67,470,110	67,470,120	67,470,130	67,470,140	67,470,150	67,470,160

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

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

(U) Alignment for group templates, BLAST Results for: XM_032794021.1 PREDICTED: Chelonoidis abingdonii...

Query_7298787
<

(U) BLAST Results for: XM_032794021.1 PREDICTED: Chelonoidis abingdonii...

Query_7298787
<

Genes, NCBI RefSeq Annotation GCF_003597395.2-RS_2025_06

SCTR

XM_032794021.1

XP_032649912.1

GTA	TGG	TTT	CCC	AAC	CTC	TAT	ATC	AGG	AAG	GTG	TTC	TTC	GGT	TGA	CAT	CAA	TCG	GAC	TTC
M	G	F	P	Q	L	Y	L	G	E	V	L	L	W	S	Y	N	A	Q	L

RNA-seq exon coverage, aggregate (filtered), NCBI RefSeq Annotation GCF_003597395.2-RS_2025_06 - log 2 scaled

0   0   0

RNA-seq intron-spanning reads, aggregate (filtered), NCBI RefSeq Annotation GCF_003597395.2-RS_2025_06 - log 2 scaled

24   24   24
8   8   8

RNA-seq intron features, aggregate (filtered), NCBI RefSeq Annotation GCF_003597395.2-RS_2025_06

7
7
10