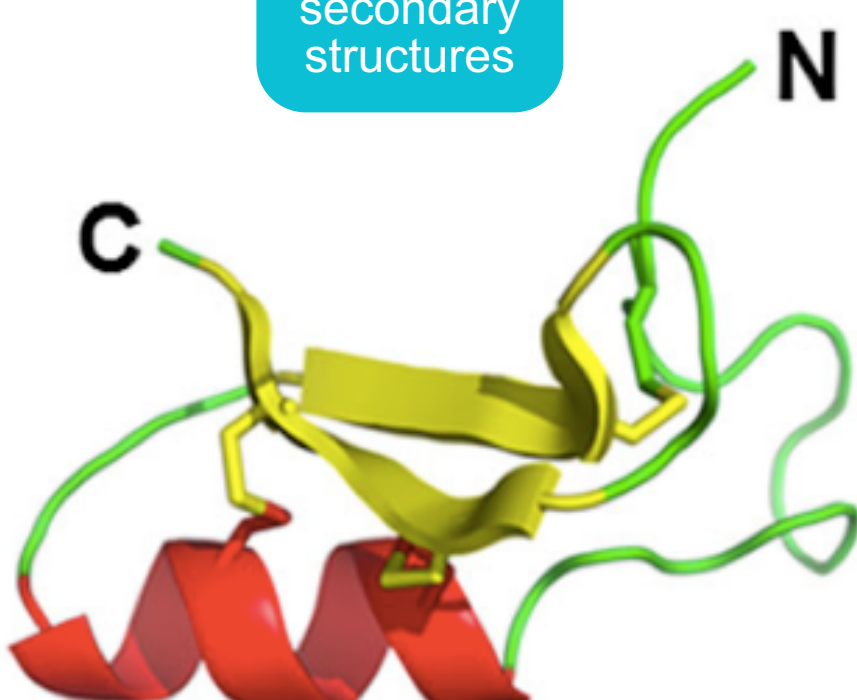
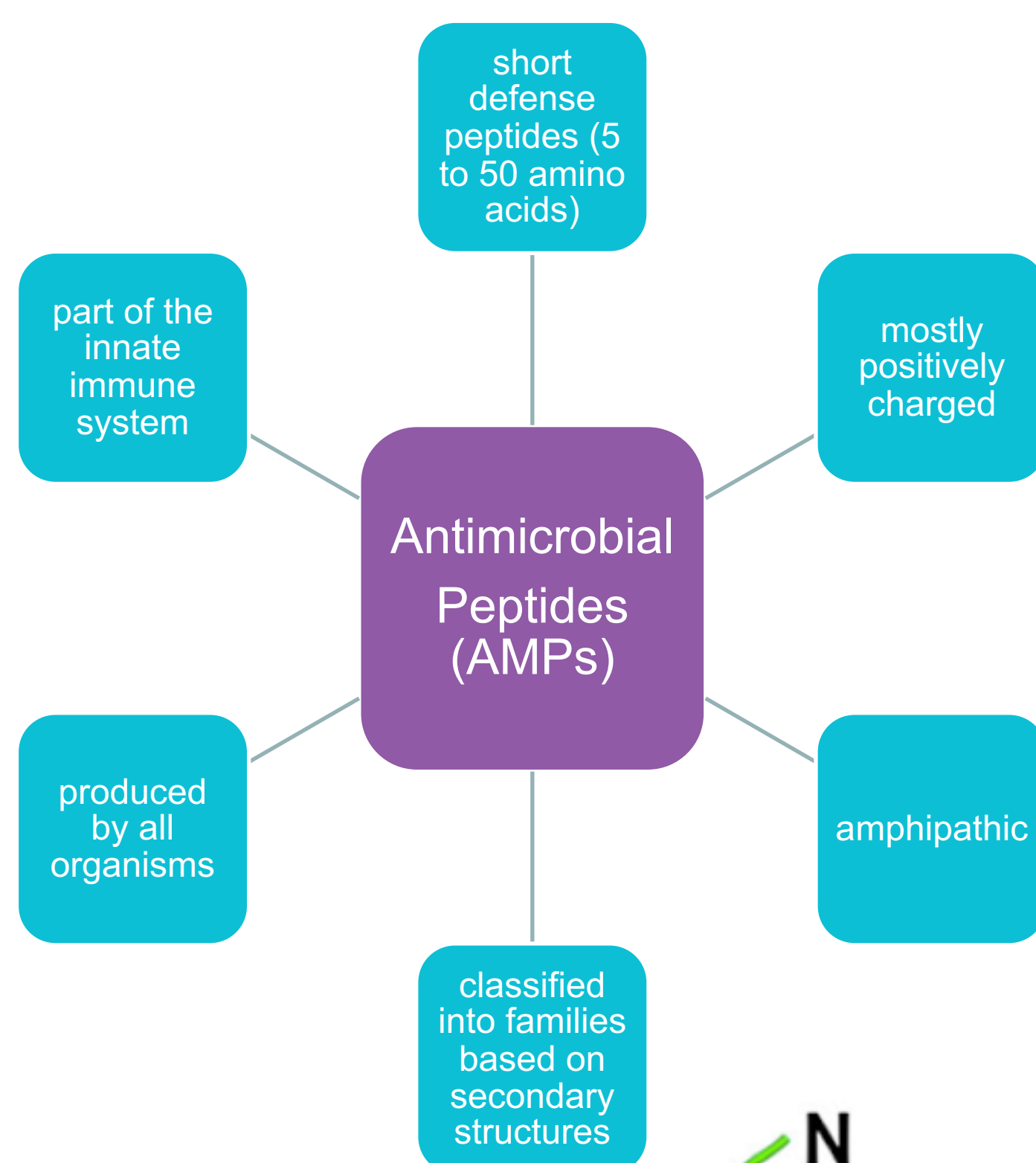


Introduction

Antimicrobial Peptides (AMPs)

Characteristics¹

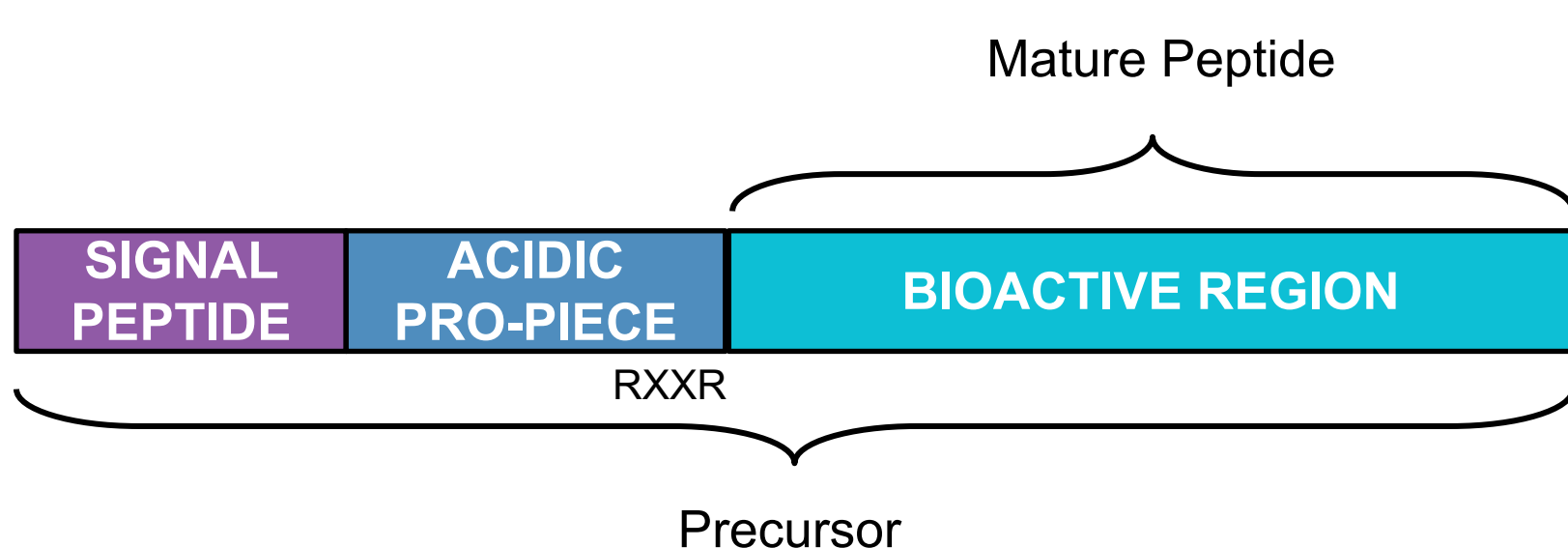


Above: Insect Defensin A (phormicin) from the Northern blowfly

<https://www.rcsb.org/structure/1ICA>

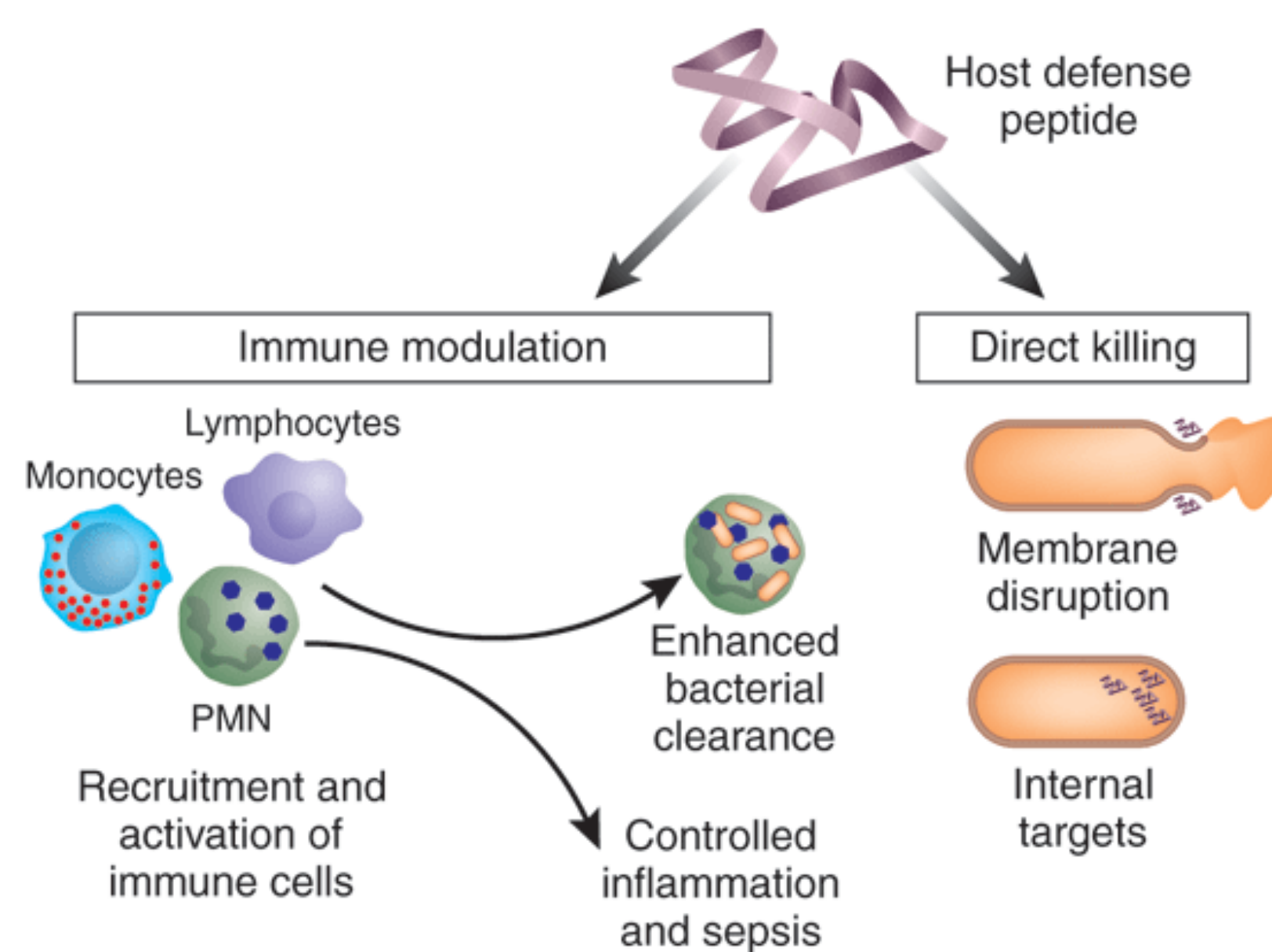
<https://www.uniprot.org/uniprot/P10891>

Peptide Structure¹



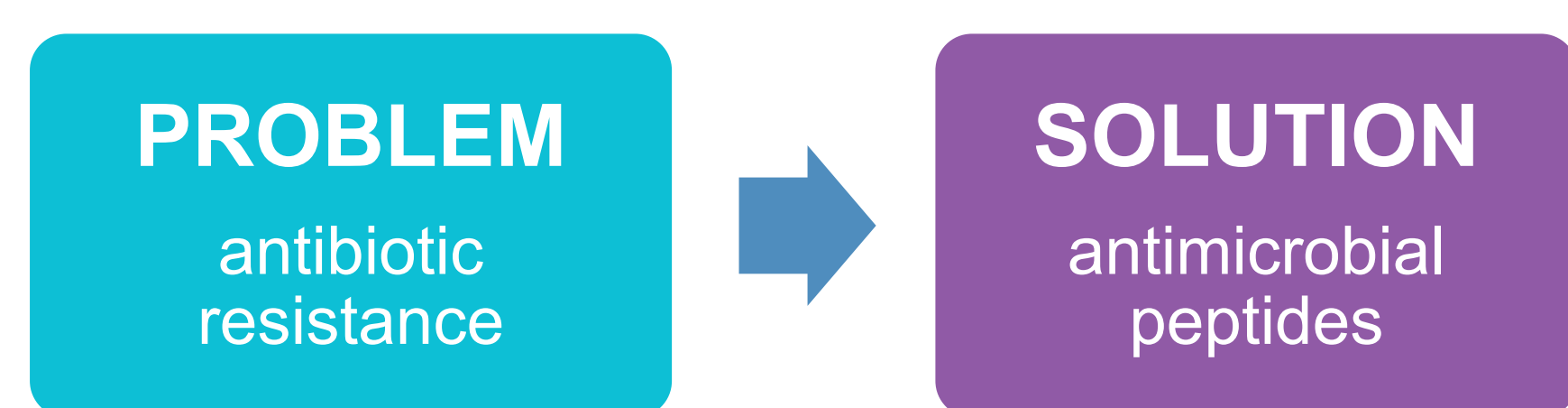
- AMPs are activated by cleavage at the RXXR motif (acidic propiece inhibits basic bioactive region)
- Cleavage separates the signal peptide and acidic propiece from the bioactive region yielding the mature peptide

Mechanisms of Action¹



Source: Hancock, R. E. W. & Sahl, H.-G. Antimicrobial and host-defense peptides as new anti-infective therapeutic strategies. *Nat. Biotechnol.* 24, 1551–1557 (2006) doi: [10.1038/nbt1267](https://doi.org/10.1038/nbt1267)

Motivation



Problem

- The rise of antibiotic resistance¹
- The antibiotic “discovery” void²: few new antibiotics, but old antibiotics less effective
- The need for novel methods to fight pathogen

Solution

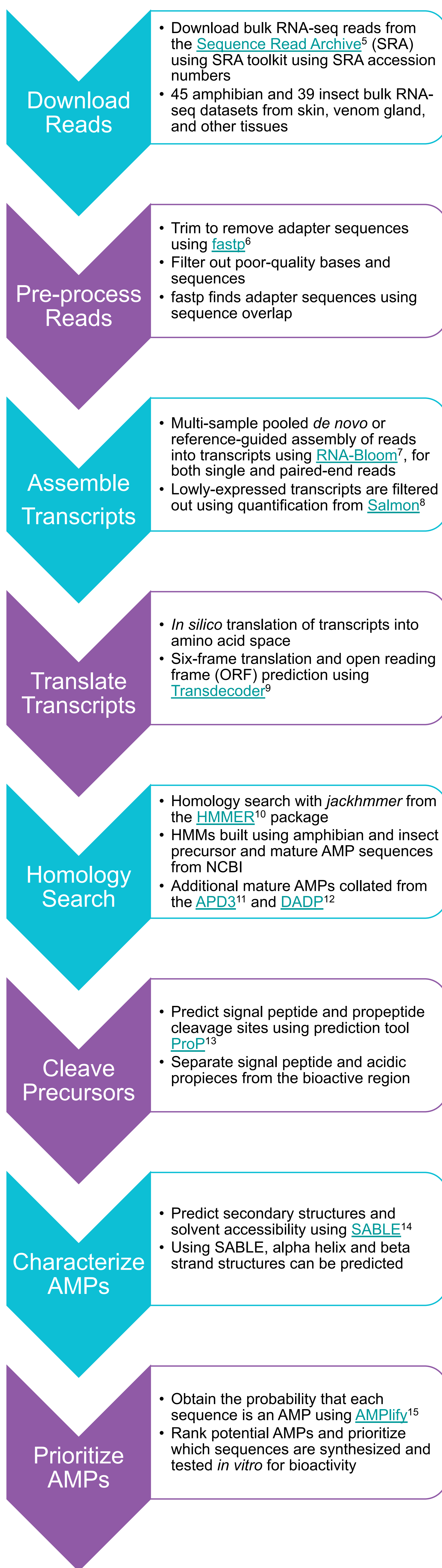
- AMPs do not confer resistance as easily as antibiotics, due to co-evolution with the human microbiome¹
- AMPs are a potential alternative to antibiotics³
- AMPs can be mined from organisms of rich AMP diversity, such as the North American bullfrog⁴

Objectives

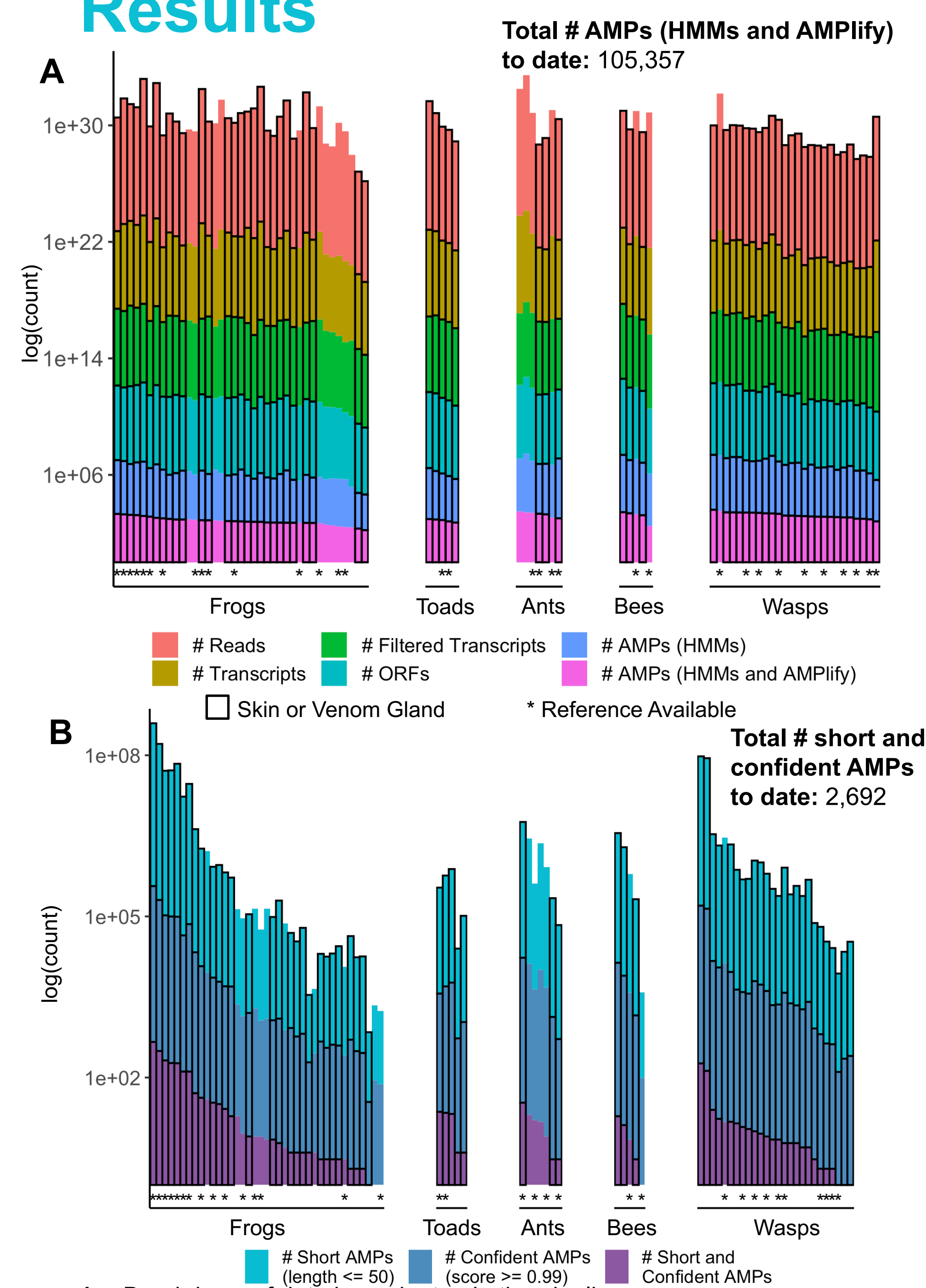
- To develop and execute a scalable bioinformatics-based AMP discovery pipeline to mine for AMP sequences in publicly available genomic resources
- To package a fully functional bioinformatics pipeline
- To obtain a list of potential AMP sequences for
 - Downstream analysis
 - In vitro* bioactivity testing
 - Drug development



Methods



Results



A. Breakdown of data in each step in the pipeline
B. Further breakdown of AMPs found using HMMs and AMPlify (pink in Fig. A), by length and AMPlify's confidence score*

*A sequence is predicted to be an AMP if its score >= 0.50

Conclusions

- In each of the assembled transcriptomes, a large set of potential AMPs using HMMs were found
- Those AMPs can be further filtered by AMPlify score (>= 0.99) and length (<= 50) to obtain shorter and higher-confidence peptides (ideal for synthesis)

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