Workflow for annotating SBP2 and SBP2L and refining incomplete SBP2 annotations

No annotated SECIS binding proteins

OR

Partially annotated SBPs proteins
(e.g. Trichoplax, Tetraodon)

→

tBLASTN taxon of interest against the non-redundant nucleotide and/or EST database with known SBP2L/SBP2

→

BLAST/BLAT search with known SBP2L or SBP2 against genome of interest

→

Link to genomic DNA

→

Input at least 20kb genomic DNA into FgenesH or GenomeScan with closest known related SBP as a guide

→

Compare predicted peptide with known orthologues

→

Refine prediction by querying CDD and ESTs from taxon of interest (or related taxa if few ESTs available)