UniqSeq v. 0.0.1

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Description: A primer design tool for identifying discriminatory targets of interest among highly similar bacterial species

Instructions:
1. Download uniqseq.py and place in working directory
2. In working directory, make a new directory for you sequences of interest
3. In working directory, make a new directory for very similar sequences that are not of interest
4. Download .fasta files for each of these sequences and place in their respective folders
5. In Terminal, run the following command: python uniqseq.py -i <seqs_of_interest_directory> -o <other_seqs_directory> -w <desired_amplicon_size> -a <desired_anneal_temp> -r <number_of_primer_sets_to_output>

Primer pairs will be output in your <seqs_of_interest> directory