discovery of novel cationic lipid biosynthesis in *Enterococcus dispar* (**Figure 6**, **Figure S3**).

One goal of this study was to find the structural determinants of Glc_N-DAG activity by MprF, and we found that hidden unit 2 from our RBM analysis was predictive of this. However, there are notable exceptions such as the *E. faecium* allele EGTF 00601, which has sequence features placing it in quadrant one yet has Glc_N-DAG activity. Therefore, identifying the exact sequence determinants of Glc_N-DAG specificity remains to be fully elucidated. One explanation could be our exclusion of the N-terminal flippase domain and the non-cytosolic region of the C-terminal domain in the RBM analysis, where important residue interactions determining specificity could occur and is under further investigation. Additionally, a challenge in experimental validation will be to standardize the method of studying *mprF* alleles from diverse organisms. When using native organisms, lipids produced may vary during the growth phase of the organisms, the media they are grown in, and whether a membrane stressor is present (i.e. inducible production of specific lipids). For this study we used stationary phase cultures of equal volume and bacteria were grown in their respective standard laboratory media. The use of a heterologous host for expression of *mprF* alleles is a method of standardization, but may result in not identifying novel lipids that would be found in their native bacteria since the appropriate lipid substrates may not be present [16, 12]. A combination of both approaches (native organisms and heterologous hosts) may be required. Additionally, spike-in controls might be implemented to help us to more

quantitatively understand the output specificity of these MprF variants. Ultimately, mutational studies of the residues identified by the RBM will allow for identification of the residues critical for specificity, though likely the residues will depend in part on the primary sequence being altered.

The general method of RBM-guided exploration has applications in enzyme design, for example, in enhancing methods like directed evolution [33]. Concretely, the residues identified through hidden units can be thought of as templates for mutational exploration, greatly reducing the search space for assessing which residues are critical for specificity determination. Enzymes like MprF that produce lipids of modified charge have potential applications in biotechnology and therapeutics, where the design of lipid nanoparticles with different charge and chemical properties of the head group have important physiological implications [34]. Notably, the identification of Lys-Glc_2-DAG opens new research avenues, particularly in the fields of antibiotic resistance and host-pathogen interactions, wherein lipid modification and cationic lipids play key roles. With respect to human health, it would be relevant to investigate whether Lys-Glc_2-DAG plays a role in enterococcal resistance to the last-line membrane-active antibiotic, daptomycin.

4 Methods and Materials

4.1 Bacterial Strains and Growth Conditions

See **Tables S1** and **S3** for a full list of bacterial strains used in this study. *Streptococcus mitis* NCTC12261 (referred to as SM61 here) [35] was grown in Todd Hewitt Broth (THB) at 37°C with 5% CO_2. *Escherichia coli* DH5*α* [36] and *Bacillus subtilis* 168 [37] was grown at 37°C with shaking at 225 rpm in lysogeny broth (LB). *Staphylococcus aureus* RN4220 [38] was grown at 37°C with shaking at 220 rpm in Trypic Soy Broth (TSB). *Streptococcus agalactiae* COH1 ATCC BAA-1176 [39] and CJB111 [40, 41] were grown in THB at 37 °C. *Enterococcus faecium* 1,231,410 [42], *Enterococcus faecalis* T11 [43] and OG1RF [44], *Enterococcus gallinarium* EG2 [42], *Enterococcus casseliflavus* EC10 [42], and *Enterococcus raffinosus* Er676 [45] were grown at 37°C in Brain Heart Infusion (BHI). *Enterococcus dispar* ATCC 51266 [46] was grown at 30°C in BHI. *Exiguobacterium acetylicum* UTDF19-27C was grown in BHI at 37 °C. *Ligilactobacillus salivarius* ATCC 11741 [47], *Lacticaseibacillus rhamnosus* ATCC 7469 [48], *Lactobacillus casei* ATCC 393 [49] and *Lacticaseibacillus paracasei* ATCC 25302 [48] were grown in Lactobacilli MRS Broth at 37°C and 5% CO_2. *Levilactobacillus brevis* ATCC 14869 [50] was grown in Lactobacilli MRS Broth at 30°C, 5% CO_2. *Bacillus licheniformis* ATCC 14580 was grown in nutrient broth at 37°C with shaking at 225 rpm [51]. A transposon mutant of *E. faecalis* OG1RF from [30] with a mini mariner transposon (EfaMarTn) insertion in OG1RF_10760 (OG1RF_10760::Tn) was grown on BHI supplemented with chloramphenicol at a concentration of 15 μ/mL. The mutant was confirmed to be erythromycin-sensitive. The transposon mutant location was confirmed through Sanger sequencing performed by the Genome Center at the University of Texas at Dallas (Richardson, TX).

Where appropriate for plasmid selection, kanamycin (Sigma-Aldrich) was added. For *E. coli*, a concentration of 50 μg/mL was used, for *S. mitis* a concentration of 300 μg/mL, and for *E. faecalis* a concentration of 500 μg/mL was used.

4.2 Routine Molecular Biology Procedures

Genomic DNA was extracted as done previously in [52] and [53]. All PCR reactions used Phusion polymerase (Thermo Fisher Scientific) and Phusion 5x HF buffer (Thermo Fisher Scientific) in a Veriti PCR machine (Applied Biosystems). List of primers used are found in **Table S4**. Gibson assemblies were completed using a 2x HI-FI Assembly master mix following the manufacturer's protocol (New England Biolabs). PCR clean-up was done using the GeneJET PCR Purification Kit (Thermo Fisher Scientific) per manufacturer protocol. Plasmid extractions were performed per manufacturer protocol using the GeneJET Plasmid miniprep kit (Thermo Fisher

Scientific). All plasmid constructs were confirmed by Sanger sequencing at the Massachusetts General Hospital CCIB DNA Core facility or by Illumina sequence at SeqCenter. DNA concentrations were measured using Nanodrop (Thermo Fisher Scientific) or Quibit 2.0 (Invitrogen by Life Technologies). Optical Density at 600 nm (OD_{600nm}) was measured in a disposable cuvette (Thermo Fisher Scientific) using a spectrophotometer (Thermo Scientific Genesys 30).

Gibson assembly was performed using pABG5 as previously described [11]. Transformation of plasmids into *E.coli, S. mitis*, and *E.faecalis* was performed as previously described in [11, 16, 54, 55].

4.3 Acidic Bligh-Dyer Lipid Extractions

Bacteria were grown for approximately 16 hours overnight in 15 mL of an appropriate culture medium. After growth, OD_{600nm} measurements were taken, and cells were pelleted at 4,280 x g for 5 minutes at room temperature in a Sorvall RC6+ centrifuge. The supernatant was tipped out, and the cell pellet was washed and resuspended in 1X Phosphate Buffered Saline (PBS). The cells were pelleted again, and all the supernatant was aspirated out. The cell pellet was stored at -80°C until lipid extraction. An acidic Bligh-Dyer lipid extraction was performed as previously reported [16, 12]. Briefly, cell pellets were resuspended in 0.8 mL of 1x Dulbecco's PBS (Sigma-Aldrich). Cells were transferred to a 9 mL glass tube with a Teflon-lined cap (Pyrex). 1 mL chloroform (MilliporeSigma) and 2 mL methanol (Thermo Fisher Scientific) were added to create the single-phase Bligh-Dyer. Tubes were vortexed every 5 minutes for 20 minutes, then centrifuged at 500 x g for 10 minutes at room temperature. The supernatant was transferred to a new 9 mL glass tube. 100 μL of Hydrochloric acid (Thermo Fisher Scientific) was added followed by 1 mL of chloroform and 0.9 mL of 1x Dulbecco's PBS to create the two-phase Bligh-Dyer. Tubes were gently mixed and centrifuged at 500 x g for 5 minutes at room temperature. After centrifuging, the bottom layer was extracted to a new tube and dried under nitrogen gas and stored at -80°C prior to lipidomic analysis. Lipid analyses were repeated in biological triplicate aside, from OG1RF_10760::Tn extractions, which were performed once.

4.4 Analysis of lysine lipids by an amino column-based Liquid Chromatography-Electrospray Ionization-Mass Spectrometry (LC-ESI MS): A new method

An amino column-based normal phase LC-ESI MS was performed using an Agilent 1200 Quaternary LC system coupled to a high-resolution TripleTOF5600 mass spectrometer (Sciex, Framingham, MA). A Unison UK-Amino column (3 μm, 25 cm × 2 mm) (Imtakt USA, Portland, OR) was used. Mobile phase A consisted of chloroform/methanol/aqueous ammonium hydroxide (800:195:5, v/v/v). Mobile phase B consisted of chloroform/methanol/water/ aqueous ammonium hydroxide (600:340:50:5, v/v/v/v). Mobile phase C consisted of chloroform/methanol/water/aqueous ammonium hydroxide (450:450:95:5, v/v/v/v). The elution program consisted of the following: 100% mobile phase A was held isocratically for 2 min and then linearly increased to 100% mobile phase B over 8 min and held at 100% B for 5 min. The LC gradient was then changed to 100% mobile phase C over 1 min and held at 100% C for 3 min, and finally returned to 100% A over 0.5 min and held at 100% A for 3 min. The total LC flow rate was 300 μl/min. The MS settings were as follows: Ion spray voltage (IS) = 5000 V, Curtain gas (CUR) = 20 psi, Ion source gas 1 (GS1) = 20 psi, De-clustering potential (DP) = 50 V, and Focusing Potential (FP) = 150 V. Nitrogen was used as the collision gas for MS/MS experiments. Data acquisition and analysis were performed using Analyst TF1.5 software (Sciex, Framingham, MA).

4.5 Generation of *mprF* expression plasmids

The *S. downei mprF* nucleotide sequence (Locus tag HMPREF9176 RS03810) and *S. ferus mprF* nucleotide sequence (Locus tag A3GY RS0106165) were used to design synthetic geneblocks (GeneWiz from Azenta Life Sciences). A 20 nucleotide 5' extension and a 20 nucleotide 3' extension complementary to the pABG5 plasmid were added to enable Gibson assembly of the inserts with pABG5. Sequences for the geneblocks can be found in **Table S5**. The *S. salivarius mprF* (Locus tag SSAL8618 04345) was amplified from *Streptococcus salivarius* ATCC 7073. A 20 nucleotide 5' extension and a 20 nucleotide 3' extension complementary to the pABG5 plasmid was added to the insert. The same protocol was used for generation of pSobrinus, pEFM-prF1, pEFMprF2, and pOGMprF2 with slight modifications. *S. sobrinus mprF* (Locus tag DLJ52 05040) was amplified from *Streptococcus sobrinus* ATCC 27352. *E. faecium mprF1* (Locus tag EFTG_00601) and *E. faecium mprF2* (Locus tag EFTG_02430) were amplified from *Enterococcus faecium* 1, 231, 410. *E. faecalis mprF2* (Locus tag OG1RF_10760) was amplified from *E. faecalis* OG1RF.

4.6 Boltzmann Machines and Restricted Boltzmann Machines for Protein Sequences

Formulation of models

The Boltzmann Machine, as described in [18], is defined as:

$$P(\mathbf{v}) = \frac{1}{Z}\exp\{\sum_{i<j} e_{ij}(v_i, v_j) + \sum_i h_i(v_i)\} \tag{2}$$

which is a probability distribution defined on the pairwise interactions (the couplings e_{ij}) between the positions (v_n) in an input sequence (**v**) and a local field term h_i. The pairwise coupling matrix is akin to a covariance matrix, and the local fields are similar to single site frequency measures.

The joint probability distribution of the Restricted Boltzmann Machine as described in [14] is as follows:

$$P(\mathbf{v}, \mathbf{h}) = \frac{1}{Z}\exp\left(\sum_{i=1}^{N} g_i(v_i) - \sum_{\mu=1}^{M} \mathcal{U}_\mu(h_\mu) + \sum_{i\mu} h_\mu w_{i\mu}(v_i)\right) \tag{3}$$

Here, the vector **v** again represents the input sequence data, $g(v_i)$ is a local field which controls the conditional probability of the input data, $\mathcal{U}_\mu$ is the hidden unit potential/activation, and the terms h_i and $w_{i\mu}(v)$ couple the input variables with the hidden unit variables. In this way, interactions between residues are mediated by a relatively smaller set of hidden units which do not interact directly with each other, leading to a bipartite structure as opposed to the Boltzmann machine's fully connected pair based formulation.

Particularly important is the potential function $\mathcal{U}$, which in this work is the dRELU function defined as:

$$\begin{aligned}\mathcal{U}_\mu(h) =& \frac{1}{2}\gamma_{\mu,+}h_+^2 + \frac{1}{2}\gamma_{\mu,-}h_-^2 + \theta_{\mu,+}h_+ + \theta_{\mu,-}h_- \quad \text{where} \\ & h_+ = \max(h, 0)\ ,\ h_- = \min(h, 0)\end{aligned} \tag{4}$$

The four parameters $\gamma_{\mu,\pm}$, $\theta_{\mu,\pm}$ are learned through the inference procedure, and allow the positive and negative components of the hidden units w_μ to be separately gated, which allows learning of bimodal distributions for the activations h_μ. Another key feature is the sparsity regularization on

the weights applied during model inference:

$$L2/L1 = \frac{\lambda_1^2}{2qN} \sum_{\mu} \left(\sum_{i,v} |w_{i\mu}(v)| \right)^2 \quad (5)$$

where q is the number of amino acids plus a gap character (21) and the hyperparameter λ_1^2 can be increased to induce sparsity and lower weight magnitude. Equations 4 and 5 together guide the representation of the hidden units to bimodal outputs with interpretable features.

Dataset acquisition and preprocessing

Multiple sequence alignment used for model training was the DUF2156 domain acquired from Pfam [25] (in later revisions renamed LPG synthase C). Starting with this MSA, it was processed to include only amino acid characters and gaps, excluding sequences with ambiguous or non-standard characters. Additionally, sequences with contiguous strings of gaps greater than 20% of the full sequence's length were removed. This left 11,507 sequences with a length of 298. After the data cleaning process described in **Figure 4**, a total of 7,865 sequences were used to train our final model.

Model training

The model previously described [14] was utilized, specifically the Python 2.7 version freely available on Github (*https://github.com/jertubiana/ProteinMotifRBM*). Extensive testing of the combinations of the number of hidden units, $L2/L1$ regularization, and learning rate were performed. Models were trained in triplicate with different random seeds, as the training procedure converges to slightly different weight values depending on their initial random configuration. Training was considered successful when the model consistently produced similar sets of weights across different random seeds, and the weights had the previously mentioned sparsity and magnitude indicating compositional representation. The final model used in this work was trained for 2000 epochs with a learning rate of 0.1, a learning rate decay of 0.33, $L2/L1$ parameter λ_1^2 set to 1.0, and 300 hidden units.

Model Weight selection

To find hidden units which were relevant to function we computed the $L1$ norm of each hidden unit individually, then ranked them. The hidden units with the largest magnitude were looked at first, and these were typically the sparsest of all hidden units. Hidden units were chosen which involved sequence coordinates implicated in our function of interest. Specifically, locations identified through Autodock [26] where the lipid was likely to interact, and a small radius around this region to select a small set of coordinates. We chose the only hidden units which had both overlap with multiple residues in this chosen radius and predictive power (separation) for the three examples we had to start with.

Software Accessibility

DUF2156 domain sequences were retrieved from Pfam33 [25]. Raw sequence datasets are available as Supplementary Material.

Acknowledgements

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Figure S1

Assessment of RBM hidden unit's reliance on total sequence identity in classification. A sliding window average is performed, where a window of width 1 is slid from the negative end to the positive of the hidden unit activation, where at each position sequence coordinates are sampled from the window. These sampled sequences are compared pairwise between themselves, computing the Hamming distance across their entire sequence length to produce an average. This sampling procedure is repeated 30 times for each window, with the light blue shading representing the 95% confidence interval.

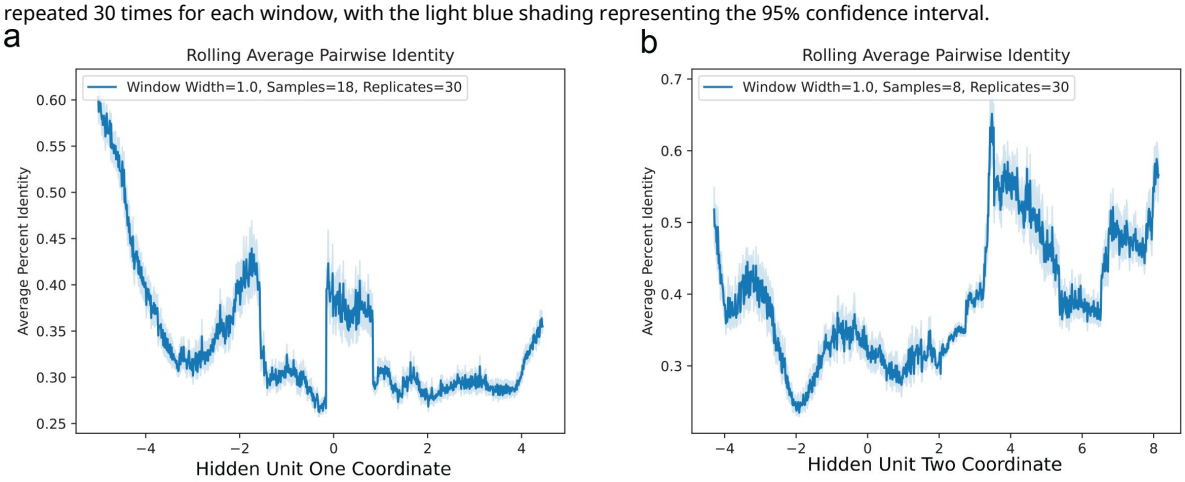

Figure S2

The full sequences of our pre-filtered multiple sequence alignment were analyzed to identify which Pfam domains were present in them. We then split these results based on the procedure in **Figure 3**, where Removed sequences indicate domain composition of sequences removed by this procedure, and Training sequences for the data we trained our final model on. We remove domains from this plot which occur in less than 1% of the sequences of their respective sets for clarity.

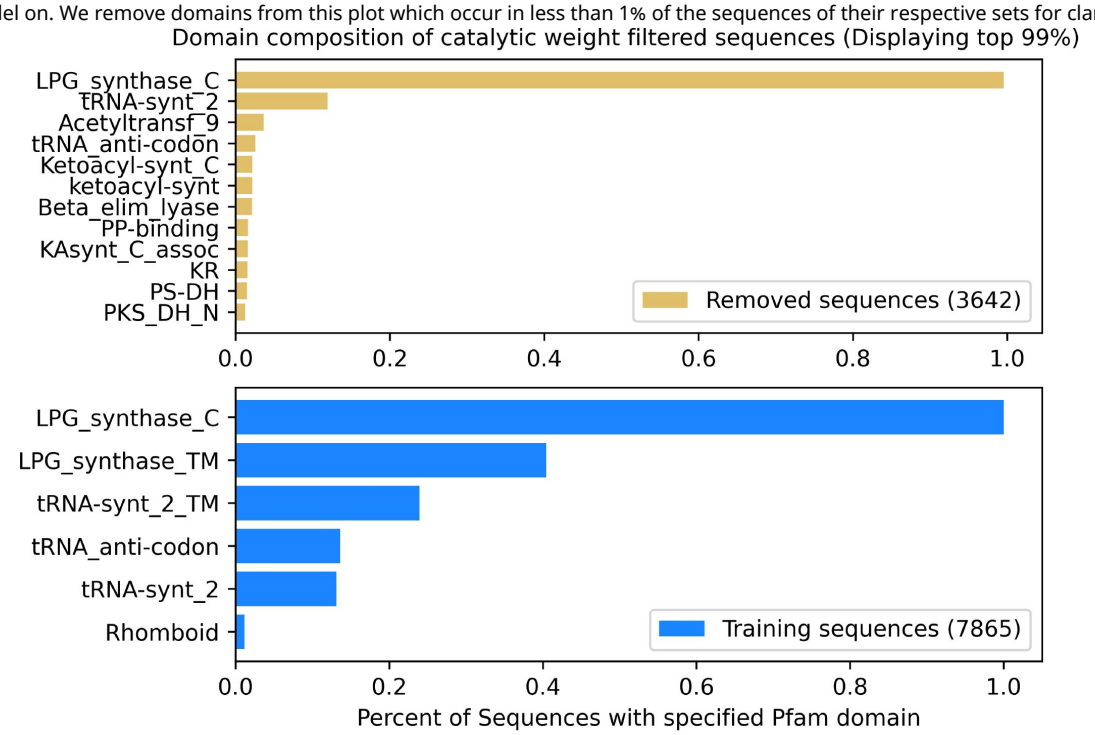

Figure S3

Identification of Lys-Glc_2-DAG which is highly retentive on a silica HPLC column. A) the total ion chromatogram of normal phase LC/MS of *E. dispar* lipids separated on a silica HPLC column. B) the positive ion mass spectrum of Lys-Glc_2-DAG eluting at the end of the LC gradient. Glc-DAG, glucosyl-diacylglycerol; Glc_2-DAG, diglucosyl-diacylglycerol; PG, phosphatidylglycerol; Lyso-Glc_2-DAG, lyso diglucosyl-diacylglycerol; Lys-PG, lysyl-phosphatidylglycerol; Lys-Glc-DAG, lysyl-glucosyl-diacylglycerol; Lyso Lys-PG, lyso lysyl-phosphatidylglycerol; Lys-Glc_2-DAG, lysyl-diglucosyl-diacylglycerol.

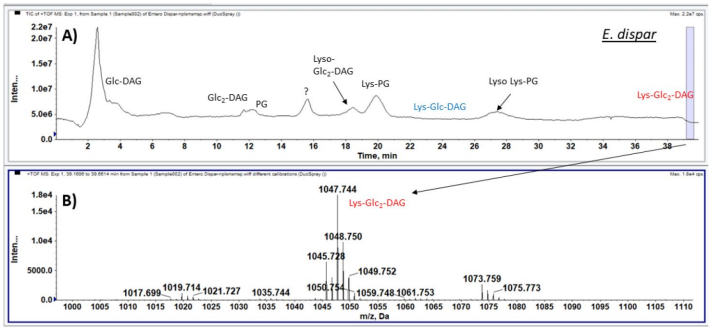

Figure S4

All *Enterococcus* sequences analyzed in the course of this study.

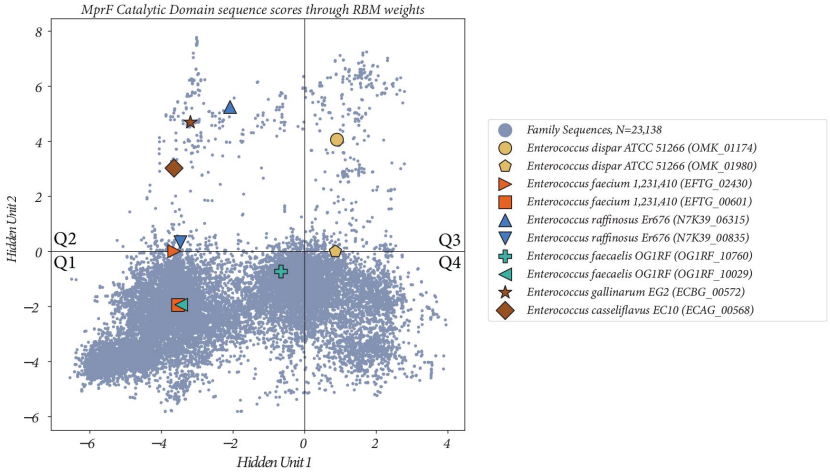

Table S1

Sequence Locus IDs for all sequences listed in Table 2. Bold denotes confirmed *mprF* allele.

Bacterial Strain	Protein ID	Locus ID	Description	Reference
Enterococcus dispar ATCC 51266 *(mprf1)*	WP_016173119	OMK_01174	Wild-type *E. dispar* strain	Collins et al. (1991)
Enterococcus dispar ATCC 51266 *(mprf2)*	WP_016172352	OMK_01980	Wild-type *E. dispar* strain	Collins et al. (1991)
Enterococcus gallinarum EG2	WP_195971496	ECBG_00572	Wild-type *E. gallinarium* strain	Palmer et al. (2010)
Enterococcus casseliflavus EC10	WP_201705909	ECAG_00568		Palmer et al. (2010)
Enterococcus faecalis T11 *(mprF1)*	EEU90403	EFMG_00309	Wild-type *E. faecalis* strain	McBride et al. (2007)
Enterococcus faecalis T11 *(mprF2)*	EEU90403	EFMG_01835	Wild-type *E. faecalis* strain	McBride et al. (2007)
Enterococcus faecalis OG1RF *(mprf1)*	WP_002414160	OG1RF_10029	Wild-type *E.faecalis* strain	Gold et al. (1975)
Enterococcus faecalis OG1RF *(mprf2)*	WP_002358907	**OG1RF_10760**	Wild-type *E.faecalis* strain	Gold et al. (1975)
Enterococcus faecium 1,231,410 *(mprf1)*	WP_002294379	**EFTG_00601**	Wild-type *E. faecium* strain	Palmer et al. (2010)
Enterococcus faecium 1,231,410 *(mprf2)*	WP_002287340	EFTG_02430	Wild-type *E. faecium* strain	Palmer et al. (2010)
Enterococcus raffinosus Er676	UXJ96875	N7K39_06315	Wild-type *E. raffinosus* strain	Sharon et al. (2023)
Streptococcus agalactiae COH1	CDN67397	GBSCOH1_1931	Wild-type *S. agalactiae* strain, serotype III	Kuypers et al. (1989)
Streptococcus agalactiae CJB111	QOW76674	ID870_10050	Wild-type *S.agalactiae* strain, serotype V	Faralla et al. (2014); Spencer et al. (2021)
Staphylococcus aureus RN4220	QWF27327	NMK49_RS06325	Wild-type *S. aureus* strain	Kreiswirth et al. (1983)
Bacillus subtilis 168	QJF41380	BSU_08425	Wild-type *B. subtilis* strain	Kunst et al. (1997)
Bacillus licheniformis ATCC 14580	WP_003179900	EJ992_04410	Wild-type *B. licheniformis* strain	Chester (1901)
Exiguobacterium acetylicum UTDF19-27C	WP_238238782	K6T22_02680	Wild-type *E. acetylicum* strain	
Ligilactobacillus salivarius ATCC 14580	EEJ74510	HMPREF0545_0714	Wild-type *L. salivarius* strain	Drucker (1979)
Lacticaseibacillus rhamnosus ATCC 7469		NHLLHDLP_02198	Wild-type *L. rhamnosus* strain	Collins et al. (1989)
Lactobacillus casei ATCC 393	BAN75198	LBCZ_2030	Wild-type *L. casei* strain	Hansen and Lessel (1971)
Levilactobacillus brevis ATCC 14869	ERK41244	HMPREF0495_02376	Wild-type *L. brevis* strain	Rogosa and Hansen (1971)
Lacticaseibacillus paracasei ATCC 25302	TDG89985	C5L26_003005	Wild-type *L. paracasei* strain	Collins et al. (1989)
Streptococcus mitis SM61 + pFerus	WP_018030543	A3GY_RS0106165	Exprssion of *S. ferus mprF* in *S. mitis*	This work
Streptococcus mitis SM61 + pDownei	WP_002997695	HMPREF9176_1523	Expression of *S. downei mprF* in *S.mitis*	This work
Streptococcus mitis SM61 + pSobrinus	WP_019781626	DL52_05040	Expression of *S. sobrinus mprF* in *S. mitis*	This work
Streptococcus mitis SM61 + pSalivarius	WP_181671155	SSALS8618_04345	Expression of the *S. salivarius mprF* in *S.mitis*	This work
Enterococcus faecalis OG1RF_10760::Tn			OG1RF with a mini-mariner transposon (EfaMarTn) inserted into MprF2 at position 787608	Dale et al. (2018)
Enterococcus faecalis OG1RF_10760::Tn + pABG5	WP_002358907	OG1RF_10760	OG1RF_10760::Tn with the empty vector pABG5 expressed	This work
Enterococcus faecalis OG1RF_10760::Tn + pOGMprF2	WP_002358907	OG1RF_10760	Complementation of the transposon. pOG.MprF2 expresses the OG1RF_10760 gene on the pABG5 vector	This work
Enterococcus faecalis OG1RF_10760::Tn + pEfMprF1	WP_002294379	EFTG_00601	Expression of MprF1 from *E. faecium* 1, 231, 410 into the OG1RF_10760::Tn	this work
Enterococcus faecalis OG1RF_10760::Tn + pEfMprF2	WP_002287340	EFTG_02430	Expression of MprF2 from *E. faecium* 1, 231, 410 into the OG1RF_10760::Tn	this work

Table S2

Fisher's exact test for determining whether positive values of Hidden Unit 2 are predictive of Glc_N-DAG specificity. p=0.028.

	Hidden Unit 2 Positive	Hidden Unit 2 Negative
Glc_N-DAG	8	4
PG Only	1	7

Table S3

***E.coli* and plasmids used**

E.coli and Plasmid	Description	Reference
E.coli DH5α (pFerus)	*E. coli* with *S. ferus mprF* in pABG5	This Study
E.coli DH5α (pDownei)	*E. coli* with *S. downei mprF* in pABG5	This Study
E.coli DH5α (pSalivarius)	*E. coli* with *S. salivarius* ATCC 7073 *mprF* in pABG5	This Study
E.coli DH5α (pSobrinus)	*E. coli* with *S. sobrinus* ATCC 27352 *mprF* in pABG5	This Study
E.coli DH5α (pEFmprF1)	*E. coli* with *E. faecium mprF1* (EFTG_00601)	Joyce et al. (2022)
E.coli DH5α (pEFmprF2)	*E. coli* with *E. faecium mprF2* (EFTG_02430) in pABG5	This Study
E.coli DH5α (pOGMprF2)	*E. coli* with *E. faecalis mprF2* (OG1RF_10760) in pABG5	This Study
E.coli DH5α (pABG5)	*E. coli* with the empty vector (pABG5)	Joyce et al. (2022)

Primer Name	Sequence	Use	Reference
pABG5-5'	GGAAAGGGACCTCTCTTCCTAAAC	Linearize pABG5 with pABG5-3'	Joyce et al. (2022)
pABG5-3'	GATAAAGGTATTGGTAAATAACAAA	Linearize pABG5 with pABG5-5'	Joyce et al. (2022)
Faec_MprF1_F	GAGAGGTCCCTTTCCTTGTTAAAAAATACCATACAATG	Primer for amplification of *E. faecium mprF*1 with Faec-MprF1_R contains complementary sequence to pABG5 for Gibson assembly	Joyce et al. (2022)
Faec_MprF1_R	ACCAATACCTTTATCTTAATACTTTCTTCGTATCC	Primer for amplification of *E. faecium mprF*1 with Faec_MprF1_R	Joyce et al. (2022)
Faec_MprF2_F	GAGAGGTCCCTTTCCGTGAAAAATAAACGATACTTG	Primer for amplification of *E. faecium mprF*2 with Faec-MprF2_R contains complementary sequence to pABG5 for Gibson assembly	This Study
Faec_MprF2_R	ACCAATACCTTTATCTTATAATTCTGTGAGCACTTC	Primer used for amplification of *E. faecium mprF*2 with Faec-MprF2_R	This Study
OG1RF_MprF2_F	GAGAGGTCCCTTTCCATGAAACAAATTATTCATTGGATC	Primer used for amplification of *E. faecalis mprF*2 with OG1RF_MprF2_R	This Study
OG1RF_MprF2_R	ACCAATACCTTTATCTTAGTCAATATTTTTTTGATCGAC	Primer used for amplification of *E. faecalis mprF*2	This Study
SalMprF_R	ACCAATACCTTTATCCTATTTCCAAAGACGTC	Primer used for amplification of *S. salivarius mprF* with SalMprF_F	This Study
SalMprF_F	GAGAGGTCCCTTTCCATGAAGCGTCTTTTAGAG	Primer used for amplification of *S. salivarius mprF*	This Study
SobMprF_F	GAGAGGTCCCTTTCCTTGAAAGCCGTTCTTG	Primer used for amplification of *S. sobrinus mprF* with SobMprF_R	This Study
SobMprF_R	ACCAATACCTTTATCTTAATTCCGAGTCACAC	Primer used for amplification of *S. sobrinus mprF*	This Study
EF1_S1	GAATAACGCTGATCAAAAGT	Primer used for sequencing pEFMprF1 insert with pABG5Fup2	Joyce et al. (2022)
EF1_S2	TGCCAAGAGAAATAGTC	Primer used for sequencing pEFMprF1 insert with EF1_S3	Joyce et al. (2022)
EF1_S3	ACAATCTCTTCGCTTG	Primer used for sequencing pEFMprF1 insert	Joyce et al. (2022)
EF1_S4	CCAACTGTTCTTCTCCAA	Primer used for sequencing pEFMprF1 insert with pABG5Fdown2	Joyce et al. (2022)
EF2_S1	CTCCTGTATGTGTGATGAAC	Primer used for sequencing pEFMprF2 insert with pABG5Fup2	This Study
EF2_S2	GGAATGGGGACTTTTGA	Primer used for sequencing pEFMprF2 insert with EF2_S3	This Study
EF2_S3	ACTGATTCGTTGCTGC	Primer used for sequencing pEFMprF2 insert	This Study
EF2_S4	CTTCGCTTGTCAGGTTAC	Primer used for sequencing pEFMprF2 insert with pABG5Fdown2	This Study
OG2_S1	TTGTAAAGAACAAACAGCC	Primer used for sequencing pOG_MprF2 insert with pABG5Fup2	This Study
OG2_S2	GCAACTTAGGTGTCG	Primer used for sequencing pOG_MprF2 insert with OG_S3	This Study
OG2_S3	GCCGAAACGATCTGT	Primer used for sequencing pOG_MprF2 insert	This Study
OG2_S4	CGTTGTGATGGGCAAC	Primer used for sequencing pOG_MprF2 insert with pABG5Fdown2	This Study
Sal_S1	GAAGGGAATAACGTAG	Primer used for sequencing pSalivarius insert with pABG5Fup2	This Study
Sal_S2	TATCTTCTCTATGATTCC	Primer used for sequencing pSalivarius insert with Sal_S3	This Study
Sal_S3	TCTTCAAGAAAGATTCCCA	Primer used for sequencing pSalivarius insert	This Study
Sal_S4	CTCTTTTGGTATCGTGTC	Primer used for sequencing pSalivarius insert with pABG5Fdown2	This Study
Sob_S1	AGGAATGACATAATAAGCCAAG	Primer used for sequencing pSobrinus insert with pABG5Fup2	This Study
Sob_S2	CGGTATTATTTCTCTGAT	Primer used for sequencing pSobrinus insert with Sob_S3	This Study
Sob_S3	TTCTACATCGGCCTCAT	Primer used for sequencing pSobrinus insert	This Study
Sob_S4	TTAGCCTTTCTGGGAGAC	Primer used for sequencing pSobrinus insert with pABG5Fdown2	This Study
Downei_S1	GAACATAATAGGCCAGGC	Sequencing primer for pDownei insert with pABG5Fup2	This Study
Downei_S2	CGGTGGGGATTATTTCC	Sequencing primer for pDownei insert with Downei_S3	This Study
Downei_S3	CTGCTTGGTTACCAGCAG	Sequencing primer for pDownei insert	This Study
Downei_S4	CAAACGCCTCTTCTG	Sequencing primer for pDownei insert with pABG5Fdown2	This Study
Ferus_S1	CCGGCAAAGAATGGCAGAATA	Sequencing primer for pFerus insert with pABG5Fup2	This Study
Ferus_S2	CACTAATCCCTGGCGG	Sequencing primer for pFerus insert with Ferus_S3	This Study
Ferus_S3	CAATGAAGGCTCTTGTAGC	Sequencing primer for pFerus insert	This Study
Ferus_S4	GTATCAGGAGGAGGGAC	Sequencing primer for pFerus with pABG5Fdown2	This Study
pABG5Fup2	CAAAAGGTTTCGACTTTTCACC	Primer used for sequencing with pABG5Fup2	Joyce et al. (2022)
pABG5Fdown2	CCAATAATAATGACTAGAGAAG	Primer used for sequencing	Joyce et al. (2022)

Table S4

Primers used in this study. Red indicates sequence complementarity to pABG5.

Name	Sequence
S. Downei mprF (Locus tag HMPREF9176_RS03810)	AGGAAGAGAGGTCCCTTTCC TTGAAAGCCCTTCTTGAAAAAATCAAGCCCCTTACCTCCATTCTTAAA ACCGTCTTCTTTGTTTCCATCATCCTCTTAATCATCATGGAAATCCTCAATCTGAGGCGGACCATTTCTGTGTCGCAACTCAAGG CGGCATTGGGTGGGGTGTCTCCTATCAATATTCTCCTGATTTTTATCATTGGAGCCCTGGCCGTCCTACCAACGACGGGCTATGA TTTTGTCCTCAATAAAATTTTGGGTACCAATAAGTCCAAGTGGTATATTTTGCAGACCTCCTGGTGTATCAATACCTTTAATAAT TTATCGGGTTTTGGCGGTCTGATTGATATTGGTCTGCGTTTGGCCTTCTACGGGCAAAAAGGAGAAGAGGAGCGCGACCTCCAGC AGGTCACGACCTTCCTCCCTTATCTGATTTCGGGCTTGTCCTTTGTCAGTCTGGCTTCTCTGGGTCTGACCTACGCCTATGGAGT CAACCGCTCTGGTCTTCCCTATTATGATATTGTTCTGATTGGAGCTAGTCTCTATTTTCCTATTCTCTATTGGTTGACGGGACGC AAGACCAAGAATTACTTTGCCAATATGCCTGTCAAGACCAGGAACCGTCTAGGGATTGTGTCCTTCTTCGAGTGGTCTTGTGCAG CGGCAGCCTTTATCATTATTGGCCGTCTGATGGGCATTGATATGCCGATTTCCGTCGTTCTGCCCTTCTTTGCCATTGGTTGTGC GGTGGGGATTATTTCCTTGATTCCTGGGGCTCTAGGGAGTTTTGACTTTGTCGTCCTGACAGGTCTGTCTGCCCACGGTTTGCCT AAGGAAACGGTTCTAGCCTGGCTCTTGCTTTACCGCCTGGCCTATTATGTTCTCCCTTTCTTTGTCGGGATTATTTTCTTTATCA GACATCTGGGTGGAAAGATTAATGAGAAATACAATGCCGTTCCCAAGCAGATGCTGGAAAGGGGCATTCATACAGTCACTATCCG TCTGATTCGCTGGTTGGGGATTTTCCTAGCCCTTTCCACCGTCTTCTTTGAAAATCTGGATTATATCACCTGGCTAAGGCCTTTT AACCCCTTGCAGAAGCAGATTATTTGGCAATTTCCAGGTCTCTTGTTGGGGATTTGTTTCATTCTTCTAGCCAGGACCATCGAAA AGAAGGTCAAGCTGGCCTATCCTCTGACCATGATTTGGTTGGTCCTGACTCTGATTTATGTCGATTTTGGAGCTATTAGTTGGGG CTTTTCCATCGCCATTTTCTTAGCTATAATTGCCCTCAATTTGGTTCGACCTCAGCTCTATAAGAAGCAGTTTATTTATTCCTGG GAGGCTAGAACCAAGGATAGCCTGATTATTGCTCTGACCCTGCTTGTGATTTTCACCTTGGCTGGAGTGATTTTCCCTGTTCGGG CCCATGAGCTCCATGAACTCGTGGAGCGGCATAAACCCATCAGTCCAGAAAGCTACCTCCTAACGCGGAAAATCGTTTTAATCAT TACGGTGATTATCACGGTCTCTTACTGGATTTTGATGCGGATTGTTCAAGGACGCAAGGTTAAGTTGGGCACGCCCTTCCAGGCT GACCGCTACCGTAAGCTCCTGGAAACCTATGGTGGTCAAGGGGATAGCGCACTTGCTTTTCTAGGTGACAAACGCCTCTTCTGGT ATCAAAAGGAAGGCGAAGACCGGGTTGCCTTTCAATTCGCTATCCGCAACAACAAATGTCTGGTGATGGGCCAACCTGCTGGTAA CCAAGCAGATGTGGAAGAAGCGATTGCTTATTTCATTGATAAGGCCGATCGGCTGGATTACGACTTGATTTTCTATAGTATCGGT CAAAAGATGACCCTCTACCTGCATGAATTCGGCTTTGAATTTATGAAGGTGGGGGAAAACGCCCTAGTGGATTTGGAAAAATTCA CCCTCAGGGGCAATAAATACAAGCCTTTCCGCAATGCCCTCAATCGGGTGGAGAAGGATGGCTTTAGCTTTGAAGTCTTGGCCAG CCCCCATAGTCCTGAGCTTTTGGCGGAAGTCAAGGCCGTTTCTGACATCTGGCTGGACGGTCGATCTGAAAAGGGCTTCTCACTA GGTTATTTTGACCAGGCCTACTTGCAGGAAGCTGCTCTGGCAGTCGTTCGCCAATCAGGAGGGCAAACTGGTTGCCTTTGCCAATG TCATGCCTAATTATCAGGAAAATATCGCTTCCATTGATATGATGCGCTATGACAAGGAGGCCATTCCAAACGGGGTCATGGACTA CCTCTTTATTTCCCTCTTTGTCTATTTCCGAGACCAAGGTATCGGTTATTTCGACTTGGGCATGGCTCCCCTATCAGGAGTTGGT CAGGTCGAGGAAAGCTTTATTCAAGAGCGTTTGGCCTATCTGGTCTATCATTTTGGCAGTCATTTTTACTCCTTTGAAGGTCTTT ATCGCTATAAGGAAAAATTCACCCCACTTTGGGACCAGCGCTATATTTCCTATTCTAGAACTTCCTGGGTCGGCTATGTCCTTAT GACCCTAGTCTTAGAGGACCGAGTGACCAGAAGTTAA GATAAAGGTATTGGTAAATA
S. ferus mprF (Locus tag A3GY_RS0106165)	AGGAAGAGAGGTCCCTTTCC AGGAAGAGAGGTCCCTTTCCTTGAAAACGATTATTGAGAAACTGAAG GCTTTTATGCCTATCATTAAGGTCATTTTTTTCACCTCAATCGTGGTCTTAATCATTGTTGAGTTAATGCACCTGAAACAAACC ATATCGGTCAAAGAGTTGGGGCAGGTGCTGCAAGGTATTTCTTGGCTTAATATCTTTCTGATTTTTTTAGTCGGCACGCTGGCC GTCTTTCCAACCACAGGATATGATTTCATTGTCAACAGGATTCTAAAAACCAACCACAGCAAATCCTATATTCTGCAGACCAGC TGGTGTATCAATACCTTTAATAATCTGACTGGTTTTGGGGGAATTATTGACATTGGCCTGCGACTTGCCTTTTACGGCAAAAAA GGCGAGGAAGAAAGGGAATTGCAGGAAGTTACCCGTTTTCTGCCCTATCTTATTTCAGGGCTGTCCTTTATCAGCCTTGTTTCC CTAGGATTGGTTTCGATCTTTCCCGTCACAAGGAGTGTCCGTTTTTACGATATCATCCTTTTGGCATCAACCCTTTATTTCCCT CTGATTTATTGGTTTTCCGGCAGAAAAAACAATCACTACTTTGGCAATATGCCCGCAAAAATCCGGCTGCAGCTTGGTCTTGTC TCCCTCTTTGAATGGACTTGTGCGGCGCTTGCTTTTATCATCATTGGCTATCTGATGGGAATTGATTTGCCCTTCTATAAAACG CTACCCCTCTTTAGTATCGCCTGTGCTGCAGGGATTGTGTCACTAATCCCTGGCGGGTTGGGAAGTTTTGAACTGGTCTTGTTT ACCGGCTTTGCTGCCGAAGGCTTGCCCAAAGAAACAGTCGTTGCCTGGCTCTTACTCTATCGTCTGGCTTATTATATTCTGCCA TTCTTTGCCGGTATTTATTTCTTTGTCCGCCATCTTGGACATCAGATTAATCAAAGGTATCAAGGGGCTCCTAGGGAGCTCCTC TCAAGCAGTCTACACAGTGTCATGATACACGCTGTTAGGTGGCTGGGAATCTCACTTGTCTTTTCAACCCTCTTTTTTGAAAAG ATCTCTCATCTCAGCTGGCTAGACGGTTTTGGTCCCTTACAAAAACAGCTTATCTGGCAATTCCCAGGGCTTTTAATCGGGGTT TGCTTTATCCTGCTGGCCAGAGCCATTGCTAATGGGGTTAAGAGGGCTTATTCTCTTATGTTTTTGGGTCTGGCAGCAACCCTT GTGTACATTAATACTGGATCTATCAGTTGGCAATGGTCACTCGCTATTGTCTTACTTGGATTGGGGACTGTCCTTATCCGAACA CACCTCTATAAAGCCCAATTTATCTATTCCTGGGAAGGACGCACCAAAGATATCATCTTGATTTCCTCCATGCTCTTTATCTTA TTCACCCTTGCCAGTCTGATTTTCCCATACCGAGCCTATGAAATGAATCAGCACCTTGGCTTCTCTCGTTACTTTTTGACGTGG AAACATATCCTGCTGGCGACCAGCTTGGTCACCCTAGCCTATGCCTGTCTGGTTAGGTATCTCTACGGTGGTAAAACTTTATTG GGTGAGACTTTTGAGCACGATCGCTACCAGCGTTTATTGAGCGAATATGGCGGCAGCGCCGACAGCGGACTCGCCTTTATAAAA AACAAGCGTCTCTTCTGGTATCAGGAGGAGGGACTTGACAAGGCAGCCTTCCAATTTTCAACTATCAATAACAAGGCTGTTGTC ATGGGAGAGCCGGCTGGAAATCCGGAAACCTTTAAAAATGCTACAAGAGCCTTCATTGAAGCTGCTGATCGCCTCAATTATGAC CTCGTCTTTTACAGTATCGGCAAAGATATGACCCTCTTTTTGCATGAATATGGCTTTGAATTCATGAAAGTGGGGGAAAATGCC CTAGTTGATTTAGATAGCTTCCATCTTAAAGGTAATAAATACAAGCCTTTCCGAAACGCTCTCAACCGTGTTCAAAAAGAAGGA TTCACCTTTGAAATAAGTCCTCAGCCTCACTCGAAAGTCTTATTAGATGAACTAGAGACTATTTCAAACAAATGGCTGGAAAAA AGACAGGAAAAAAGATTCTCACTCGGTTTCTTTGATAGAGACTATTTCCAAGAGGCACCGCTGGCGCTGGTTAAAAATAAGGAA CAGGAAATTGTTGCCTTTGCCAATATTATGCCCAATCACCAGAACGGTATCGTCTCCATCGACTTGATGCGCTACGATGCCAAA AAAATTCCAAATGGGGTCATGGACTACCTCTTCTTATCTCTTTTTATCCATTTTAAGGAAGAAGGACTGGCCTACTTTGACCTT GGAATGGCACCCTTGTGGGGGGTTGGGCAAGTCAAGGAAAGTTTCCTCCACGAACGGCTGGCCTATCTGCTCTACAATTTCGGA ACCCATTTTTATTCCTTTGAAGGACTGCACCAGTACAAAAAGAAATTCAACCCGATTTGGGAGGAACGCTATGTCTCTGTTGCC AAATCCTCTTGGCTGCTCTACGCCATCTTGGGCATTTTCTTACTGGATACCAAACTGTTTAACAAAAAAAGAAGATCCTCTTAG GATAAAGGTATTGGTAAATA

Table S5

mprF sequences synthesized by Genewiz.

Red indicates sequence complementarity pABG5.

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Editors

Reviewer #1 (Public review):

The manuscript by Christensen, et al. presents an application of restricted Boltzmann machines to analyze the MprF family of enzymes, which catalyze the addition of amino acids to lipid substrates in bacteria. Overall the manuscript is an interesting and very compelling combination of advanced statistical analysis of sequences and experimental determination of MprF function. One notable outcome is (as stated in the title) the identification of a novel substrate/product. I expect that other researchers interested in using advanced methods to connect sequence to lipid synthesis functions will find the work of significant value and that others interested in microbial resistance will find inspiration in the results. This is an excellent contribution that will be of great value to the field, and which is improved following revisions.

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Reviewer #3 (Public review):

Summary:

After the previous identification that the Streptococcus agalactiae MprF enzyme can synthesize also lysyl-glucosyl-diacylglycerol (Lys-Glc-DAG), besides the already known lysyl-phosphatidylglycerol (Lys-PG), the authors aim for the current manuscript was to investigate the molecular determinants of MprF lipid substrate specificity, for which MprF from a variety of bacterial species were used. This then led to the coincidental discovery of a novel lipid species.

The manuscript is well constructed and easy to follow, especially taking into account the multidisciplinary aspect of it (computational machine learning combined with lipid biology). The Restricted Boltzmann machines (RBM) approach enables the successful, although not perfect, classification and categorization of MprF activity. The computational approach is validated by lab experiments in which LC-MS analysis reveals the specific activity of the lipid synthesizing enzymes. In a few cases lipid synthesis activity is completely absent. Due to the lack of protein expression data, it is unclear if this is caused by enzyme inactivity or the overall absence of enzyme.

Overall, the authors largely achieved their goals, as the applied RBM approach led to specific sequence determinants in MprF enzymes that could categorize the specificity of these enzymes. The experimental data could largely confirm this categorization, although a stronger connection between synthesized lipids and enzyme activity would have further strengthened the observations.

The work now focuses only on MprF enzymes, but could in theory be expanded to other categories of lipid synthesizing enzymes. In other words, the RBM approach could have an impact on the lipid synthesis field, if it would be a tool that is easy applicable. Moreover, the lipids synthesized by MprF (Lys-PG, but also other cationic lipids) play an important role in the bacterial resistance against certain antibiotics.

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Author response:

The following is the authors' response to the original reviews.

> ***Reviewer 1 (Public Review):***
>
> *The contribution of individual resides is shown in Figure 3c, which highlights one of the strengths of this RBM implementation - it is interpretable in a physically meaningful way. However, there are several decisions here, the justification of which is not entirely clear.*
>
> *i) Some of the residues in Fig 3c are stated as "relevant" for aminoacylated PG production. But is this the only such hidden unit? Or are there others that are sparse, bimodal, and involve "relevant" AA?*

Thanks for bringing this important question to our attention. In fact, this was the only hidden unit involving the combination of positions 152 and 212. Although we don't have knowledge of all relevant amino acids for this catalytic process, the residues we uncover were however shown through experimental analysis to be critical for the catalytic function of two MprF variants, and thus since our protein of interest involved this function, any domain which did not contain these residues were excluded. We can't rule out that the domains we excluded from further analysis could be performing similar catalytic functions, but we found it unlikely considering the amino acids found in the negative portion of the weight were chemically unlikely to form a complex with the amino acid lysine. We have clarified in the text, that this selection is probably a subset of all important amino acids, however, this selection provided predictive power.

> *ii) In order to filter the sequences for the second stage, only those that produce an activation over +2.0 in this particular hidden unit were taken. How was this choice made?*

The +2.0 was chosen as it ensured that the bimodal distribution was split into two distinct distributions.

> *iii) How many sequences are in the set before and after this filtering? On the basis of the strength of the results that follow I expect that there are good reasons for these choices, but they should be more carefully discussed.*

We started with 11,507 sequences and after filtering we had 7,890 to train our model with. We think this number still maintains robust statistics. This is noted in the Dataset acquisition and pre-processing section of the Methods section.

> *iv) Do the authors think that this gets all of the aminoacylated PG enzymes? Or are some missed?*

This is an interesting question that prompted us to do further analysis. We have added a new supplemental figure providing more details to this question. Based on the Uniprot derived annotations and the Pfam domain-based analysis of these sequences, the large majority of sequences that were excluded were proteins which included the *LPG_synthase_C* domain but **not** the transmembrane flippase domain required by the MprF class of enzymes, and were instead accompanied by different domains which seem less relevant to our enzyme of interest. It is true though, and related to question (i), that variants which might retain the functionality despite losing experimentally determined key catalytic residues could have been excluded by this method, but such sequences could still be reasonably excluded due to their dissimilarity with MprF from *Streptococcus agalactiae*.

> *However, some similar criticisms from the last point occur here as well, namely the selection of which weights should be used to classify the enzymes' function. Again the approach is to identify hidden unit activations that are sparse (with respect to the input sequence), have a high overall magnitude, and "involve residues which could be plausibly linked to the lipid binding specificity."*
>
> *(i) Two hidden units are identified as useful for classification, but how many candidates are there that pass the first two criteria? Indeed, how many hidden units are there?*

We note in the Model training section of the methods that our final model used had 300 hidden units in total. As to the first part of your question, rather than systematically test the predictive power of all other hidden units to this task, we decided to use the weights that we did because of their connection to a proposed lipid binding pocket found through Autodocking experiments. While another weight might provide predictive power, it might lack this critical secondary information. Moreover, the direction of our research necessitated finding weights which first satisfied our lipid-binding pocket plausibility before using these weights to propose MprF variants to test for our novel functionality. Given the limited information we had early in the research process, to go in reverse would have provided too many options for experimental testing with reduced mechanistic justification. We included a brief explanation of our rationale in section " Restricted Boltzmann Machines can provide sensitive, rational guidance for sequence classification “ in the updated manuscript.

> *ii) The criterion "involve residues which could be plausibly linked to the lipid binding specificity" is again vague. Do all of the other candidate hidden units *not* involve significant contributions from substrate-binding residues? Maybe one of the other units does a better job of discriminating substrate specificity. (As indicated in Figure 8, there are examples of enzymes that confound the proposed classification.) Why combine the activations of two units for the classification, instead of 1 or 3 or…?*

In fact, it is true that the other hidden units do not involve significant contribution to substrate-binding residues, and we will clarify this. The weights found through this RBM methodology are biased to be probabilistically independent, meaning that the residues and amino acids implicated by each weight are not shared among the other weights through the design of the model. We will update the Model Weight selection section to clarify that the weights we chose had more significantly weighted residues overlapping with the residues near the lipid-binding region than the other weights we checked. We combined these two because they were the only ones which had both overlap with these residues and predictive power of lipid activity with the few sequences we had detailed knowledge of at the time of decision (Figure 5b).

The Model Weight section reads as follows:

“Weights were chosen which involved sequence coordinates implicated in our function of interest. Specifically, locations identified through Autodock (Hebecker et al., 2015) where the lipid was likely to interact, and a small radius around this region to select a small set of coordinates. We chose the only weights which had both overlap with multiple residues in this chosen radius and predictive power (separation) for the three examples we had to start with.”

> ***Author Recommendations:***
>
> *The manuscript will likely be read by many membrane biologists/biochemists, and they might like to better understand how the RBM might be useful in their own approach. Here are some suggestions along these lines. The overall goal is to explain the RBM in *plain English* - the mathematical description in Eqs 2-4 is not easily interpretable.*
>
> *(1a) Explain that the RBM is a two-layer structure, in which one layer is the "visible" elements of the input sequence, and the other is called "hidden units." Connections are only made between visible and hidden units, but all such connections are made.*
>
> *(1b) The strengths of these connections are called "weights", and are determined in a statistical way based on a large set of input sequences. Once parametrized, the RBM is capable of capturing correlations among many positions in an input sequence - a significant advantage over the DCA approach.*

We agree with this assessment, and have updated the section of the text where we introduce the RBM with a non-technical explanation of what this method is doing. It reads as:

“The design of this RBM can be seen in Figure 4, where the model architecture is represented by purple dots and green triangles. The dots are the “visible” layer, which take in input sequences and encode them into the “hidden” layer, where each triangle represents a separate hidden unit. The lines connecting the visible and hidden layers show that each hidden unit can see all the visible units (the statistics are global), but they cannot see any of the other hidden units, meaning the hidden units are mutually independent. This global model with mutually independent hidden units (see also the marginal distribution form shown in Equation 3) has the following useful properties: higherorder couplings between... “

> *(1c) Although strictly true that the DCA model is a Boltzmann machine, it's not a typical Boltzmann machine, because all of the units are visible. Typically a Boltzmann machine would also include hidden units, in order to increase its capacity/power.*

We have clarified the relationship between DCA and Boltzmann machines, and this section now reads as:

This class of models is closely related to another model termed the Boltzmann machine. The Boltzmann machine formulation is closely related to the Potts model from physics, which was successfully applied in biology to elucidate important residues in protein structure and function (Morcos et al., 2011), and another example being the careful tuning of enzyme specificity in bacterial two-component regulatory systems (Cheng et al., 2014; Jiang et al., 2021). The Boltzmann machine-like formulation from Morcos et al. (2011), termed Direct Coupling Analysis (DCA), stores patterns...

> *(1d) Throughout, the authors refer to the activation of the hidden units as weights, but this is not a typical usage of this terminology. Connections between units are weights and have two subscripts. Given an input sequence, the sum over these weights for a given*

> *hidden unit is its activation (Eq. 1). I suggest aligning the description with the typical usage in order to make the presentation easier to follow. Hereafter I will refer to these hidden unit activations as simply activations.*

We agree with you, the hidden units are a collection of edge weights. We have modified the terminology in the text and in our figures to consistently refer to the collections of weights as hidden units and refer to the hidden unit outputs given a sequence input as activations.

> *(1e) How many hidden units are there?*

The final model was trained with 300 hidden units.

> *(2) It is redundant to say that lipids are both amphiphiles and hydrophobic…amphiphile already means hydrophobic plus hydrophilic.*

This is true, we have edited the manuscript to reflect this.

> *(3) What does this mean, and what's the point of this remark? "They [lipids] are relatively smaller than other complex biomolecules, such as proteins, thereby allowing a larger portion of their surface to interact with other macromolecules."*

We have removed this sentence.

> ***Reviewer 2 (Author Recommendations):***
>
> *While the idea of filtering out a part of the sequence data obtained with BLAST makes sense per se, it would be nice if the authors could comment on the nature of the sequences corresponding to the left peak in Figure 3b. It is hypothesised in conclusion that these sequences could lack any catalytic function. Could the authors experimentally check that this is the case or provide further evidence for this hypothesis?*

Yes, in this revision we provide further evidence as a new supplementary figure S2. At the time we performed domain analysis of the sequences we excluded; most of these sequences lacked the flippase domain associated with MprF function, and instead were combined with different domains. On this basis we excluded them due to their lack of relevance to the MprF from *Streptococcus agalactiae* we were interested in. Although there is possibility that some relevant sequences might be excluded, our assessment is that we gained specificity by reducing the set of sequences.

> *A key step in the RBM-based approach is the identification of "meaningful" hidden units, i.e. whose values are related to biological function. In Methods, the authors explain how they selected these units based on the L1 norms of the weights and the region of interaction with the lipid. While these criteria are reasonable, I wonder whether they are too stringent. In particular, one could think that regions in the proteins not in direct contact with the lipid could also be important for binding. It is known for instance that the length of loops can affect flexibility and help regulate activity in some catalytic enzymes. So my question is: if one relaxes the criterion about the coordinates of large weight values, what happens? Are other potentially interesting hidden units identified?*

We completely agree that other regions of the protein are likely involved in determining enzyme specificity, and that focusing on solely regions which interact with the lipid is perhaps missing important contributions to the catalytic function; we hypothesize that the flippase domain itself and its interaction with the catalytic domain are involved, especially considering the concerted mechanism by which they must operate. We are currently

investigating these theories and will be the subject of future work. As an initial step, we present this current work with restricted information that led to concrete predictions. We focused on the lipid binding pocket because it was one of just a few bits of information we had from the start, but as the reviewer suggests, we plan to follow up our research to try to identify other relevant hidden units and domains.

> *From a purely machine-learning point of view, it would be good to see more about cross-validation of the model. More precisely, could the authors show the log-likelihood of test set data compared to the one of training sequence data?*

We agree this is an important piece of information. We will update our methods section with this information. We performed a parameter sweep to search for the parameter's we used in our final model, and in that testing with a random 80/20% training/test split we had a training log probability loss of -0.91, and a test loss of -0.98. However, for our final model we used all available data and did not perform a split; the final result did not change dramatically by including the additional data, and the weight structure and composition was consistent with the results presented in the paper.

> ***Reviewer 3 (Public Review):***
>
> *In many of the analyzed strains, the presence of the lipid species Lys-PG, Lys-Glc-DAG, and Lys-Glc2-DAG is correlated to the presence of the MprF enzyme(s), but one should keep in mind that a multitude of other membrane proteins are present that in theory could be involved in the synthesis as well. Therefore, there is no direct evidence that the MprF enzymes are linked to the synthesis of these lipid species. Although, it is unlikely that other enzymes are involved, this weakens the connection between the observed lipids and the type of MprF.*

While there are a number of proteins found on the membrane that could play a role, we have specifically used a background strain that has a transposon in *mprF* that makes the bacteria incapable of synthesizing Lys-lipids (Figure 7B) unless complemented back with a functional MprF (Figure 7D-E). This led us to conclude that MprF is responsible for Lys-lipid synthesis.

> *Related to this, in a few cases MprF activity is tested, but the manuscript does not contain any information on protein expression levels. Heterologous expression of membrane proteins is in general challenging and due to various reasons, proteins end up not being expressed at all. As an example, the absence of activity for the E. faecalis MprF1 and E. faecium MprF2 could very well be explained by the entire absence of the protein.*

The genes were expressed on the same plasmid to control for expression. While we did not run a western blot to examine expression levels the plasmid backbone was used as a control for protein expression. Previous research supports *E. faecalis* MprF1 and *E. faecium* MprF2 not synthesizing Lys-lipids and instead most likely play a different role in the cell membrane.

> *The title is somewhat misleading. The sequence statistics and machine learning categorized the MprFs, but the identification of a novel lipid species was a coincidence while checking/confirming the categorization.*

We believe the title is appropriate given that the identification of *Enterococcus dispar* was through computational methods that led to the discovery Lys-Glc2-DAG. In other words, the categorization of potential organisms that produce lipids related to MprF has been driven by the proposition from the computational method. We agree, however, that the discovery was unexpected but would not have happened without the suggested organisms coming from the methodology presented here.

> *Please read the manuscript one more time to correct textual errors.*
>
> *The example of the role of LPS in delivering siRNA to targeted cancer cells is a bit farfetched as LPS is very different from the lipids that are being discussed here. I would rather focus on the role of Lysyl-lipids in antibiotic resistance in the introduction.*

We included LPS here to explain that natural lipids/components of the bacterial cell membrane could be used for drug delivery systems. While it is true LPS is quite different from Lys-lipid compounds, our goal was to create an emphasis on how the bacterial domain is a rich untapped source of lipids that could be used in biotechnology. In this way we wanted our statement to be more broadly about bacterial lipids and the importance of their continued study for diverse applications like pharmaceuticals.

> *The MS identification of Lys-Glc2-DAG is convincing, especially in combination with the fragmentation data, but the ion counts suggest low abundance. The observation would be strengthened if the identification of Lysyl-Glc2-DAG with different acyl-chain configurations has been observed. This should be then mentioned or visualized in the manuscript.*

We agree and have added an updated Figure 8A to demonstrate the presence of different acyl-chain configurations in *Enterococcus dispar*.

> *Further analysis of the Enterococcus strains shows the presence of the three lipids Lys-PG, Lys-Glc-DAG, and LysGlc2-DAG, although the Lys-Glc-DAG is only detected in trace amounts. This raises questions on the specificity of the MprF for the substrate Glc-DAG. If the ratio of Glc2-DAG compared to Glc-DAG abundance is similar to the ratio of Lys-Glc2-DAG vs. Lys-Glc-DAG abundance, this would strengthen the observation that the enzyme has equal affinity. However, if there is a rather large amount of Glc-DAG but a small amount of Lys-Glc-DAG, the production of Lys-Glc-DAG might be a side-reaction.*

The reviewer brings a relevant point of discussion, however, a clear resolution might be part of future work as we do not use spike in controls when completing lipid extractions. Because of this, it it is not possible for us to compare lipid levels across different samples. We now include a note clarifying this in the discussion section.

> *The plotting of the MprF sequence variants using the chosen RBM weights reveals a rather complex distribution over the quadrants (Figure 8). It is rather unclear in Figure 8 why only 1 sequence is plotted for Enterococcus faecalis and faecium, while 2 different MprFs are present (and tested) for these two organisms. This should be clarified.*

We agree this can be a source of confusion. We have further clarified this in the text that only the functional alleles were plotted in Figure 8 and that all Enterococcal alleles are plotted in Figure S3 regardless of function.

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