

Anas platyrhynchos mitochondrion, complete genome

NCBI Reference Sequence: NC_009684.1

FASTA Graphics

Go to:

LOCUS NC_009684 16604 bp DNA circular VRT 07-JUN-2021

DEFINITION Anas platyrhynchos mitochondrion, complete genome.

ACCESSION NC_009684

VERSION NC_009684.1

DBLINK BioProject: PRJNA20199

KEYWORDS RefSeq.

SOURCE mitochondrion Anas platyrhynchos (mallard duck)

ORGANISM Anas platyrhynchos

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
Coelurosauria; Aves; Neognathae; Galloanserae; Anseriformes;
Anatidae; Anatinae; Anas.

REFERENCE 1 (bases 1 to 16604)

AUTHORS Tu,J.F., Huang,Y.H. and Li,N.

TITLE Complete mitochondrial genome sequence analysis of pekin and the
origin of duck

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 16604)

CONSRTM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (24-JUL-2007) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (bases 1 to 16604)

AUTHORS Tu,J.F., Huang,Y.H. and Li,N.

TITLE Direct Submission

JOURNAL Submitted (30-JUN-2007) State Key Laboratory for Agribiotechnology,
China Agricultural University, Yunamingyuan West Road 2, Beijing
100094, China

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The
reference sequence was derived from EU009397.

COMPLETENESS: full length.

FEATURES Location/Qualifiers

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/organelle="mitochondrion"
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/db_xref="taxon:8839"
/common="mallard duck"

	/breed="Pekin duck"
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SAALGGWMGLNQTQTRKILAFSSISHLGWIAIILVYSPKLALLTFYLYTIMTSAVFMA	
LNKIKALNLSMILTSWTKTPVLNATLMLVLLSLAGLPPLTGFMKWLIIQELTKQEMT	
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gene	complement(6168..6236) /locus_tag="KEG62_t08" /db_xref="GeneID:64987710"
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tRNA	/db_xref="GenelD:64987713" complement(6377..6448) /locus_tag="KEG62_t11" /product="tRNA-Tyr"
gene	/db_xref="GenelD:64987713" 6450..8000 /gene="COX1" /locus_tag="KEG62_p11"
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FWLLPPSLLLLASSTVEAGAGTGWTVYPPLAGNLAHAGASVDLAIFSLHLAGVSSIL
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AMLSIGFLGFIWAAHMFVGMVDVDRAYFTSATMIIAIPGTGIKVFSLATLHG GTIK
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GFTHWFPLLTGFTLHQTWAKAHFGVMFTGVNLTFFPQHFLGLAGMPRRYS DYPDAYTL

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PAFVQVQE"

gene	complement(7992..8064) /locus_tag="KEG62_t12" /db_xref="GenelD:64987697"
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MLMEKLSSNAVDAQEVELIWTLPAIVLVLLALPSLQILYMMDEIDEPDLTLKAIGHQ

WYWSYEYTDKDLSDSYMIPTDLPNGHFRLLVDHRVVPMESPIRVITAGDVLH

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MALAFPLWLATLLTGLRNKPSASLAHLLPEGTPPTPLIPALILIETTSLIRPLALGVR	
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HALTLTILLGFYFTALQAMEYHEAPFSIADSVYGSTFFVATGFHGLHVIIGSTFLTV

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gene 10520..10588
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tRNA 10520..10588
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gene 10589..10940
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/db_xref="GenelD:5405822"

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Mol. Biol. Evol., 15:1568-1571)"
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/translation="MNMLTFMFSLSLVLSAILTALNFWLAQMTPDSEKLSPYECGFDP

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LAYEWAQGGLEWAE"

gene 10942..11011


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LRQTDKSLIAYSSVSHMGLVIAAGMIQTHWSFSGAMILMISHGLTSSMLFCLANTNY
ERTHSRILLLTRGLQPLLPLMATWWLLANLTNMALPPTTNLMAELTIMITLFNWSALT

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gene	12885..14708 /gene="ND5" /locus_tag="KEG62_p03" /db_xref="GenelD:5405820"
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LAAAGKSAQFGLHPWLPAAMEGPTPVSALLHSSTMVAGIFLLIRMHPLLASNQTALT

ACLCLGALSTLFAATCALTQNDIKKIIAFSTSSQLGLMMVAIGLNLPQLAFLHISTHA

FFKAMLFLCSGSIHSLNGEQDIRKMGGGLQKTLPVTTSCLTIGNLALMGTPFLAGFYS

KDLIESLNTSYLNTWALSLLATAFTATYSIRMTLLVQAGRTRIPPITPMNENNPL

ITAPLTRLALGSIMAGMLITSFITPTKTPPMTMPLITKTAAILVTVLGVILALELSNM

THTLTHPKPSRLVNFSSLLGYFNPLVHRFCSKTLEKGQNIALHLIDLSWLKKGPEG

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gene 14708..15850

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/gene="CYTB"

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/db_xref="GenelD:5405813"

/translation="MAPNIRKSHPLLKMINNSLIDLPAPSNISAWWNFGSLLAICLAT

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FYYGSYLYKETWNTGVILLTLMATAFVGYVLPWGQMSFWGATVITNLFSAIPYIGQT

LVEWAWGGFSVDNPTLTRFFAIHFLLPFLIAGITLVHLTFLHESGSNNPLGLVSDCDK

IPFHPYFSFKDILGFILMLTPLMALALFSPNLLGDPENFTPANPLVTPPHIKPEWYFL

FAYAILRSIPNKLGGVLALAASVLILFLVPFLHKSQRTMTFRPLSQLLFWTLVANLL
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 /db_xref="GenelD:5405816"

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gene complement(16534..16604)
 /locus_tag="KEG62_t22"
 /db_xref="GenelD:64987703"

tRNA complement(16534..16604)
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 /product="tRNA-Glu"
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961 gaaactccag cactaaagac gatccaaacc cgatgacaat cattacttg acctaaaa
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