

NC\_086252.1:30255593..30255725 *Prinia subflava* isolate CZ2003 ecotype Zambia chromosome 6, Cam Psub 1.2, whole genome shotgun sequence

30 255 600 | 30 255 610 | 30 255 620 | 30 255 630 | 30 255 640 | 30 255 650 | 30 255 660 | 30 255 670 | 30 255 680 | 30 255 690 | 30 255 700 | 30 255 710

AGGGAAAAAAGCAAGGAGGGAAAAGGATGAAGTAAAAGAGCTACGAGCCACGCTGGAGAGCATACAAACAGCCTGCTGACCTCTGATGCATGAGGGATGAAGAAAACAGACTGTGTTGACTATGTGGACCT  
TCCCTTTTCGTTCCCTCCCTTCCATTCTCGATGCTCGGTGCGACCTCTCGTATGTTGTCGGACGACTGGAGACTACGTACTCCCTACTTCTTTGTCGACACAAACTGATAACACCTGG

(U) Alignment for group templates. BLAST Results for: XM\_063400925.1:1-1530 PREDICTED: Prinia subflava...

Query 201861

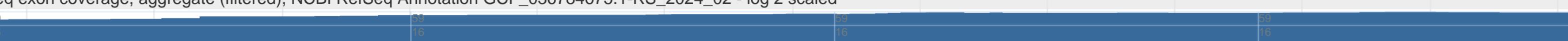
(LI) BLAST Results for: XM\_063400035.1;1\_1530 PREDICTED: Brinjal subfamily

Query 301861

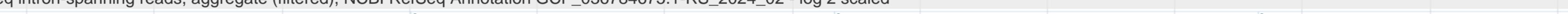
Genes NCBI RefSeq Annotation GCF\_021018805 1-BS 2024\_02

The diagram illustrates the structure of the SCTR gene. It features a green box at the top representing the gene body, with black arrows pointing from left to right along its length. Below this, two transcripts are shown as colored horizontal lines: a blue line for XM\_063400925.1 and an orange line for XP\_063256995.1. Both transcripts have black arrows indicating their direction of transcription. The XM transcript is positioned above the gene body, while the XP transcript is below it. The sequence labels at the bottom (AGG, GAA, AAA, GCA, AGG, AGG, GAA, AAG, GAT, GAA, GTA, AAA, AGA, GCT, ACG, AGC, CAC, GCT, GGA, GAG, CAT, AAA, CAG, CCT, GCT, CTC, TGC, ATG, AGG, GAT, GAA, AAC, AGA, CTG, TGT, TTG, ACT, ATG, TGG, ACC) correspond to the sequence of the XM transcript.

RNA-seq exon coverage aggregate (filtered) - NCBI RefSeq Annotation GCF\_026784675.1\_RS\_2024-02 - Log 2 scaled



RNA-seq intron spanning reads\_aggregates (filtered)\_NCBI\_RefSeq\_Annotation\_GCF\_036784675.1\_RS\_2024-03\_Jag\_3\_sealed



RNA-seq intron features\_aggregate (filtered)\_NCBI\_RefSeq\_Annotation\_GCF\_036784675.1\_RS\_2024\_02