

NC_092593.1:8352663..8352795 Anas platyrhynchos isolate ZD024472 breed Pekin duck chromosome 7, IASCAA5 PekinDuck T2T, whole genome shotgun sequence

8,352,670 | 8,352,680 | 8,352,690 | 8,352,700 | 8,352,710 | 8,352,720 | 8,352,730 | 8,352,740 | 8,352,750 | 8,352,760 | 8,352,770 | 8,352,780 | 8,352,790

AGGAAAAAAAGCAAGGAGGGAAAGGAATGAAGTGAAAGGAGCTGAGAGGCCAGGCTGGAGAGCACGCAGACAGCCTGGTGACCTCTGGTGTATGAAGGATGAAGGAAGCAGACTGAGTGACTATGTGGACCGCTTCCTTTTCGTTCCCTCCCTTCCCTTACTTCACTTCCCTCGACTCTCGGTCCGACCTCTCGTGCCTGTCGGACCACACTGGAGACCCACATACTTCCTTCGTTGACTCACTGATAACACCTGGCG

(U) Alignment for group templates, BLAST Results for: XM_038181962.2:2009-3541 PREDICTED: Anas platyrhynchos...

Query_7585021

(LI) BLAST Results for: XM_038181063.3;2009_3541_PREDICTED; Apis melliferae

(U) BLAST Results for: XM_038181962.2:2009-3541 PREDICTED: Anas platyrhynchos... Query_7585021

Genes, NCBI RefSeq Annotation GCF_047663525.1-RS_2025_03

- ► XM_038181962.2 ► - ► XP_038037890.2 ►

AGG AAA AAA GCA AGG AGG GAA AGG AAT GAA GTG AAA GGA GCT GAG AGC CAG GCT GGA GAG CAC AGA AGG

RNA-seq exon coverage, aggregate (filtered), NCBI RefSeq Annotation GCF_047663525.1-RS_2025_03 - log 2 scaled

472	472	472	472
32	32	32	32

RNA-seq intron-spanning reads, aggregate (filtered), NCBI RefSeq Annotation GCF_047663525.1-RS_2025_03 - log 2 scaled

RNA-seq intron features, aggregate (filtered), NCBI RefSeq Annotation GCF_047663525.1-RS_2025_03