

NC_089983.1:40294344..40294406 *Apteryx mantelli* isolate bAptMan1 chromosome 6, bAptMan1.hap1, whole genome shotgun sequence

|40-294-350

|40 294 360

|40-294-37

40-294

40-29

403

A G G A A A A A C G C T A G G A A A G G A T G G A G T G A G C G A A C G G A G G T C C T C T G A G C C T C A G G A C C T C T C G C G

T C C T T T T T G C G A T C C T C C C T A C C T C A C T C G C T T G C C T C T C C A G G A G C C T C T C G C G

(U) Alignment for group templates BLAST Results for: XM_067298584.1 PREDICTED: Apterix mantelli

uery_1699519

(II) BLAST Results for: XM_067298584.1 PREDICTED: *Apertrix mantelli*

query_1699519

Genes NCBI RefSeq Annotation GCF_036417845.1-RS 2024_08

The figure displays a genomic track for the SCTR gene. The top green bar represents the gene structure, with exons shown as green boxes and introns as green lines. The gene name 'SCTR' is centered above the first exon. Below the gene structure, two horizontal blue bars represent different protein variants:

- The top blue bar is labeled 'XM_067298584.1' and corresponds to the sequence shown in the bottom row.
- The bottom blue bar is labeled 'XP_067154685.1' and corresponds to the sequence shown in the row above it.

The bottom row shows the amino acid sequence for each variant. The sequence is: AAA, K, CGC, P, TAG, X, GAG, E, GGA, C, AAG, K, GGA, C, TGG, W, AGT, S, GAG, E, CGA, P, ACG, T, GAG, E, AGG, P, TCC, S, TCT, S, GGA, C, GAG, E. The 'X' in the sequence indicates a stop codon.

RNA-seq exon coverage aggregate (filtered) NCBI RefSeq Annotation GCF_041075295.1_RS_2024_08_Jeg_3_scaled



RNA-seq intron-spanning reads, aggregate (filtered) NCBI RefSeq Annotation GCF_041075295.1-BS_2024_08 - Log 2 scaled



RNA-seq intron features_aggregate (filtered)_NCBI_RefSeq_Annotation_GCF_041075295_1-BS_2024_08