40,294,350	40,294,360	40,294,370	40,294,380	40,294,390	40,294,400

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

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

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

Query_1699519

∨

(U) BLAST Results for: XM_067298584.1 PREDICTED: Apteryx mantelli...

Query_1699519

∨

Genes, NCBI RefSeq Annotation GCF_036417845.1-RS_2024_08

SCTR

XM_067298584.1

XP_067154685.1

| AGG | AAA | AAA | CGC | TAG | GAG | GGA | AAG | GGA | TGG | AGT | GAG | CGA | ACG | GAG | AGG | TCC | TCT | GGA | GAG |
| R | K | K | R | X | E | G | K | G | W | S | E | R | T | E | R | S | S | G | E |

RNA-seq exon coverage, aggregate (filtered), NCBI RefSeq Annotation GCF_041075295.1-RS_2024_08 - log 2 scaled

0   0   0   0

RNA-seq intron-spanning reads, aggregate (filtered), NCBI RefSeq Annotation GCF_041075295.1-RS_2024_08 - log 2 scaled

0   0   0

RNA-seq intron features, aggregate (filtered), NCBI RefSeq Annotation GCF_041075295.1-RS_2024_08