STEP 1: Create the local database of supercontigs of the *I. scapularis* genome

STEP 2: Perform a local BLASTX search of the supercontig database using other tick serpin downloads as queries to identify serpin encoding supercontigs

STEP 3: Assemble Use genomic (g) DNA coding domains. Use GenomeScan analysis to align tick serpin protein sequences with supercocontig sequences to identify exons. Use VectorNTI DNA analysis software to manually assemble into genomic (g) DNA coding domains

STEP 4: Assemble cDNA sequences. Perform BLASTN scanning of exons or gDNA coding domains against trace archive database to retrieve ESTs and their mates. Use the VectorNTI contig assembly to assemble ESTs and their mates into cDNA sequences

STEP 5: Determine the gene map. With parameters set to *Drosophila melanogaster* use the SPIDEY software to delineate exon and intron boundaries based on the GT-AG donor splice sites.

STEP 6: Perform BLASTN scanning of assembled coding sequences against the whole shotgun genome database to retrieve accession numbers of primary sequences used to assemble supercontigs used in this study