



# Cyclopeptide Sequencing

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## The Problem:

# Cyclopeptide Sequencing

Relies on a "branching and bounding algorithm"

Every time the while loop runs, each peptide grows in length by one amino acid

Then the spectrum each peptide in the list is be compared to the spectrum of the mystery peptide. If it contains a peak value that is not in the spectrum, it is removed from the list

This continues until the peptide whose spectrum exactly matches the given spectrum is identified

Pros:

Faster than a brute force algorithm

Cons:

Still very slow

Only worked if the given spectrum was perfect and didn't have any missing or extraneous peaks.



### Leaderboard w/Spectral Convolution

Spectral convolution narrows down the number of amino acids that are added to the peptides each time.

Calculate the difference between each peak in the spectrum Based on the numbers between 57 a  $\sim$ 

#### References

- 1. Compeau, P., & Pevzner, P. (2015). *BIOINFORMATICS ALGORITHMS: An active learning approach* (Vol. 1). S.I.: ACTIVE LEARNING.
- 2. "Tyrocidine." *Wikipedia*, Wikimedia Foundation, 30 Apr. 2018, en.wikipedia.org/wiki/Tyrocidine. [Source of Image on 2nd Slide]