

Identification of Novel Peptides from the Venom Duct Transcriptome of Marine Snail *Cinguloterebra Anilis*

Molecules produced in nature that are biologically active continue to be the source and inspiration for a vast number of drugs, diagnostics, and pharmacological tools. However, it remains challenging not only to find new organisms that produce natural products, but also to identify all of the bioactive molecules produced by these organisms.

Marine snails have proven to be good sources of neuroactive peptides in the past. Whereas toxins from species like cone snails have been moderately well categorized, toxins from the vermivorous *Terebrid* snails remain more poorly characterized.

Working in collaboration with the Holford Lab at the Hunter College of CUNY, I focus on discovering neuroactive peptides from the venom tissues of the snail *Cinguloterebra anilis*. We are working on Illumina RNA-Seq data of the *anilis* venom duct, and aim to assemble, annotate and filter our way to discovering new toxins, later progressing to physiological assays.

As shown in the flowchart below, this pipeline involves the process of assembling RNA-Seq data *de novo*, evaluating assembly quality, generating open reading frames from assembled contigs and mining for putative toxins with a new algorithm that we are putting together. We also aim to create a re-usable pipeline that can be employed to mine for similar data in any species that is known to produce venom with a framework similar to terebrids.

