

NC_073704.1:33039361..33039423 Falco cherrug isolate bFaIChe1 chromosome 8, bFaIChe1.pri, whole genome shotgun sequence

(1) Alignment for group templates BLAST Results for: XM_005431780.3:2215-3849 PREDICTED: Falco

(S) Alignment for group template, BEAS1 Results for: KM_0001011003.22 10-00-10 1 PREdicted P-values...
Query_338815

(U) BLAST Results for: XM_005431780.3:2215-3849 PREDICTED: Falco...

Page 1 of 1

Genes, NCBI RefSeq Annotation GCF_023634085.1-RS_2023_04

◀ ▶ ▶ ▶ ▶ ▶ SCTR ▶ ▶ ▶ ▶ ▶ ▶ ▶

► ► ► ► ► ► XP_005431837.2 ► ► - - ► ► ► ►

GAA AGG GAC GAA GTG AAA GGA GCT AGG AAC CAA ACT GGA GAG CAT AGA CAG ACC AGT GAC

RNA-seq over-coverage aggregate (filtered) - NCBI RefSeq Annotation GCF_022827615.1_RS_2023-04 - Log 2 scaled

RNA-seq exon coverage, aggregate (filtered), NCBI RefSeq Annotation GCF_029876125.1-RS_2023_04 - log₂ scaled

81 81 81 81 81

RNA-seq transcriptome analysis (filter) in NCBLB (S. A. et al., GSE32687; GSE32688; GSE32689; GSE32690)

RNA-seq intron-spanning reads, aggregate (filtered), NCBI RefSeq Annotation GCF_029876125.1-RS_2023_04 - log 2 scaled

0 0 0 0