

NC_071536.1:30072626..30072688 *Vidua chalybeata* isolate OUT-0048 chromosome 7, bVidCha1 merged haplotype, whole genome shotgun sequence

30 072 630

30 072 640

|30 072 650

30 072 660

30 072 670

30 072 680

(U) Alignment for group templates. BLAST Results for: XM_053947471.1:1-1533 PREDICTED: Vidua chalybeata...

Query 3571797

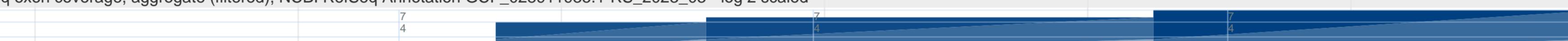
(Li) BLAST Results for: XM_053947471.1; 1-1533 PREDICTED: Vidua chalybeata

Query_3571797

Genes NCBI RefSeq Annotation CCF_026070E6F_1 RS_2023_03

The figure displays a genomic track diagram for the SCTR gene. The top track shows the gene structure with exons in green and introns in blue. The gene name 'SCTR' is centered above the first exon. Below the tracks, individual nucleotide positions are labeled with their corresponding codons and amino acids. Two alternative transcripts are shown: XM_053947471.1 (top) and XP_053803446.1 (bottom). Both transcripts start with GAA (E), followed by different sequences. XM_053947471.1 continues with AAA (K), GCA (A), AAG (K), AGG (R), GAA (E), AAG (K), GAT (D), GAA (E), GTG (V), AAA (K), AAG (K), AGC (S), TAG (X), GAG (E), CCA (R), CGC (P), TGG (W), and AGA (R). XP_053803446.1 continues with a dash (-), followed by the same sequence as XM_053947471.1.

RNA-seq exon coverage_aggregate (filtered)_NCBI_RefSeq_Annotation_GCF_028911935.1_RS_2023-03-Jag_3-cooled



RNA-seq intron spanning reads, aggregate (filtered), NCBI RefSeq Annotation GCF_028911935.1_RS_2023_03_Img_3_scaled



RNA-seq intron features aggregate (filtered) NCBI RefSeq Annotation GCF_028911935 1-RS 2023_03