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Synthetic-bioinformatic natural product-inspired peptides†

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Covering: 2016 to 2024

Natural products, particularly cyclic peptides, are a promising source of bioactive compounds. Nonribosomal peptide synthetases (NRPSs) play a key role in biosynthesizing these compounds, which include antibiotic and anticancer agents, immunosuppressants, and others. Traditional methods of discovering natural products have limitations including cryptic biosynthetic gene clusters (BGCs), low titers, and currently unculturable organisms. This has prompted the exploration of alternative approaches. Synthetic-bioinformatic natural products (*syn*-BNPs) are one such alternative that utilizes bioinformatics techniques to predict nonribosomal peptides (NRPs) followed by chemical synthesis of the predicted peptides. This approach has shown promise, resulting in the discovery of a variety of bioactive compounds including peptides with antibacterial, antifungal, anticancer, and proteasome-stimulating activities. Despite the success of this approach, challenges remain especially in the accurate prediction of fatty acid incorporation, tailoring enzyme modifications, and peptide release mechanisms. Further work in these areas will enable the discovery of many bioactive peptides that are currently inaccessible.

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1. Introduction

Natural products are a bountiful source of bioactive compounds, with many being utilized as therapeutics. As of 2019, approximately two-thirds of FDA-approved small molecules are derived from natural products,[1] highlighting the significance of natural products in the drug discovery pipeline. Bacteria, particularly *Actinomycetota*, are a prolific source of bioactive compounds,[2] with over 13 000 bacterial natural products discovered to date.[3,4]

Among the bioactive natural products, cyclic peptides are a promising class of therapeutics, with over 40 FDA-approved cyclic peptides, many derived from natural products, targeting a range of bioactivities.[5–9] Since 2000, approximately one cyclic peptide has been approved each year,[6–8] highlighting their growing importance in the pharmaceutical industry. Compared to their linear counterparts, cyclic peptides typically exhibit heightened bioactivity due to enhanced cell permeability, binding affinity, and proteolytic stability.[10–14]

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In biological systems, peptide natural products are primarily synthesized *via* two main pathways: ribosomally synthesized and post-translationally modified peptides (RiPPs)[15] and non-ribosomal peptide synthetases (NRPSs).[16] RiPPs have been recently reviewed elsewhere.[17–19] This review focuses on NRPSs, which produce nonribosomal peptides (NRPs) with potential for a broad range of therapeutic applications, including antifungals such as caspofungin, antibiotics such as daptomycin and colistin, chemotherapeutics such as actinomycin D, and immunosuppressants such as cyclosporine (Fig. 1). Despite the considerable number of NRPs discovered thus far, bioinformatics analyses of sequenced bacterial genomes suggest that there remains immense potential for unearthing novel bioactive molecules from *Actinomycetota*.[20–22]

Traditional methods of natural product discovery, such as phenotypic screening,[23] co-cultivation,[24] and one strain many compounds (OSMAC),[25] have yielded valuable insights, but suffer from limitations such as low yields, high rediscovery rates, and time intensive isolations.[26,27] To address these challenges, alternative approaches such as heterologous expression of biosynthetic gene clusters (BGCs) and promoter engineering have been employed.[28] However, challenges persist, including choice of chassis and promoters, as well as frequent low yields.

Recently, a new technique was developed, which focuses on bioinformatics predictions of NRP structures followed by chemical synthesis and biological testing to generate bioactive natural product-inspired metabolites (Fig. 2A). This method was initially developed by Brady and coworkers and was named the synthetic-bioinformatic natural product (*syn*-BNP) approach.[29] The goal of the *syn*-BNP method is not to generate the exact natural product. Instead, it aims to quickly and more easily access the core scaffold of the natural product that is hopefully "close enough" in that it retains the biological activity of the natural product. This goal is well supported by the many natural product derivatives that are used as medicines (*e.g.* eribulin, doxycycline, rezafungin, as well as many others). While there are natural products that are directly used as medicines, most must be modified to improve properties such as pharmacokinetics or decrease toxicity. This is well evidenced by the number of natural products (71) *versus* natural product derivatives (356) approved by the FDA as drugs from 1981 to 2019.[1] The use of direct chemical synthesis allows access to many (oftentimes between 10 and a few hundred) peptides on reasonable scales for screening (usually a few milligrams). This is in contrast to isolation where one or a few molecules are isolated, oftentimes at submilligram quantities resulting in limited numbers of biological assays being performed. Additionally, the synthetic approach allows for easy modification for rapid structure activity relationship analyses and is generally easier to scale-up than isolation for further analyses.

Overall, the *syn*-BNP approach complements more historical approaches including bioactivity-guided fractionation of organisms (either collected or cultured) as well as heterologous expression. In particular, it overcomes many of the limitations of these more traditional approaches, including supply limitations, costly rediscovery of known natural products, the high percentage of currently unculturable organisms, and the challenges of finding appropriate hosts for heterologous expression. However, *syn*-BNP is currently limited by our ability to predict natural product structures, with highly modified bioactive molecules likely being missed by this approach. It also limits the source of the natural products explored. While it is possible to apply the *syn*-BNP method to fungal or plant genomes, it is more challenging to predict natural product structures when biosynthetic genes are not clustered, thus limiting our ability to apply the *syn*-BNP method to these organisms. As natural

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Elizabeth I. Parkinson

Elizabeth (Betsy) Parkinson attended Rhodes College, where she obtained her BS in chemistry in 2010. She conducted graduate research with Prof. Paul Hergenrother at the University of Illinois at Urbana-Champaign (UIUC) on the synthesis of bioactive natural products and their mechanisms of action. After obtaining her PhD in 2015, she joined the laboratory of Prof. William Metcalf in Microbiology at UIUC for her postdoctoral studies, where she studied the biosynthesis of natural products from Streptomyces*. Betsy started her independent career as an assistant professor in the Departments of Chemistry and Medicinal Chemistry and Molecular Pharmacology at Purdue University in the Fall of 2018. In her lab, research focuses on the discovery of natural products from cryptic biosynthetic gene clusters and elucidating the function of natural product biosynthetic enzymes.*

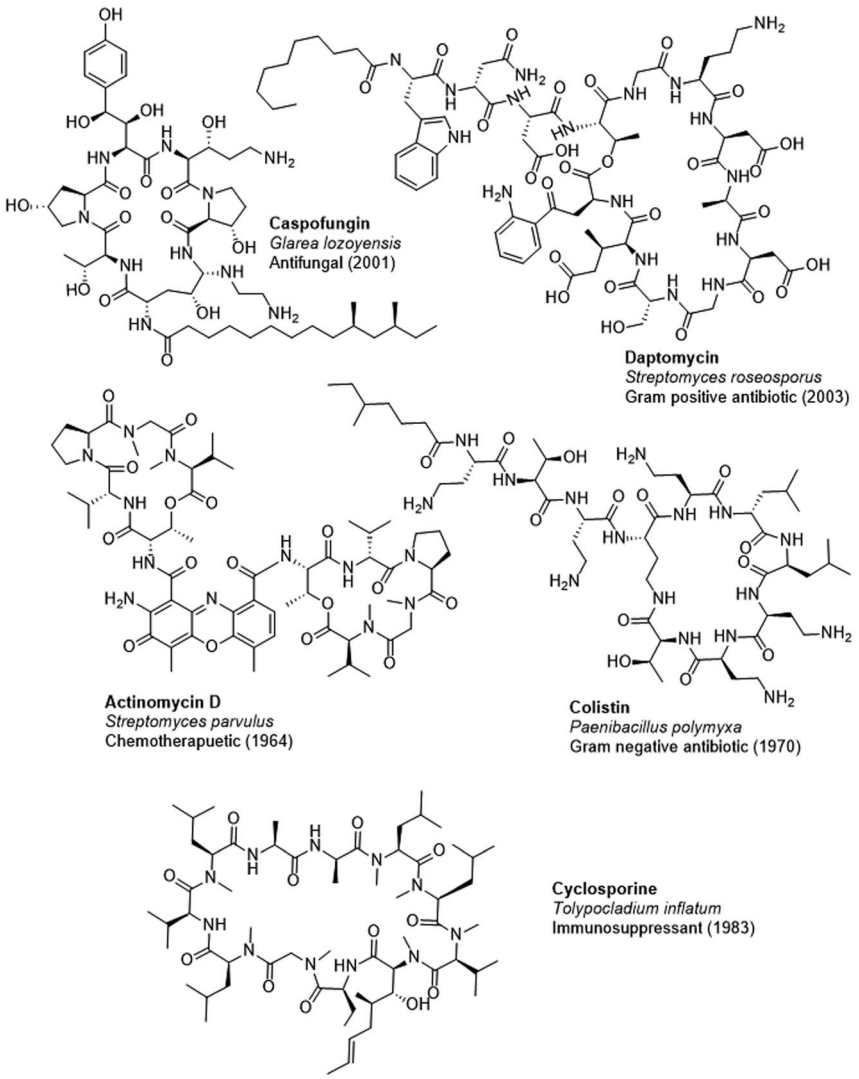

Fig. 1 A selection of FDA approved NRPs with their approval date, bioactivity, and species of origin.

product structure predictions improve, we expect that *syn*-BNP will be more widely applied to natural products from different domains and kingdoms. *Syn*-BNP, along with other BGC targeted approaches such as heterologous expression, also suffers from the fact that we are often unable to predict whether a natural product will be bioactive based solely on its BGC. For this reason, there is a need to screen molecules from a wide variety of BGCs in a large number of assays to identify bioactive natural products. While this is very challenging using heterologous expression, this is an area where the *syn*-BNP method excels. Specifically, the synthetic approach of *syn*-BNP allows for rapid generation of medium sized libraries of natural product-like molecules for biological testing. Additionally, the fact that *syn*-BNPs are pure molecules is another advantage compared to traditional screening of extracts. In particular, it avoids the challenges of crude extracts or fractions, such as molecules that directly interfere with screens (*e.g.* pan-assay interference compounds, PAINS) or compounds that synergize and lose activity upon isolation. Since the initial inception of the *syn*-BNP approach in 2016, the technique has resulted in the identification of many bioactive molecules such as antibacterial, antifungal, and anticancer compounds (ESI Table 1†), showcasing its potential in expanding the repertoire of bioactive molecules derived from natural sources. In this review, we cover the *syn*-BNP method and papers published on the topic from 2016 to August 2024.

2. Bioinformatics prediction of NRPs

NRPSs are multimodular enzyme complexes that possess distinct domains responsible for loading and coupling amino acids. The essential domains include adenylation (A), thiolation (T), and condensation (C) domains (Fig. 2B). The A domain selects and activates the amino acid *via* adenylation. These activated amino acids are then loaded onto the phosphopantetheinyl arm of the T (also known as the peptidyl carrier protein, PCP) domain, which is responsible for carrying the growing peptide chain. Finally, the C domain is responsible for peptide bond formation between the amino acids on the upstream and downstream T domains. In addition to the

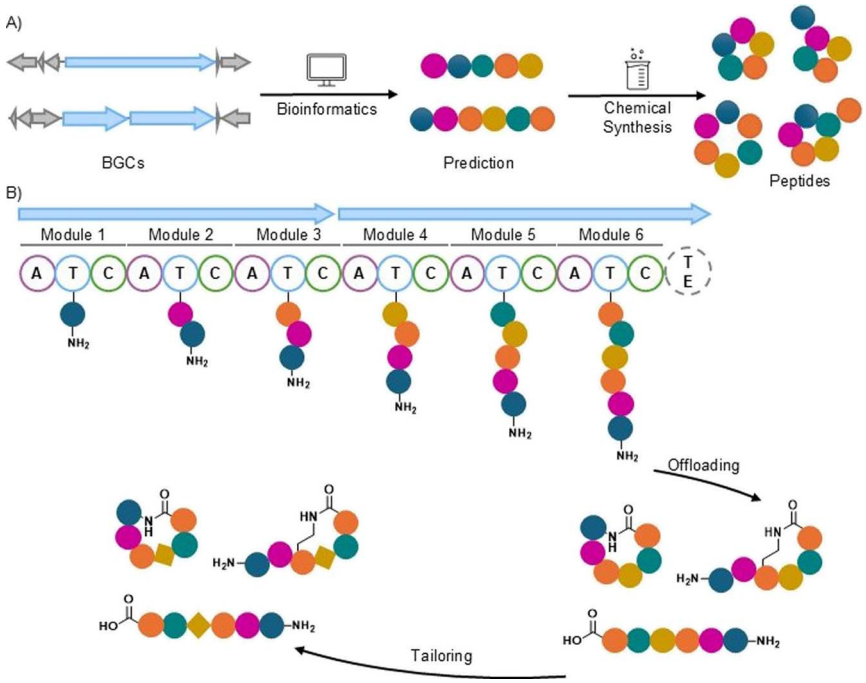

Fig. 2 (A) General workflow of the *syn*-BNP approach. (B) General NRPS machinery. Rectangles denote modifications installed by tailoring enzymes. Abbreviations: adenylation (A), thiolation (T), condensation (C), thioesterase (TE), biosynthetic gene cluster (BGC).

essential domains, several other domains are often present on NRPSs including epimerization (E, epimerizes L amino acids to D amino acids), methylation (M, often *N*-methylates an amino acid), heterocyclization (Cy, cyclodehydrates between a Cys, Ser, or Thr and backbone carbonyl), reduction (R, offloads the peptide as an aldehyde) and thioesterase (TE, offloads peptide as either a carboxylic acid, lactone, or lactam) domains.[16,30,31] These additional domains and in *trans* tailoring enzymes facilitate additional modifications to give the final NRP.

2.1. Strategies for peptide structure prediction

Accurate predictions of amino acid sequences of NRPs are essential for the *syn*-BNP method to be successful. Many methods for adenylation domain specificity predictions have been developed over the years. Initially, Stachelhaus developed a predictive method based on the A domain active site residues.[32] It was discovered that certain residues (positions 235, 236, 239, 278, 299, 301, 322, 330, 331, and 517) are essential for substrate selectivity. The amino acids at these locations within the substrate binding pocket generally correlate with the class of amino acids that are loaded. This study helped identify rules that can be utilized to predict the amino acids that will be loaded by a specific adenylation domain. More recently, tools such as AntiSMASH,[33,34] PRISM,[35,36] SANDPUMA,[37] Norine,[38] and NRPSPredictor2 (ref. 39) (Table 1) leverage machine learning techniques, including profile hidden Markov models, to predict the amino acid associated with the adenylation domain. These models are robust and widely employed for predicting the amino acid affiliated with a specific A domain.[58]

In addition to predicting the amino acid sequence, it is necessary to predict other modifications to the NRP, such as those performed by the non-essential domains and in *trans* tailoring enzymes. Both antiSMASH and PRISM provide valuable insights into these modifications. For instance, they both predict E, M, and Cy domains within the NRPS, enabling epimerization, methylation, and heterocycle formation to be predicted. They can also predict starter C (Cs) domains, which are present at the beginning of the initiation module. Cs domains are typically indicative of a lipopeptide, a distinct class of NRPs with an N-terminal fatty acid tail. However, accurate prediction of the identity of the chain remains challenging. These programs can also predict the presence of likely peptide tailoring enzymes, such as hydroxylases, glycosyltransferases,

Table 1 Bioinformatics tools employed in studies utilizing the *syn*-BNP approach and corresponding references

Bioinformatics tools	Reference paper
AntiSMASH v.6.1	40
AntiSMASH v.5.1.2	41–45
AntiSMASH v.5.0	46–49
AntiSMASH v.3.0	50
AntiSMASH v.2.0	29 and 51–53
PRISM 4	47–50
Minowa	54 and 55
NRPSPredictor2	54 and 55
Stachelhaus	55 and 56
SANDPUMA	45 and 56
Norine	45
MIBiG v.2.0	45
In-house method	41, 42, 45 and 57

Table 2 Databases used in studies utilizing the *syn*-BNP strategy along with bioactivities discovered and reference papers

Repository	Mechanism	Reference paper
GenBank	Amoebicidal, antibiotic, antifungal, chemotherapeutic, proteasome stimulator	41–45, 47–49, 51, 53 and 57
Joint genome institute	Antibiotic	57
Human microbiome project	Antibiotic, chemotherapeutic	29, 52 and 55
Human oral microbiome database	Antibiotic, chemotherapeutic	29, 52 and 55
Soil metagenome	Antibiotic, chemotherapeutic	40, 46 and 56

and halogenases but are typically not able to accurately predict how these tailoring enzymes will modify the NRP. For this reason, BGCs with multiple tailoring enzymes are usually avoided in the *syn*-BNP method.

Once the linear NRP is predicted, determining the method of release becomes crucial. Two primary enzymes have been utilized to date in the *syn*-BNP approach: traditional TEs and penicillin-binding protein (PBP)-like TEs (PBP-TEs). Traditional TE domains often act in *cis* and catalyze the release of peptides from the final T domain of the NRPS, either through hydrolysis or cyclization. Several types of cyclization are possible such as: head-to-tail, head-to-sidechain, or head-to-fatty acid. While a single TE will usually only perform one of these offloading methods, predicting this process based solely on TE sequence remains a challenge.[59] This results in many predicted NRPs for each NRPS BGC. For the *syn*-BNP approach with traditional TE containing NRPSs, either the linear peptide is exclusively synthesized[29,53–55] or multiple cyclized products per predicted linear NRP (*i.e.*, head-to-tail, head-to-sidechain, and/or head-to-fatty acid) are produced.[51,52] This can make the synthesis process laborious as multiple derivatives must be synthesized to identify the correct molecule of interest. While the majority of NRPS BGCs found to date end in a traditional TE domain, other offloading methods exist. One such method is *via* PBP-TEs, which act in *trans* to the NRPS. Multiple PBP-TEs have been studied (*e.g.*, SurE,[60,61] Ulm16,[62] PenA,[63] WolJ,[64] and DsaJ[65]) with several studies having utilized derivatives of their native substrates to determine the scope of the PBP-TEs. To date, these studies have only found PBP-TEs to catalyze head-to-tail cyclization.[60,62,63,66] Therefore, when utilizing a PBP-TE for bioinformatics predictions, only one peptide needs to be synthesized per linear prediction.[47–50]

2.2. Sources of biosynthetic gene clusters

To generate bioinformatics predictions, genome libraries are essential. For the *syn*-BNP approach, three major sources of genomes have been investigated: genomes from isolated soil bacteria, soil metagenomes, and the human microbiome. For the studies that used genomes from isolated bacteria, most have relied on either the GenBank[67] or the Joint Genome Institute (JGI)[68] database (Table 2). Others have focused on particular bacterial species such as *Streptomyces* sp. H-KF8 (ref. 50) and *Paenibacillus mucilaginosus* K02.[54] The soil metagenome and the microbiome projects are particularly interesting sources because they do not require the isolation of an organism. Given that approximately 1% of bacterial species are thought to be currently culturable, the natural products in the other 99% of bacterial species are currently inaccessible.[69] The culture-independent nature of the *syn*-BNP method facilitates access to these otherwise very challenging to attain molecules.

The work with soil metagenomes has exclusively been performed by Brady and co-workers using their extensive soil metagenome libraries.[29,52,59] For the microbiome work, genomes have primarily been accessed from resources like the Human Microbiome Project[70] and the Human Oral Microbiome Database.[71] These diverse sources of microorganisms have led to the identification of unique and novel *syn*-BNPs. Given the vast amount of genome sequences that exist and the continuing growth of these libraries, we hypothesize that there are still many bioactive *syn*-BNPs yet to be discovered.

3. Synthesis of NRPs

The second step of the *syn*-BNP method is the chemical synthesis of the predicted peptides. Given that *syn*-BNP has only been performed on NRPS substrates, except for the NRPS-PKS hybrid albicidin, the major steps of the synthesis are the generation of the linear peptide substrate and the subsequent cyclization strategy, if applicable. The following sections delve into the synthetic techniques employed in these areas. Another important area, which will not be discussed in depth here, is the synthesis of non-canonical amino acids. The synthesis of *syn*-BNPs can be greatly complicated by predictions of non-commercially available non-canonical amino acids. Continued development of efficient methods to access non-canonical amino acids will help to expedite these syntheses.[72,73]

3.1. Linear peptide synthesis

The synthesis of linear peptides is often the first step of *syn*-BNP synthesis. Solid-phase peptide synthesis (SPPS)[74] is nearly always employed (Fig. 3A). The exceptions to this are the highly modified lapcin and PABA-containing *syn*-BNPs, which were synthesized using batch methods.[40,43,46] Many fantastic reviews of SPPS exist[75–77] and thus we will only outline the methods used to generate *syn*-BNPs. Chlorotrityl or Wang resin is most often employed because either can be used to generate C-terminal carboxylic acids, yielding completed linear peptides that can be further activated for cyclization reactions if desired.[77] Specific reagents for SPPS have included common coupling reagents HATU, HBTU, Oxyma, or PyBOP for amide bond

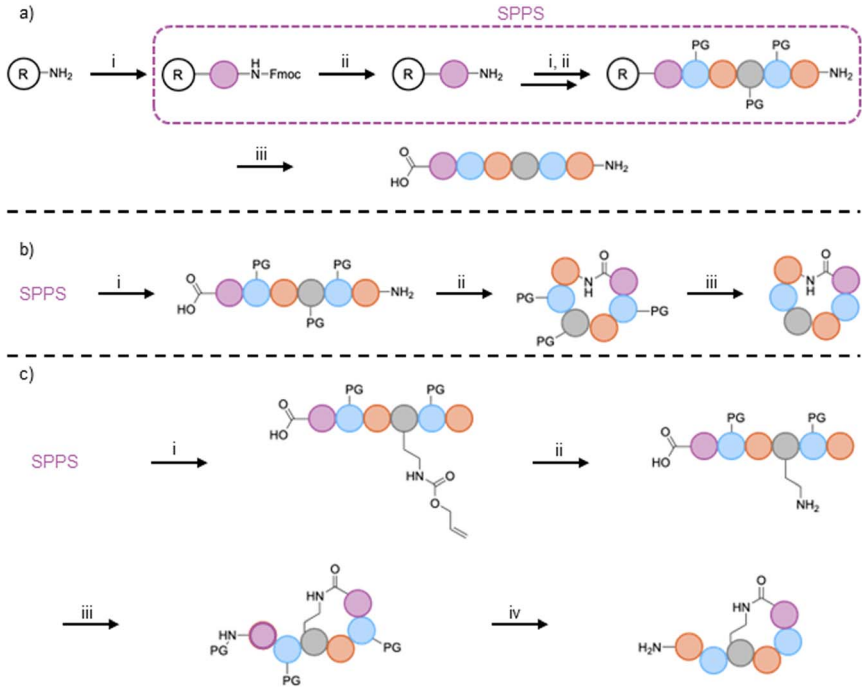

Fig. 3 (A) General scheme for synthesizing linear peptides. Starting with a resin pre-loaded with the C-terminal amino acid, the steps for SPPS include: (i) activation of the amino acid with an amide coupling reagent and (ii) deprotection of the Fmoc-protecting group with piperidine. Steps i and ii are repeated until all amino acids are coupled. (iii) Removal of the protecting groups and cleavage of the peptide from the resin. (B) General scheme for synthesizing head-to-tail cyclized peptides. After completion of SPPS: (i) cleavage of the peptide from resin using a method that retains sidechain protecting groups, (ii) cyclization of the peptide using a coupling agent, and (iii) global deprotection of the peptide. (C) General scheme for synthesizing head-to-sidechain cyclized peptides. After completion of SPPS with the desired coupling sidechain having an orthogonal protecting group: (i) deprotection of the allyloxycarbonyl group, (ii) cyclization with a coupling agent, and (iv) cleavage from resin and global deprotection to obtain the final product. Acronyms: solid-phase peptide synthesis (SPPS), resin (R), protecting group (PG).

formation with piperidine for Fmoc-deprotection. Once the full linear peptide is synthesized, it can be cleaved from the resin using HFIP or TFA, depending on whether a side chain protected or fully deprotected peptide is desired. N-terminal modifications such as fatty acid installation occur during SPPS (*e.g.* cilagicin,[41] lapcin,[43] macolacin[44]). While these methods work well for generation of linear peptides, future studies should consider greener alternatives to SPPS, which requires the use of large amounts of toxic organic solvents as well as explosive coupling reagents and allergenic additives.[78]

3.2. Cyclization strategies

Many of the *syn*-BNPs generated to date are cyclic peptides, including head-to-tail, head-to-sidechain, and head-to-fatty acid cyclic peptides. Head-to-tail cyclized peptides are generally made using chlorotrityl resin followed by cleavage from the resin with HFIP or TFA and DIEA, to retain the sidechain protecting groups and thus prevent unwanted sidechain cyclization (Fig. 3B). The specific conditions for the TFA deprotection are important to retain the protecting groups on the designated sidechains, typically using short exposure to 1% TFA in DCM with neutralization by DIEA.[41,44,51,52] Head-to-tail cyclization is then catalyzed using PyBOP or HATU in solution, usually at low concentrations to avoid oligomerization. After successful cyclization, the sidechain protecting groups are removed with TFA resulting in the final cyclic peptide.[47–49]

Head-to-sidechain and head-to-fatty acid syntheses both rely on orthogonal protecting strategies (Figs. 3C, *e.g.*, an allyloxycarbonyl (Alloc) protecting group for an amine that can be removed using palladium, leaving the other Fmoc-protected amines protected). This ensures a selective cyclization of the previously Alloc-protected amine with the activated carboxyl group on the peptide. While utilization of the orthogonal protecting group strategy for peptide cyclization can be employed off-resin, performing the cyclization on-resin is often advantageous due to the pseudodilution effect.[79] Specifically, peptides are much less likely to oligomerize, thus giving higher yields of correctly cyclized products.[41,42,44,45,51,52,56,57] One example of on-resin cyclization for *syn*-BNPs added a monomethoxytrityl protected lysine to the C-terminus of the linear peptide during SPPS. Glutaric anhydride was then coupled to the N-terminus using DMAP. Cleavage of the monomethoxytrityl group on the lysine was performed using TFA, and on-resin cyclization was performed with PyBOP or HATU resulting in the final product.[50]

4. Examples of *syn*-BNP libraries and bioactivities

4.1. Unbiased *syn*-BNP predictions and bioactivities

After predicting and synthesizing the *syn*-BNP libraries, they are screened for bioactivities. This screening process has yielded peptides exhibiting a wide spectrum of bioactivities (Table 2

and ESI Table 1†), underscoring the versatility and potential of this technique.

4.1.1. *Syn*-BNPs with antibiotic activity. The primary emphasis of most unbiased *syn*-BNP studies has been on uncovering antibiotics, with nearly every paper investigating the antibacterial activity of their *syn*-BNPs. Through this approach, 17 antibiotics effective against Gram-negative and/or Gram-positive pathogens have been unearthed with diverse MIC values ranging from 1 to 248 μg mL^{-1} from 2016 to 2024.[29,50,51,53,54] Of the 17 discovered antibiotics, 15 have MIC values less than 10 μg mL^{-1}. In the initial paper describing the *syn*-BNP approach, both human commensal and pathogenic bacteria were analyzed for the presence of NRPs.[29] NRPs predicted to have more than 5 residues, appeared to be complete clusters, and did not contain PKS domains were taken forward, leading to 30 target *syn*-BNPs. Of these, 25 linear peptides were successfully synthesized and tested for antibiotic activity against both pathogens and human commensals. From this, two *N*-acylated linear heptapeptides named humimycin A and humimycin B were found to have potent activity against Gram-positive bacteria including *Firmicutes*, *Actinomycetota*, *Staphylococcus*, and *Streptococcus* (Fig. 4). Resistance to humimycin was developed and suggested that the mechanism of action was likely inhibition of a homolog of MurJ, a flippase that translocates peptidoglycan precursors. This was further supported by the fact that humimycin A resensitized β-lactam resistant strains to dicloxacillin, suggesting they are likely acting on the peptidoglycan biosynthesis pathway. A follow up paper explored the structure activity relationship and identified 17S, which replaced all three aromatic residues in humimycin A with tryptophan, as a broader spectrum, more potent antibiotic.[55] It also retained the ability to synergize with β-lactams and had a lower rate of resistance.

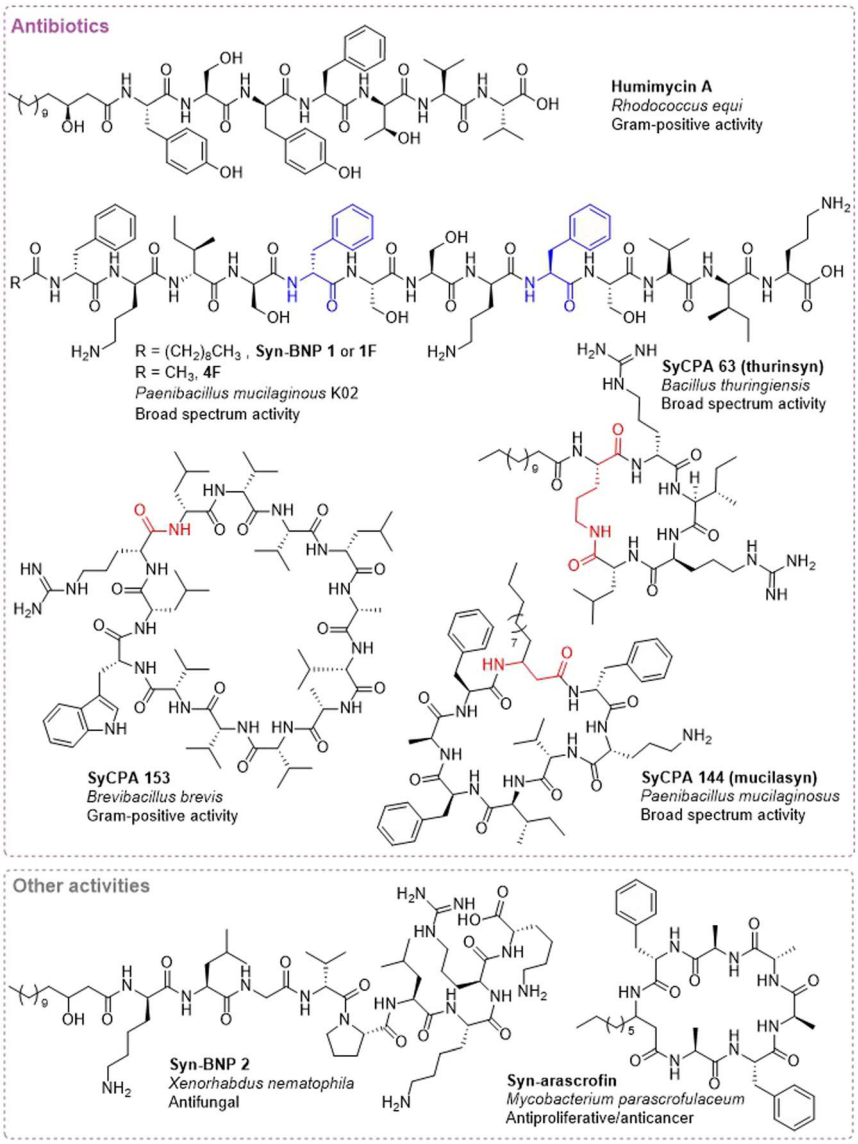

Fig. 4 Structures of a subset of the bioactive *syn*-BNPs identified from unbiased libraries. Under each structure is the name, species of origin and bioactivity of the molecule. Blue indicates residues with differing predictions. Red is the cyclization site.

In another early *syn*-BNP study, a library of 288 linear *syn*-BNPs from the NCBI database yielded 5 antibiotic agents with MIC values less than 8 μg mL^{-1} against ESKAPE pathogens.[53] The most potent compound, *syn*-BNP 1 (Fig. 4), was discovered from the *Paenibacillus mucilaginosus* K02 genome. *Syn*-BNP 1 demonstrated activity against Gram-positive bacteria, as well as the Gram-negative *Acinetobacter baumanii*. This compound mimics tridecaptins, with 5 of the 13 amino acids being shared. Interestingly, no resistance to *syn*-BNP 1 could be developed *via* direct plating or serial passaging methods. Because this is often indicative of a membrane based mechanism, *syn*-BNP 1 was tested for its ability to depolarize cells using a fluorescence DiBAC4 assay. Similar to tridecaptin, no depolarization of the membrane was observed. Tridecaptin has previously been shown to bind lipid II, and it is hypothesized that *syn*-BNP 1 is acting similarly. However, additional experimentation is needed to verify this hypothesis. Derivatives of *syn*-BNP 1 were explored in a follow up paper where differences in amino acid predictions as well as alternate fatty acid chains were investigated.[54] Interestingly, the choice of fatty acid chain greatly affected the activity profile. For example, replacement of the decanoyl of *syn*-BNP 1 (aka compound 1F) with an acetyl group (compound 4F, Fig. 4) resulted in decreased potency against most of the Gram-positive strains and greatly increased potency against the Gram-negative strains. 4F showed good selectivity for bacterial cells over mammalian cells and strong activity in a rat cutaneous model of multidrug resistant *A. baumannii*. To explore the mechanism of 4F, resistant mutants were developed using *A. baumannii* ATCC 17978. These mutants generally grew slower and had a different morphology compared to the parent strains. Sequencing revealed that mutations occurred in the cell membrane phospholipid metabolism network (*e.g.* phospholipase A and D and phosphatidyltransferase), suggesting that 4F targets the membrane. Interestingly, several mutations in the *adeS* gene, which encodes for a histidine kinase in a two-component regulatory system, and in the lipopolysaccharide biosynthesis pathway further supported the membrane as a target of 4F. Additionally, while only moderate membrane depolarization was observed upon treatment with 4F, extensive pore formation was observed.

Another unbiased *syn*-BNP library was developed from bacterial genomes found in GenBank.[51] After excluding known NRPS biosynthetic gene clusters as well as clusters containing a large number of tailoring enzymes or fewer that 3 adenylation domains, 96 linear peptide predictions were explored. This work differed from previous publications in that it focused on cyclic peptides. Specifically, for each linear peptide predicted, a head-to-tail (or head-to-fatty acid for predicted *N*-acyl containing peptides) and head-to-side chain cyclic peptides were explored. This resulted in 157 cyclic peptides, which were screened against ESKAPEE pathogens and *Mycobacterium tuberculosis*. Impressively, this relatively small library resulted in 9 bioactive *syn*-BNP cyclic peptides (4 Gram-positive specific and 5 with both Gram-positive and Gram-negative activity), with 7 showing minimal to no cytotoxicity to mammalian cells. These *syn*-BNP cyclic peptide antibiotics (syCPAs) were found to have various mechanisms of action including cell lysis (syCPA 12, 102, and 123), membrane depolarization (syCPA 63), inhibition of cell wall biosynthesis (syCPA 4), and ClpP protease dysregulation (syCPA 116). Three active molecules (syCPA 2, 144, and 153) currently have undetermined mechanisms of action (Fig. 4).

Overall, these findings suggest that *syn*-BNPs are a great source of antibiotics with interesting mechanisms that have the potential to target multidrug-resistant bacteria. Future screening efforts should continue to explore and expand on this activity. Additionally, in the future, standardized conditions for testing peptides for antibiotic activity should be developed. Many are screened using conditions originally optimized for small molecules. These conditions can sometimes result in degradation of the peptides and thus the community may be missing some promising compounds.

4.1.2. *Syn*-BNPs with antifungal activity. Antifungal activity has only been screened in a handful of studies,[45,50,52,53] with one antifungal *syn*-BNP hit being discovered to date.[53] Specifically, the linear nono-lipopeptide (*syn*-BNP 2) has activity against *Candida albicans* at 3.23 μg mL^{-1} with no cytotoxicity displayed at 128 μg mL^{-1} against HT-29 and HeLa cells. *Syn*-BNP 2 also displayed good activity (2–4 μg mL^{-1}) against other fungal strains (*Stachybotrys chartarum*, *Cryptococcus albidus*, *Cryptococcus neoformans*, *Schizosaccharomyces pombe*, and *Saccharomyces cerevisiae*). A handful of derivatives of *syn*-BNP 2 based on alternative predictions from the Stachelhaus code as compared to the NRPSPred2 and Minowa algorithms were synthesized. None showed superior activity to the parent compound. Preliminary mechanism of action studies revealed that *syn*-BNP 2 does not disrupt the cell wall nor ergosterol biology, and the mechanism currently remains unknown. Overall, there is a need for additional testing of *syn*-BNPs for antifungal activity given that many antifungal agents are peptide natural products.

4.1.3. *Syn*-BNPs with anticancer activity. Given that many peptidic natural products have previously been shown to have anticancer activity,[80] screening the *syn*-BNP library is a logical step. Many *syn*-BNPs have been evaluated for their anticancer activity, with five having activity at 2 μM or less.[40,43,48,52,56] Interestingly, a library based on human microbiome NRPS BGCs resulted in the discovery of several anticancer agents.[52] Analysis of approximately 1300 human associated bacteria for BGCs containing greater than 5 modules with strong bioinformatics predictions and few tailoring enzymes resulted in 30 linear *syn*-BNPs and 86 cyclic *syn*-BNP target structures. 72 of these 86 targets were successfully synthesized and tested for antibiotic, antifungal, and anticancer activities. Interestingly, in contrast to studies performed with libraries of soil-dwelling bacteria, no antibiotic or antifungal molecules were observed. Instead, in a screen against the HeLa cervical cancer cell line, four *syn*-BNPs (*syn*-hoagimin B, *syn*-rhodomin, *syn*-parascrofin, and *syn*-kroppenstin) with anticancer activity were identified.[52] Excitingly, *syn*-parascrofin and *syn*-kroppenstin demonstrated IC_{50} values below 1 μM against HeLa cells as well as a colorectal adenocarcinoma cell line (HT-29) and two non-small cell lung cancer cell lines (A549 and NCI-H1299).[52] Unfortunately, neither toxicity to normal cells nor the mechanisms of action were investigated. Overall, this study demonstrates the selective

discovery of anticancer agents from human associated microbes, especially opportunistic pathogens. This is quite intriguing and suggests that the origin of the bacteria is likely to influence the activities observed.

4.2. Targeted derivative predictions

While many of the papers utilizing the *syn*-BNP method employ an unbiased approach (*i.e.* synthesizing any NRP with between 4 or 5 and 13 amino acids),[47–54] some have employed a targeted strategy to identify more potent analogs of either a certain peptide class or molecule. Nearly all of these studies, with the exception of the head-to-tail cyclized peptides, have focused on antibiotic activity. Below we have described some of the targeted approaches, specifically focusing on those that went after specific NRP classes or NRPs containing certain non-canonical amino acids.

4.2.1. Lipopeptides. Lipopeptides are clinically used as both antibiotics (*e.g.* colistin and daptomycin) and antifungals (*e.g.* caspofungin). For this reason, Brady and co-workers chose to selectively search for NRPS BGCs that contained a Cs domain, which install fatty acids on lipopeptides.[42,81] They generated a phylogenetic tree from NRPSs found in ~10 000 bacterial genomes in Genbank using the Cs domain as the query. From this tree, they identified a clade with no characterized lipopeptides that fell into a larger group with Cs domains from known antibiotic BGCs. As it is difficult to predict the release of an NRP by a TE, they synthesized two linear and six cyclic peptides identified in this clade. The fatty acid utilized for each peptide family was determined based on the lipid most commonly observed in the most closely related Cs domain. For example, when peptides were similar to the paenibactins, myristic acid was utilized. This led to the discovery of cilagicin (Fig. 5), a dodecalipodepsipeptide antibiotic with potent activity against Gram-positive, antibiotic-resistant pathogens.[42] Cilagicin was found to bind both undecaprenyl phosphate (C55:P) and undecaprenyl pyrophosphate (Cff:PP), essential carrier lipids required for the translocation of cell wall intermediates, resulting in disrupted cell wall synthesis. To date, no resistance has been developed to cilagicin, likely due to its ability to bind to multiple non-peptidic targets.[42] Furthermore, cilagicin did not demonstrate cytotoxic activity against HEK-293 cells at up to 64 μg mL^{-1}.[57] Due to this very promising activity, cilagicin was evaluated for *in vivo* efficacy in neutropenic mouse thigh models with *S. aureus* and *S. pyrogens*, where it demonstrated very promising reductions in bacterial burden. Unfortunately, high serum binding likely reduced efficacy *in vivo*.[42]

To discover peptides with similar or enhanced activity compared to cilagicin, a screen was conducted using both the Joint Genomic Institute (JGI) and GenBank databases to identify compounds with highly homologous BGCs to the cilagicin BGC.[57] Of the 25 they screened, only five highly similar (>50% shared amino acids) NRPs were identified, with two being identical to cilagicin. The three predicted NRPs (paenilagicin, bacilagicin, and virgilagicin) were found to have similar, if slightly less potent, Gram-positive antibiotic activity (0.12 to 8 μg mL^{-1}) to cilagicin. Interestingly, cilagicin, paenilagicin, and virgilagicin did not lead to resistance after prolonged antibiotic exposure.[57] More recently, Brady and coworkers have put forth efforts to optimize cilagicin for clinical development. The myristic acid at the N-termini was replaced with a biphenyl moiety, which in turn reduced the serum binding and improved *in vivo* efficacy. A robust structure activity relationship campaign identified a derivative called dodecacilagicin which improved potency, reduced serum binding, and exhibited low MICs.[82]

4.2.2. *n*-Cinnamoyl containing peptides. While most lipopeptide *syn*-BNPs have focused on peptides with simple fatty acids, recently Brady and co-workers have investigated *syn*-BNPs containing the cinnamoyl fatty acid (*i.e.* cinnamoyl containing peptides, CCPs).[56] CCPs such as the Gram-positive antibiotic cinnapeptin and the antitubercular agent atratumycin are just two recent examples highlighting the promise of CCPs.[83–85] To identify *syn*-BNPs containing the cinnamoyl fatty acid, the biosynthetic subcluster responsible for the production of cinnamoyl (specifically the ketosynthase alpha, ketoreductase, and isomerase) were used as query sequences, resulting in the identification of hundreds of CPP-encoding BGCs. These BGCs were initially analyzed using the standard *syn*-BNP approach,

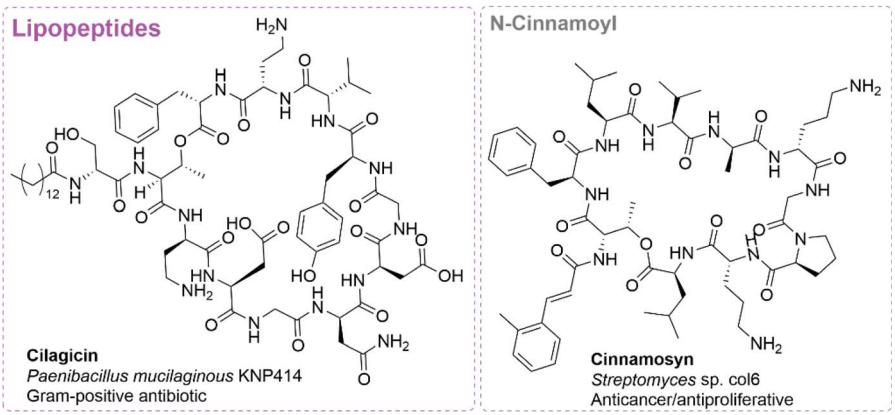

Fig. 5 Structures of bioactive *syn*-BNPs identified by the lipopeptide and *n*-cinnamoyl targeted approaches. Under each structure is the name, species of origin and bioactivity of the molecule.

with amino acids being predicted based on the substrate binding pocket of the A-domain. BGCs corresponding to known CCPs, duplicates, and those with many tailoring enzymes were removed from further analysis. The *cnn* BGC, which is predicted to encode for production of a decapeptide CCP, was chosen for further analysis. While six adenylation domains had perfect matches to characterized A-domains using the Stachelhaus code, four more variant positions were further analyzed using SANDPUMA. Ultimately, the SANDPUMA predictions agreed with two positions but predicted ornithine at the other two. The SANDPUMA predictions were used for the synthesis. Cyclization was predicted to occur at the N-terminal *allo*-threonine due to similar cyclization sites in other CCPs, resulting in the final molecule cinnamosyn (Fig. 5). Cinnamosyn displayed moderate antibiotic activity against *E. coli* and *B. subtilis* as well anticancer activity against a variety of cancer cell lines (*e.g.* HeLa, U-2 OS, LS-411, RKO, HT-29, HCT-116, and HCC1806) with an IC_{50}s ranging from 4 to 21 μM. However, it also potently killed two healthy cells lines (Uero E6 and HEK-293), suggesting that it is likely to not be selective for cancerous over healthy tissues. Replacement of the cinnamic acid with a hexanoic acid resulted in greatly reduced potencies for both cancerous and healthy cell lines, demonstrating the importance of the cinnamic acid for activity.

4.2.3. Cationic lipopeptides. Another antibiotic class that has been utilized as a hook for *syn*-BNPs is the cationic lipopeptides.[86,87] One of the most well-known cationic lipopeptides is colistin (aka polymixn E), which has activity against multidrug-resistant Gram-negative pathogens.[86] Brady and coworkers screened for new cationic lipopeptides by screening for NRPS BGCs that contained a Cs domain (*i.e.* encoded for production of a lipopeptide) and were predicted to incorporate two or more positively charged amino acids.[41] Of the ~10 000 strains screened, over 15 000 BGCs contained Cs domains, and 395 were predicted to have ≥5 amino acids with 2 or more amino acids being positively charged. Analysis of uncharacterized BGCs that were in the same Cs clade as known cationic lipopeptides led to the discovery of derivatives of laterocidine (*syn*-CNRLP1, -2, and -3), tridecaptin (*syn*-CNRPL4, -5, and -6), and paenibacterin (*syn*-CNRLP7, Fig. 6). The cationic lipopeptides *syn*-CNRLP1, -5, and -7 displayed antibiotic activity against ESKAPEE pathogens ranging from 0.25 to 64 μg mL^{-1}. The laterocidine derivative, *syn*-CNRLP1, was active against Gram-negative bacteria, while the tridecaptin derivative *syn*-CNRLP5 and the paenibacterin derivative *syn*-CNRLP7 exhibited activity against both Gram-negative and Gram-positive bacteria. Interestingly, tridecaptin A was only active against Gram-negative bacteria, demonstrating that the *syn*-BNP method was able to identify *syn*-CNRLP5 as a more broad-spectrum tridecaptin. Similarly, while *syn*-CNRLP7 has weaker activity against Gram-negative bacteria compared to paenibacterin, it has increased activity against WT *S. aureus*, three strains of multidrug-resistant *S. aureus*, and three strains of vancomycin-resistant *E. faecium*. The mechanism of action for these molecules is currently unknown,[41] but given that they are cationic lipopeptides it is reasonable to assume that their activity is likely at least in part due to membrane interactions.

Another cationic lipopeptide *syn*-BNP with antibiotic activity is macolacin (Fig. 6), which has potent activity against ESKAPEE pathogens, including those resistant to colistin.[44] Colistin is a cationic lipopeptide that works by binding to lipid A in lipopolysaccharides, resulting in membrane disruption and cell death. Recently, resistance to colistin has been rising, in large part due to the plasmid-borne mobilized colistin resistance gene *mcr-1*, which encodes phosphoethanolamine transferase.[88] This transferase modifies lipid A with the positively charged

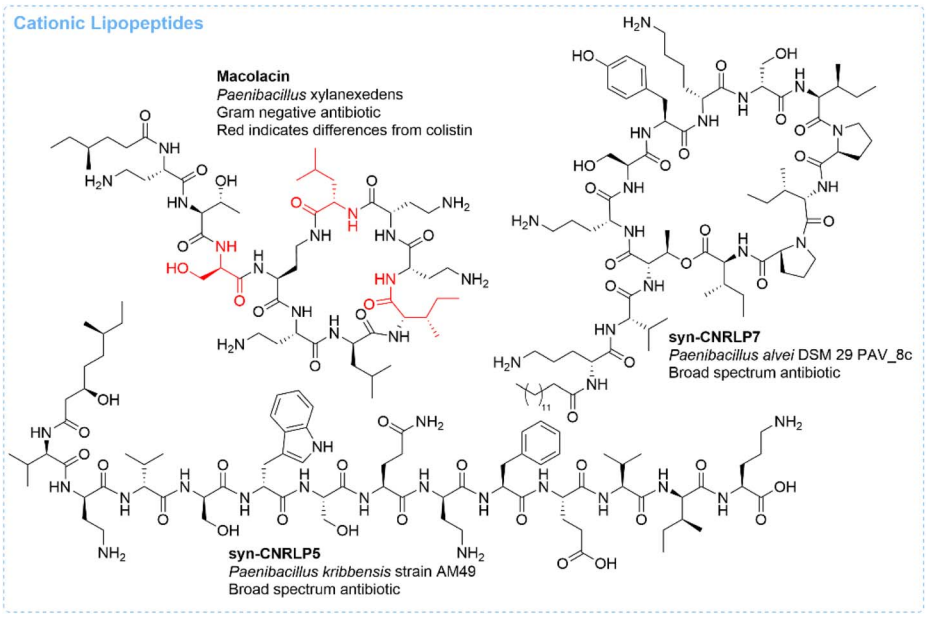

Fig. 6 Structures of *syn*-BNPs identified by the cationic lipopeptide targeted approach. Under each structure is the name, species of origin and bioactivity of the molecule.

phosphoethanolamine, resulting in the loss of colistin binding. Brady and co-workers specifically searched for colistin-like BGCs. 35 *syn*-BNPs from colistin-like BGCs were synthesized and tested for activity against pairs of colistin-sensitive and colistin-resistant *K. pneumoniae* and *A. baumannii*. This resulted in the discovery that macolacin has similar potency as colistin against colistin-sensitive strains and much improved activity against colistin-resistant strains (~16-fold, single-digit $\mu g\ mL^{-1}$ activities). Additionally, macolacin has improved activity against strains with a 4-amino-4-deoxy-L-arabinose modification compared to colistin and other polymyxins. Due to these very promising results, derivatives of macolacin were synthesized, including one that replaced the linear fatty acid tail with a biphenyl. Biphenyl-macolacin proved to be more potent than macolacin *in vitro* and was shown to be effective *in vivo* in a neutropenic thigh mouse model of infection using colistin-resistant *A. baumannii* strains.[44]

4.2.4. Head-to-tail cyclic peptides. Head-to-tail cyclized peptides biosynthesized by PBP-TEs are a valuable source of bioactive agents. PBP-TE cyclized peptides, including peptides with antibiotic activity (ulleungmycin,[66] mannopeptimycin,[89,90] desotamide[65,91]) and cathepsin B inhibition (surugamides),[60,92,93] have been isolated from diverse strains of *Streptomyces*. For this reason, we chose to focus our *syn*-BNP efforts on NRPS BGCs that contain PBP-TEs. PBP-TEs associated with known natural products localize near NRPSs, making PBP-TEs a rational focus for the initial bioinformatics screen. A BlastP search for the well-studied PBP-TE SurE was performed to identify novel PBP-TEs, and the BGCs associated with the top 500 SurE hits was further analyzed. The hits included BGCs that synthesize the NRPs associated with known PBP-TEs such as the mannopeptimycins, the ulleungmycins, desotamide B, and the surugamides, showcasing the effectiveness of this method in identifying PBP-TE NRPs. From the 500 hits, 131 unique and novel cyclic peptides were identified, and 52 structurally diverse cyclic peptides were synthesized.[48] This library, which we named the SNaPP (Synthetic Natural Product Inspired Cyclic Peptides) library, has since been screened for a variety of bioactivities. Specifically, the SNaPP library has been explored for antibiotic activities with 14 of the 51 molecules screened having activity against at least one multidrug-resistant ESKAPEE pathogens (pNP-23, -43, -51, -111, Fig. 7). Of the antibiotics identified, 9 were active against Gram-positive strains, 4 against Gram-negative strains, and one broad spectrum antibiotic. Derivatives of pNP-43 were synthesized to determine a structure activity relationship, with derivative pNP-43d (modifying the ornithine with a lysine) showing increased activity against WT and R *A. baumannii*. Additionally, preliminary mechanistic studies were performed and demonstrated that pNP-43 results in the lysis of Gram-negative bacteria, but not Gram-positive bacteria or human red blood cells.[48] However, given that cell lysis occurred at ~4 times the MIC, it is likely that there are additional mechanisms involved.

When natural products are screened for activities, they are most often tested in phenotypic assays for their antimicrobial and anticancer activities. However, many other important targets and interesting assays exist. To date, the SNaPP library

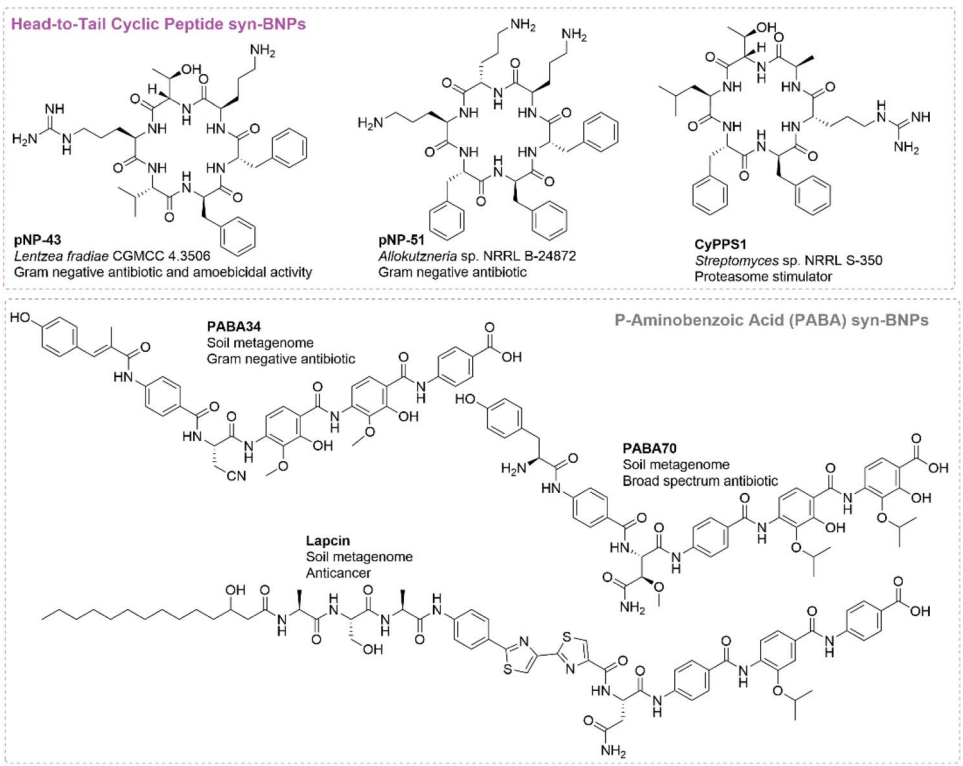

Fig. 7 Structures of bioactive NRPs identified by the head-to-tail and *p*-aminobenzoic acid (PABA) containing targeted approach.

has been explored in a handful of other activity assays including proteasome stimulation and antiamoebic activity.

The accumulation of disordered proteins such as Tau and α-synuclein has been implicated in neurodegenerative diseases such as Alzheimer's[94,95] and Parkinson's Disease.[96–98] Stimulation of the 20S core particle (CP) of the proteasome has shown promise in enhancing the clearance of highly disordered and misfolded proteins through ubiquitin-independent proteolysis.[99] Screening of the SNaPP library in an *in vitro* proteasome stimulation assay resulted in the discovery of molecules that lead to selective degradation of misfolded and highly disordered protein α-synuclein at 10 μM.[49] These molecules have been renamed the Cyclic Peptide Proteaseome Stimulators (CyPPSs). Several CyPPSs (CyPPS-1, -13, -14, and -23, Fig. 7) are cell-permeable and stimulate cytosolic 20S CP at 10 μM in cell culture. Additionally, they exhibit no cytotoxic effects at up to the highest concentration tested (15 μM).[49]

Balamuthia mandrillaris is a pathogenic free-living amoeba that has a fatality rate of approximately 92%.[100] A primary screen of the SNaPP library targeting the free-living amoebas *Balamuthia mandrillaris*, *Acanthamoeba castellanii*, and *Naegleria fowleri* was conducted.[47] Eight hits were identified for *Balamuthia mandrillaris*, sixteen for *Acanthamoeba castellanii*, and one against *Naegleria fowleri* at 16 μg mL^{-1}. One hit, pNP-43 (Fig. 7), displayed significant potency against *Balamuthia mandrillaris* with an IC_{50} of 4.6 μM. Furthermore, this molecule exhibited no cytotoxicity, showing no activity against A549 cells nor causing hemolysis at 100 μM.[47] Overall, these two examples demonstrate that *syn*-BNPs have activities outside of the traditionally tested antimicrobial and anticancer activities. This should inspire further testing of these molecules in additional assays in the future.

4.2.5. *p*-Aminobenzoic acid containing peptides. Structurally related albicidin[101] and cystobactamid[102] are DNA-gyrase inhibitors that contain multiple *p*-aminobenzoic acid (PABA) monomers. Three studies thus far have focused on identifying NRPS BGCs that have at least one A domain that is predicted to activate PABA for inclusion in an NRP.[40,43,46] These studies investigated PABA containing NRPs from soil metagenome libraries. After construction of a PABA A-domain phylogenetic tree, 12 NRPS BGCs most closely related to the cystobactamid or albicidin BGCs were subjected to the *syn*-BNP method. In addition to predictions of the A domains, the presence (albicidin-like) or absence (cystobactamid-like) of a polyketide synthase (PKS) module and PABA modification enzymes (*e.g.* oxygenases, methyltransferases, and B12-dependent radical SAM enzymes) were also considered in the structure predictions. This resulted in three cystobactamid analogues (PABA48, PABA70, and PABA57) and three albicidin congeners (PABA34, PABA157, and PABA95, Fig. 7). These molecules were screened for antibiotic activity against the ESKAPEE pathogens.[46] Interestingly, several showed improved activity compared to the parent molecules. Specifically, PABA48 had improved activity against the Gram-positive strains and *K. pneumoniae*, while PABA34 is more potent against Gram-negative bacteria compared to the parent. As might be expected, all molecules demonstrated potent inhibition of DNA gyrase. Interestingly, the compounds retained activity against mutant DNA gyrase with resistance to the fluoroquinolones, suggesting that they target a different site. One of the major limitations of albicidin is its degradation by the endopeptidase AlbD, resulting in resistance. Interestingly, PABA34 contains AHMBA rather than PABA in position D which prevents hydrolysis by AlbD because it is adjacent to the endopeptidase cleavage site. This suggests that PABA34 is an excellent lead going forward.[46]

In addition to derivatives of albicidin and cystobactamid, Brady and co-workers also investigated novel NRPS BGCs with PABA A domains found in their metagenomic library.[43] They identified an NRPS BGC encoding a decapeptide with a Cs domain, suggesting it is a lipopeptide. The NRPS BGC also contained two Cy domains and an FMN-dependent dehydrogenase, suggesting the presence of two thiazole rings. Overall, this prediction was for a unique NRP, which they named lapcin (Fig. 7). Lapcin was successfully synthesized, but heterologous expression of the BGC was unsuccessful, preventing confirmation of the actual natural product.[43] Interestingly, lapcin was found to be a potent anticancer agent (nM to pM IC_{50}) with generally good selectivity for cancerous over non-cancerous cell lines. It was particularly potent against cell lines with mutant p53. Unlike the other PABA-containing natural products albicidin and cystobactamid, lapcin had little-to-no DNA gyrase inhibition nor antibiotic activity. Instead, it was found to be a potent and selective human topoisomerase inhibitor. Another decalipopeptide similar to lapcin (tapcin) was also identified from a soil metagenome library that has a BGC with high similarity to the lapcin BGC.[43] The two major differences of the new BGC are the lack of a serine at the two site and an additional Cy domain. The molecule resulting from this BGC was named tapcin and contains three thiazole rings. Similar to lapcin, tapcin is a potent chemotherapeutic through inhibition of human topoisomerase.[40] Tapcin has similar efficacy to the clinically used topoisomerase irinotecan in both hollow fiber models and xenograft murine models of colorectal adenocarcinoma.

4.2.6. Menaquinone-binding antibiotics. Menaquinones are redox active molecules that are electron carriers in the electron transport chain for many bacteria, enabling them to adapt to low oxygen and other stressors,[103] and are involved in biofilm formation. Three structurally related cyclic lipopeptides lysocin E,[104] WAP-8294A2,[105] and WBP-29479A1 (ref. 106–109) bind directly to menaquinone, leading to membrane disruption, cell lysis, and ultimately bacteria cell death. Brady and coworkers searched a soil metagenome cosmid library for novel menaquinone-binding peptides by querying for six conserved amino acids in the known menaquinone-binding peptides.[45] From the initial query, they identified six BGCs of interest. From these six BGCs, ten cyclic peptides with a 3-hydroxy-octanoic acid fatty acid were generated: six cyclized to the hydroxyl on the fatty acid and four cyclized to nucleophilic side chains at the first or second amino acid. The *syn*-BNPs based on these previously discovered binders were screened for activity against ESKAPEE pathogens.[45] Several were found to be active against Gram-positive pathogens, as would be expected based on the crucial role that menaquinone plays in their electron transport

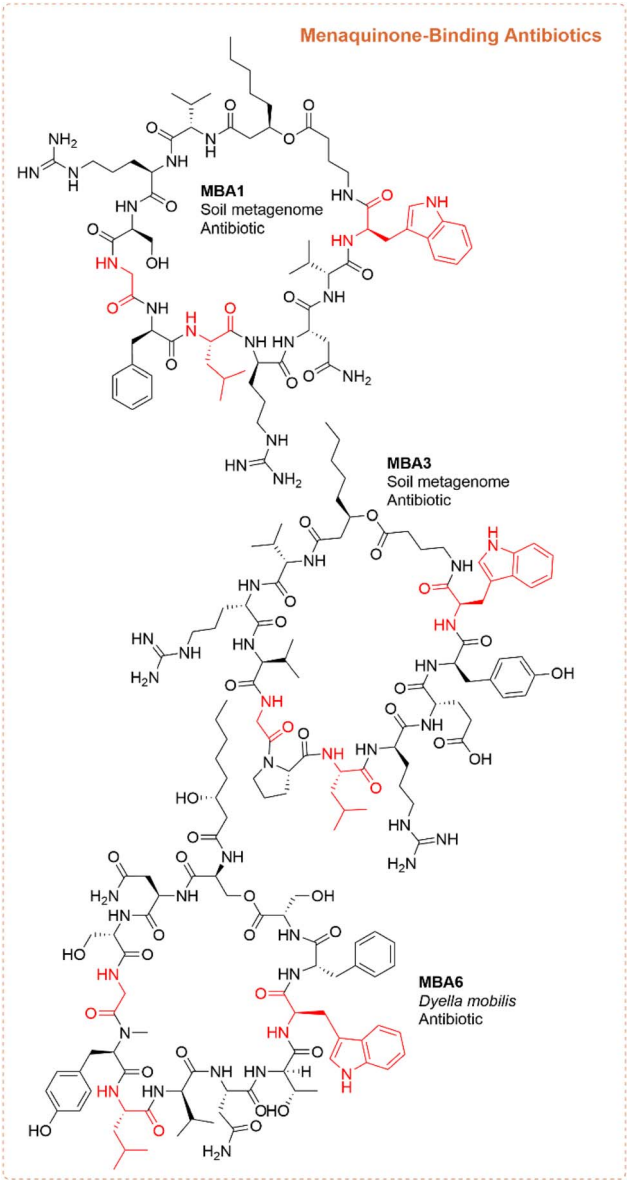

Fig. 8 Structures of bioactive NRPs identified by the cationic menaquinone-binding antibiotics targeted approach.

system. Additionally, they were tested for activity against *M. tuberculosis* and found to have very promising activity against several multidrug-resistant strains. From these peptides, they were able to identify a shared motif (GXLXXXW)—which they named the menaquinone-binding motif (Fig. 8). The mechanism was confirmed to be binding to menaquinone using strains with knockouts of the menaquinone biosynthesis pathway and by direct binding to menaquinone, along with other tests. Additionally, two *syn*-BNPs (MBA3 and -6, Fig. 8) were screened using a peritonitis-sepsis mouse, with both molecules drastically increasing the survival rate.

5. Future direction

Synthetic-bioinformatic natural product-inspired peptides have proven to be a valuable tool in identifying novel peptides with unique mechanisms of action and bioactivity.[29,40–53,55–57] This approach has led to the discovery of compounds with antibiotic,[29,41,42,44–46,48,50,51,53–57] anticancer,[40,43,52,56] amoebicidal,[47] and proteasome stimulation activity.[49] Many of these compounds are potent, and some have demonstrated activity *in cellulo* and/or *in vivo*. However, several challenges persist.

One such challenge arises from the presence of a Cs domain in the NRPS, indicating the presence of a fatty acid at the N terminus.[110] To the best of our knowledge, current NRPS predictions cannot accurately determine which fatty acid will be added to the NRP, complicating the design and synthesis of the predicted peptide. When only a few peptides are being targeted, the synthesis of several peptides, each with a different fatty acid chain, is manageable. However, simplification become more necessary in cases where a large library is being synthesized, often resulting in the same fatty acid being added to all the peptides predicted to possess a starter Cs domain.[51] This approach likely limits the number of identified bioactive peptides, since the identity of the fatty acid often has a large effect on the bioactivity of the molecule.[111,112] Improvements in bioinformatics predictions of Cs fatty acid specificity will enable access to *syn*-BNPs that more closely resemble the true natural products, and are thus more likely to have interesting bioactivities.

Another challenge for accurate *syn*-BNP predictions is tailoring enzymes. Tailoring enzymes frequently are located within the same genomic neighborhood as the NRPS and are responsible for the synthesis of non-canonical amino acids or the modification of the NRP during or after its assembly. Common tailoring enzymes include halogenases (halogenation), glycosyltransferases (addition of a sugar moiety), hydroxylases (addition of hydroxyl), and P450s (various oxidation reactions).[113] Unfortunately, precise predictions of the modifications that these tailoring enzymes will introduce is challenging. Currently, many researchers refrain from incorporating modifications due to the inability to predict if or how the tailoring enzymes will act. Since many of these modifications are essential to bioactivity (*e.g.* the antibiotic activity of vancomycin and proteasome inhibition by salinosporamide A both are dependent on the incorporation of halogen atoms by halogenases),[114] their exclusion likely limits the discovery of bioactive molecules. As predictions for these tailoring enzymes improve, their incorporation into *syn*-BNP predictions will likely aid in the discovery of bioactive compounds. However, the requirement for modified non-canonical amino acids is likely to complicate the synthesis of these molecules.

Finally, the release of an NRP from an NRPS by a TE domain presents another significant challenge for predictions. While there are a handful of programs that attempt to predict the cyclization method of an NRP based on the peptide structure,[115] the methods developed to date are based on small libraries and are thus biased and lack accuracy.[59] This necessitates the synthesis of multiple peptides per predicted linear substrate when a traditional TE is present. Improvements of these predictions, perhaps through machine learning analyses of known TEs, will help to overcome this challenge, further streamlining the *syn*-BNP approach.

Overall, to address all of these challenges, more data about the biosynthesis of known molecules combined with predictions, likely through machine learning models, will enhance the efficiency and accuracy of peptide design and synthesis in the future.

6. Data availability

No primary research results, software or code have been included and no new data were generated or analysed as part of this review.

7. Author contributions

S. N. and E. I. P. conceptualized and wrote the article.

8. Conflicts of interest

The authors have no conflicts of interest to report.

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10. References

1 D. J. Newman and G. M. Cragg, *J. Nat. Prod.*, 2020, **83**, 770–803.
2 E. Patridge, P. Gareiss, M. S. Kinch and D. Hoyer, *Drug Discovery Today*, 2016, **21**, 204–207.
3 A. S. Abdel-Razek, M. E. El-Naggar, A. Allam, O. M. Morsy and S. I. Othman, *Processes*, 2020, **8**, 470.
4 J. A. van Santen, E. F. Poynton, D. Iskakova, E. McMann, T. A. Alsup, T. N. Clark, C. H. Fergusson, D. P. Fewer, A. H. Hughes, C. A. McCadden, J. Parra, S. Soldatou, J. D. Rudolf, E. M-L Janssen, K. R. Duncan and R. G. Linington, *Nucleic Acids Res.*, 2021, **50**, D1317–D1323.
5 J. L. Lau and M. K. Dunn, *Bioorg. Med. Chem.*, 2018, **26**, 2700–2707.
6 H. Zhang and S. Chen, *RSC Chem. Biol.*, 2022, **3**, 18–31.
7 D. Al Shaer, O. Al Musaimi, F. Albericio and B. G. de la Torre, *Pharmaceuticals*, 2024, **17**, 243.
8 O. Al Musaimi, D. Al Shaer, F. Albericio and B. G. de la Torre, *Pharmaceuticals*, 2023, **16**, 336.
9 A. Zorzi, K. Deyle and C. Heinis, *Curr. Opin. Chem. Biol.*, 2017, **38**, 24–29.
10 S. Jackson, W. Degrado, A. Dwivedi, A. Parthasarathy, A. Higley, J. Krywko, A. Rockwell, J. Markwalder, G. Wells, R. Wexler, S. Mousa and R. Harlow, *J. Am. Chem. Soc.*, 1994, **116**, 3220–3230.
11 J. J. Devlin, L. C. Panganiban and P. E. Devlin, *Science*, 1990, **249**, 404–406.
12 K. Deyle, X.-D. Kong and C. Heinis, *Acc. Chem. Res.*, 2017, **50**, 1866–1874.
13 X. Ji, A. L. Nielsen and C. Heinis, *Angew. Chem., Int. Ed.*, 2024, **136**, e202308251.
14 D. A. Price, H. Eng, K. A. Farley, G. H. Goetz, Y. Huang, Z. Jiao, A. S. Kalgutkar, N. M. Kablaoui, B. Khunte, S. Liras, C. Limberakis, A. M. Mathiowetz, R. B. Ruggeri, J. M. Quan and Z. Yang, *Org. Biomol. Chem.*, 2017, **15**, 2501–2506.
15 M. Montalbán-Lopez, T. A. Scott, S. Ramesh, I. R. Rahman, A. J. van Heel, J. H. Viel, V. Bandarian, E. Dittmann, O. Genilloud, Y. Goto, M. José Grande Burgos, C. Hill, S. Kim, J. Koehnke, J. A. Latham, J. A. Link, B. Martínez, S. K. Nair, Y. Nicolet, S. Rebuffat, H.-G. Sahl, D. Sareen, E. W. Schmidt, L. Schmitt, K. Severinov, R. D. Süssmuth, A. W. Truman, H. Wang, J.-K. Weng, G. P. van Wezel, Q. Zhang, J. Zhong, J. Piel, D. A. Mitchell, O. P. Kuipers and W. A. van der Donk, *Nat. Prod. Rep.*, 2021, **38**, 130–239.
16 R. D. Süssmuth and A. Mainz, *Angew. Chem., Int. Ed.*, 2017, **56**, 3770–3821.
17 I. P. M. Pfeiffer, M. P. Schröder and S. Mordhorst, *Nat. Prod. Rep.*, 2024, **41**, 990–1019.
18 H. Li, W. Ding and Q. Zhang, *RSC Chem. Biol.*, 2024, **5**, 90–108.
19 C. Ongpipattanakul, E. K. Desormeaux, A. Dicaprio, W. A. Van Der Donk, D. A. Mitchell and S. K. Nair, *Chem. Rev.*, 2022, **122**, 14722–14814.
20 A. Gavriilidou, S. A. Kautsar, N. Zaburannyi, D. Krug, R. Müller, M. H. Medema and N. Ziemert, *Nat. Microbiol.*, 2022, **7**, 726–735.
21 E. Kalkreuter, S. A. Kautsar, D. Yang, C. D. Bader, C. N. Teijaro, L. L. Fluegel, C. M. Davis, J. R. Simpson, L. Lauterbach, A. D. Steele, C. Gui, S. Meng, G. Li, K. Viehrig, F. Ye, P. Su, A. F. Kiefer, A. Nichols, A. J. Cepeda, W. Yan, B. Fan, Y. Jiang, A. Adhikari, C.-J. Zheng, L. Schuster, T. M. Cowan, M. J. Smanski, M. G. Chevrette, L. P. S. De Carvalho and B. Shen, *bioRxiv*, preprint, 2023, DOI: 10.1101/2023.12.14.571759.
22 B. S. Jian, S. L. Chiou, C. C. Hsu, J. Ho, Y. W. Wu and J. Chu, *ACS Chem. Biol.*, 2023, **18**, 476–483.
23 J. G. Moffat, F. Vincent, J. A. Lee, J. Eder and M. Prunotto, *Nat. Rev. Drug Discovery*, 2017, **16**, 531–543.
24 Z. Q. Tan, H. Y. Leow, D. C. W. Lee, K. Karisnan, A. A. L. Song, C. W. Mai, W. S. Yap, S. H. E. Lim and K. S. Lai, *Open Biotechnol. J.*, 2019, **13**, 18–26.
25 H. B. Bode, B. Bethe, R. Höfs and A. Zeeck, *ChemBioChem*, 2002, **3**, 619–627.
26 A. Y. Alwali, D. Santos, C. Aguilar, A. Birch, L. Rodriguez-Ordunea, C. B. Roberts, R. Modi, C. Licona-Cassani and E. I. Parkinson, *J. Ind. Microbiol. Biotechnol.*, 2024, **51**, kuae014.
27 L. Katz and R. H. Baltz, *J. Ind. Microbiol. Biotechnol.*, 2016, **43**, 155–176.
28 P. J. Rutledge and G. L. Challis, *Nat. Rev. Microbiol.*, 2015, **13**, 509–523.

29 J. Chu, X. Vila-Farres, D. Inoyama, M. Ternei, L. J. Cohen, E. A. Gordon, B. V. B. Reddy, Z. Charlop-Powers, H. A. Zebroski, R. Gallardo-Macias, M. Jaskowski, S. Satish, S. Park, D. S. Perlin, J. S. Freundlich and S. F. Brady, *Nat. Chem. Biol.*, 2016, **12**, 1004–1006.
30 L. Du and L. Lou, *Nat. Prod. Rep.*, 2010, **27**, 255–278.
31 M. A. Fischbach and C. T. Walsh, *Chem. Rev.*, 2006, **106**, 3468–3496.
32 T. Stachelhaus, H. D. Mootz and M. A. Marahiel, *Chem. Biol.*, 1999, **6**, 493–505.
33 K. Blin, S. Shaw, A. M. Kloosterman, Z. Charlop-Powers, G. P. Van Wezel, M. H. Medema and T. Weber, *Nucleic Acids Res.*, 2021, **49**, W29–W35.
34 M. H. Medema, K. Blin, P. Cimermancic, V. de Jager, P. Zakrzewski, M. A. Fischbach, T. Weber, E. Takano and R. Breitling, *Nucleic Acids Res.*, 2011, **39**, W339–W346.
35 M. A. Skinnider, C. A. Dejong, P. N. Rees, C. W. Johnston, H. Li, A. L. H. Webster, M. A. Wyatt and N. A. Magarvey, *Nucleic Acids Res.*, 2015, **43**, 9645–9662.
36 M. A. Skinnider, N. J. Merwin, C. W. Johnston and N. A. Magarvey, *Nucleic Acids Res.*, 2017, **45**, W49–W54.
37 M. G. Chevrette, F. Aicheler, O. Kohlbacher, C. R. Currie and M. H. Medema, *Bioinformatics*, 2017, **33**, 3202–3210.
38 A. Flissi, E. Ricart, C. Campart, M. Chevalier, Y. Dufresne, J. Michalik, P. Jacques, C. Flahaut, F. Lisacek, V. Leclère and M. Pupin, *Nucleic Acids Res.*, 2020, **48**, D465–D469.
39 M. Röttig, M. H. Medema, K. Blin, T. Weber, C. Rausch and O. Kohlbacher, *Nucleic Acids Res.*, 2011, **39**, W362–W367.
40 Z. Wang, A. Kasper, M. Takahashi, A. Morales Amador, A. Bhattacharjee, J. Kan, Y. Hernandez, M. Ternei and S. F. Brady, *Angew. Chem., Int. Ed.*, 2024, **63**, e202317187.
41 Z. Wang, B. Koirala, Y. Hernandez and S. F. Brady, *Org. Lett.*, 2022, **24**, 4943–4948.
42 Z. Wang, B. Koirala, Y. Hernandez, M. Zimmerman and S. F. Brady, *Science*, 2022, **376**, 991–996.
43 Z. Wang, N. Forelli, Y. Hernandez, M. Ternei and S. F. Brady, *Nat. Commun.*, 2022, **13**, 842.
44 Z. Wang, B. Koirala, Y. Hernandez, M. Zimmerman, S. Park, D. S. Perlin and S. F. Brady, *Nature*, 2022, **601**, 606–611.
45 L. Li, B. Koirala, Y. Hernandez, L. W. MacIntyre, M. A. Ternei, R. Russo and S. F. Brady, *Nat. Microbiol.*, 2022, **7**, 120–131.
46 Z. Wang, A. Kasper, R. Mehmood, M. Ternei, S. Li, J. S. Freundlich, S. F. Brady, Z. Wang, A. Kasper, R. Mehmood, M. Ternei, S. F. Brady, S. Li and J. S. Freundlich, *Angew. Chem., Int. Ed.*, 2021, **60**, 22172–22177.
47 C. Lu, S. Nelson, G. Coy, C. Neumann, E. I. Parkinson and C. A. Rice, *bioRxiv*, preprint, 2024, DOI: **10.1101/2024.05.03.592372**.
48 M. A. Hostetler, C. Smith, S. Nelson, Z. Budimir, R. Modi, I. Woolsey, A. Frerk, B. Baker, J. Gantt and E. I. Parkinson, *ACS Chem. Biol.*, 2021, **16**, 2604–2611.
49 S. Nelson, T. J. Harris, C. S. Muli, M. E. Maresh, B. Baker, C. Smith, C. Neumann, D. J. Trader and E. I. Parkinson, *ChemBioChem*, 2023, **25**, e202300671.
50 L. I. Beyer, A.-B. Schäfer, A. Undabarrena, I. Mattsby-Baltzer, D. Tietze, E. Svensson, A. Stubelius, M. Wenzel, B. Cámara and A. A. Tietze, *ACS Infect. Dis.*, 2023, **10**, 79–92.
51 J. Chu, B. Koirala, N. Forelli, X. Vila-Farres, M. A. Ternei, T. Ali, D. A. Colosimo and S. F. Brady, *J. Am. Chem. Soc.*, 2020, **142**, 14158–14168.
52 J. Chu, X. Vila-Farres and S. F. Brady, *J. Am. Chem. Soc.*, 2019, **141**, 15737–15741.
53 X. Vila-Farres, J. Chu, D. Inoyama, M. A. Ternei, C. Lemetre, L. J. Cohen, W. Cho, B. B. Vijay Reddy, H. A. Zebroski, J. S. Freundlich, D. S. Perlin and S. F. Brady, *J. Am. Chem. Soc.*, 2017, **139**, 1404–1407.
54 X. Vila-Farres, J. Chu, M. A. Ternei, C. Lemetre, S. Park, D. S. Perlin and S. F. Brady, *mSphere*, 2018, **3**, e00528.
55 J. Chu, X. Vila-Farres, D. Inoyama, R. Gallardo-Macias, M. Jaskowski, S. Satish, J. S. Freundlich and S. F. Brady, *ACS Infect. Dis.*, 2018, **4**, 33–38.
56 L. W. MacIntyre, B. Koirala, A. Rosenzweig, A. Morales-Amador and S. F. Brady, *Org. Lett.*, 2024, **26**, 4433–4437.
57 A. F. Rosenzweig, Z. Wang, A. Morales-Amador, K. Spotton and S. F. Brady, *ACS Infect. Dis.*, 2023, **9**, 2394–2400.
58 K. Blin, H. U. Kim, M. H. Medema and T. Weber, *Brief. Bioinform*, 2019, **20**, 1103–1113.
59 M. E. Horsman, T. P. A. Hari and C. N. Boddy, *Nat. Prod. Rep.*, 2016, **33**, 183–202.
60 Y. Zhou, X. Lin, C. Xu, L. Li, H. Deng and H.-W. Lin Correspondence, *Cell Chem. Biol.*, 2019, **26**, 737–744.
61 T. Kuranaga, K. Matsuda, A. Sano, M. Asakazu Kobayashi, A. Ninomiya, K. Takada, S. Matsunaga and T. Wakimoto, *Angew. Chem., Int. Ed.*, 2018, **130**, 9591–9595.
62 Z. L. Budimir, R. S. Patel, A. Eggly, C. N. Evans, H. M. Rondon-Cordero, J. J. Adams, C. Das and E. I. Parkinson, *Nat. Chem. Biol.*, 2023, **20**, 120–128.
63 K. Matsuda, K. Fujita and T. Wakimoto, *J. Ind. Microbiol. Biotechnol.*, 2021, **48**, kuab023.
64 M. Kobayashi, K. Fujita, K. Matsuda and T. Wakimoto, *J. Am. Chem. Soc.*, 2023, **145**, 3270–3275.
65 Q. Li, Y. Song, X. Qin, X. Zhang, A. Sun and J. Ju, *J. Nat. Prod.*, 2015, **78**, 944–948.
66 S. Son, Y.-S. Hong, M. Jang, K. T. Heo, B. Lee, J.-P. Jang, J.-W. Kim, I.-J. Ryoo, W.-G. Kim, S.-K. Ko, B. Y. Kim, J.-H. Jang and J. S. Ahn, *J. Nat. Prod.*, 2017, **80**, 3025–3031.
67 D. A. Benson, M. Cavanaugh, K. Clark, I. Karsch-Mizrachi, J. Ostell, K. D. Pruitt and E. W. Sayers, *Nucleic Acids Res.*, 2018, **46**, D41–D47.
68 I. V. Grigoriev, H. Nordberg, I. Shabalov, A. Aerts, M. Cantor, D. Goodstein, A. Kuo, S. Minovitsky, R. Nikitin, R. A. Ohm, R. Otillar, A. Poliakov, I. Ratnere, R. Riley, T. Smirnova, D. Rokhsar and I. Dubchak, *Nucleic Acids Res.*, 2012, **40**, D26–D32.
69 L. L. Ling, T. Schneider, A. J. Peoples, A. L. Spoering, I. Engels, B. P. Conlon, A. Mueller, T. F. Schäberle, D. E. Hughes, S. Epstein, M. Jones, L. Lazarides, V. A. Steadman, D. R. Cohen, C. R. Felix, K. A. Fetterman, W. P. Millett, A. G. Nitti, A. M. Zullo, C. Chen and K. Lewis, *Nature*, 2015, **517**, 455–459.

70 J. Peterson, S. Garges, M. Giovanni, P. McInnes, L. Wang, J. A. Schloss, V. Bonazzi, J. E. McEwen, K. A. Wetterstrand, C. Deal, C. C. Baker, V. Di Francesco, T. K. Howcroft, R. W. Karp, R. D. Lunsford, C. R. Wellington, T. Belachew, M. Wright, C. Giblin, H. David, M. Mills, R. Salomon, C. Mullins, B. Akolkar, L. Begg, C. Davis, L. Grandison, M. Humble, J. Khalsa, A. Roger Little, H. Peavy, C. Pontzer, M. Portnoy, M. H. Sayre, P. Starke-Reed, S. Zakhari, J. Read, B. Watson and M. Guyer, *Genome Res.*, 2009, **19**, 2317–2323.
71 T. Chen, W. H. Yu, J. Izard, O. V. Baranova, A. Lakshmanan and F. E. Dewhirst, *Database*, 2010, **2010**, baq013.
72 S. I. Toh, C. L. Lo and C. Y. Chang, *Acta Crystallogr., Sect. F: Struct. Biol. Commun.*, 2023, **79**, 193–199.
73 D. J. Atkinson, B. J. Naysmith, D. P. Furkert and M. A. Brimble, *Beilstein J. Org. Chem.*, 2016, **12**, 2325.
74 R. B. Merrifield, *J. Am. Chem. Soc.*, 1963, **85**, 2149–2154.
75 R. Behrendt, P. White and J. Offer, *J. Pept. Sci.*, 2016, **22**, 4–27.
76 J. M. Palomo, *RSC Adv.*, 2014, **4**, 32658–32672.
77 J. A. Moss, *Curr. Protoc. Protein Sci.*, 2005, **40**, DOI: **10.1002/0471140864.ps1807s40**.
78 K. G. Varnava and V. Sarojini, *Chem.–Asian J.*, 2019, **14**, 1088–1097.
79 C. J. White and A. K. Yudin, *Nat. Chem.*, 2011, **3**, 509–524.
80 M. S. Donia, B. Wang, D. C. Dunbar, P. V Desai, A. Patny, M. Avery and M. T. Hamann, *Int. J. Mol. Sci.*, 2021, **22**, 3973.
81 I. Nouioui, A. Zimmermann, O. Hennrich, S. Xia, O. Rössler, R. Makitrynskyy, J. Pablo Gomez-Escribano, G. Pötter, M. Jando, M. Döppner, J. Wolf, M. Neumann-Schaal, C. Hughes and Y. Mast, *Front. Bioeng. Biotechnol.*, 2024, **12**, 1255151.
82 A. Rosenzweig, K. Spotton, A. Bhattacharjee, A. Morales-Amador and S. F. Brady, *ACS Infect. Dis.*, 2024, **10**, 1536–1544.
83 C. Zhang and M. R. Seyedsayamdost, *Angew. Chem., Int. Ed.*, 2020, **59**, 23005–23009.
84 J. Shi, C. L. Liu, B. Zhang, W. J. Guo, J. Zhu, C.-Y. Chang, E. J. Zhao, R. H. Jiao, R. X. Tan and H. M. Ge, *Chem. Sci.*, 2019, **10**, 4839–4846.
85 Q. Liu, Z. Liu, C. Sun, M. Shao, J. Ma, X. Wei, T. Zhang, W. Li and J. Ju, *Org. Lett.*, 2019, **21**, 2634–2638.
86 S. Biswas, J. M. Brunel, J. C. Dubus, M. Reynaud-Gaubert and J. M. Rolain, *Expert Rev. Anti-Infect. Ther.*, 2012, **10**, 917–934.
87 S. A. Cochrane and J. C. Vederas, *Med. Res. Rev.*, 2016, **36**, 4–31.
88 Y.-Y. Liu, C. E. Chandler, L. M. Leung, C. L. Mcelheny, R. T. Mettus, R. M. Q. Shanks, J.-H. Liu, D. R. Goodlett, R. K. Ernst, Y. Doi, C. Liu, C. Ce, L. Lm, M. Cl, M. Rt, S. Rmq and J.-H. Liu, *Antimicrob. Agents Chemother.*, 2017, **61**, e00580.
89 N. A. Magarvey, B. Haltli, M. He, M. Greenstein and J. A. Hucul, *Antimicrob. Agents Chemother.*, 2006, **50**, 2167–2177.
90 H. He, R. T. Williamson, B. Shen, E. I. Graziani, H. Y. Yang, S. M. Sakya, P. J. Petersen and G. T. Carter, *J. Am. Chem. Soc.*, 2002, **124**, 9729–9736.
91 Y. Song, Q. Li, X. Liu, Y. Chen, Y. Zhang, A. Sun, W. Zhang, J. Zhang and J. Ju, *J. Nat. Prod.*, 2014, **77**, 1937–1941.
92 F. Xu, B. Nazari, K. Moon, L. B. Bushin and M. R. Seyedsayamdost, *J. Am. Chem. Soc.*, 2017, **139**, 9203–9212.
93 K. Takada, A. Ninomiya, M. Naruse, Y. Sun, M. Miyazaki, Y. Nogi, S. Okada and S. Matsunaga, *J. Org. Chem.*, 2013, **78**, 6746–6750.
94 K. Gadhave, N. Bolshette, A. Ahire, R. Pardeshi, K. Thakur, C. Trandafir, A. Istrate, S. Ahmed, M. Lahkar, D. F. Muresanu and M. Balea, *J. Cell. Mol. Med.*, 2016, **20**, 1392–1407.
95 G. Palmieri, E. Cocca, M. Gogliettino, R. Valentino, M. Ruvo, G. Cristofano, A. Angiolillo, M. Balestrieri, M. Rossi and A. Di Costanzo, *J. Alzheimer's Dis.*, 2017, **60**, 1097–1106.
96 L. Stefanis, *Cold Spring Harbor Perspect. Med.*, 2012, **2**, a009399.
97 K. St. P. McNaught and P. Jenner, *Neurosci. Lett.*, 2001, **297**, 191–194.
98 K. St. P. McNaught, R. Belizaire, O. Isacson, P. Jenner and W. C. Olanow, *Exp. Neurol.*, 2003, **179**, 38–46.
99 R. A. Coleman, R. Mohallem, U. K. Aryal and D. J. Trader, *RSC Chem. Biol.*, 2021, **2**, 636–644.
100 J. R. Cope, J. Landa, H. Nethercut, S. A. Collier, C. Glaser, M. Moser, R. Puttagunta, J. S. Yoder, I. K. Ali and S. L. Roy, *Clin. Infect. Dis.*, 2019, **68**, 1815–1822.
101 S. Cociancich, A. Pesic, D. Petras, S. Uhlmann, J. Kretz, V. Schubert, L. Vieweg, S. Duplan, M. Marguerettaz, J. Noëll, I. Pieretti, M. Hügelland, S. Kemper, A. Mainz, P. Rott, M. Royer and R. D. Süssmuth, *Nat. Chem. Biol.*, 2015, **11**, 195–197.
102 S. Baumann, J. Herrmann, R. Raju, H. Steinmetz, K. I. Mohr, S. Hüttel, K. Harmrolfs, M. Stadler and R. Müller, *Angew. Chem., Int. Ed.*, 2014, **53**, 14605–14609.
103 J. M. Johnston and E. M. Bulloch, *Curr. Opin. Struct. Biol.*, 2020, **65**, 33–41.
104 H. Hamamoto, M. Urai, K. Ishii, J. Yasukawa, A. Paudel, M. Murai, T. Kaji, T. Kuranaga, K. Hamase, T. Katsu, J. Su, T. Adachi, R. Uchida, H. Tomoda, M. Yamada, M. Souma, H. Kurihara, M. Inoue and K. Sekimizu, *Nat. Chem. Biol.*, 2014, **11**, 127–133.
105 H. Itoh, K. Tokumoto, T. Kaji, A. Paudel, S. Panthee, H. Hamamoto, K. Sekimizu and M. Inoue, *J. Org. Chem.*, 2018, **83**, 6924–6935.
106 M. Sang, H. Wang, Y. Shen, N. Rodrigues De Almeida, M. Conda-Sheridan, S. Li, Y. Li and L. Du, *Org. Lett.*, 2019, **21**, 6432–6436.
107 C. Rausch, I. Hoof, T. Weber, W. Wohlleben and D. H. Huson, *BMC Evol. Biol.*, 2007, **7**, 1–15.
108 N. Sakura, T. Itoh, Y. Uchida, K. Ohki, K. Okimura, K. Chiba, Y. Sato and H. Sawanishi, *Bull. Chem. Soc. Jpn.*, 2004, **77**, 1915–1924.
109 H. Tsubery, I. Ofek, S. Cohen and M. Fridkin, *Peptides*, 2001, **22**, 1675–1681.
110 C. T. Walsh, *Nat. Prod. Rep.*, 2023, **40**, 326–386.

111 C. S. Neumann, D. G. Fujimori and C. T. Walsh, *Chem. Biol.*, 2008, **15**, 99–109.
112 P. Agrawal and D. Mohanty, *Bioinformatics*, 2021, **37**, 603–611.
113 C. T. Walsh, *Nat. Prod. Rep.*, 2023, **40**(2), 326–386.
114 C. S. Neumann, D. G. Fujimori and C. T. Walsh, *Chem. Biol.*, 2008, **15**(2), 99–109.
115 P. Agrawal and D. Mohanty, *Bioinformatics*, 2021, **27**(5), 603–611.