* Using NCBI
  + General search for ***accession number*** of assumed protein:
    - Taxa: insect, moth, pyralidae (and bactrocera dorsalis)
    - filtering terms: arylphorin, storage protein, riboflavin binding, methionine rich, hexamerin, diapause associated, juvenile hormone binding hexamerin
    - This will provide me with a list of the protein FASTAs that I can blast my fragments against
  + Blast fragments against ***accession numbers***
    - Using the protein fragments as the search term(s)
    - Blast the search term(s) against the accession numbers
    - ***Aligned results*** will be the proteins associated with the accession numbers collected.
  + Blast the proteins with identity
    - Using the protein ***identity FASTAs*** from the aligned results as the search term(s)
    - Blast the search term(s) against the Ostrinia nubilalis EST database
    - ***Identity EST*** will result and provide me with a list of sequence reads that are putative mRNA for the *O. nubilalis* storage proteins!!!!!