Ensembl mRNA annotation spliced from genomic DNA

1. Align to Refseq mRNA or complete Unigene consensus with BLASTN: e < 10^{-10} and alignment length > 100 nt > 99% sequence identity

2. Align both to best-matching non-hypothetical SWISSPROT protein (aligned subsequence must be conserved in a non-mammalian vertebrate) BLASTP e < 10^{-4} and FASTA e < 0.01

3. These SWISSPROT protein aligned subsequences are parsed at the first ORF disablement to check for BLAST alignment e < 10^{-4}

4. mRNAs are also aligned to SCOP protein domains BLAST e < 10^{-4}