Rattus norvegicus isolate 436 mitochondrion, complete genome

GenBank: KM820834.1

FASTA Graphics

LOCUS KM820834 955 bp DNA linear ROD 25-JAN-2015

DEFINITION Rattus norvegicus isolate 436 mitochondrion, complete genome.

ACCESSION KM820834 REGION: 2746..3700

VERSION KM820834.1

KEYWORDS .

SOURCE mitochondrion Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 955)

AUTHORS Huang,C.

TITLE Direct Submission

JOURNAL Submitted (01-OCT-2014) Fudan University, China

FEATURES Location/Qualifiers

source 1..955

/organism="Rattus norvegicus"

/organelle="mitochondrion"

/mol_type="genomic DNA"

/isolate="436"

/db_xref="taxon:10116"

gene 1..955

/gene="ND1"

CDS 1..955

/gene="ND1"

/note="TAA stop codon is completed by the addition of 3' A residues to the mRNA"

/codon_start=1

/transl_except=(pos:3700,aa:TERM)

/transl_table=2

/product="NADH dehydrogenase subunit 1"

/protein_id="AJE61378.1"

/translation="MYFINILTLLIPILIAMAFLTLVERKILGYMQLRKGPNIVGPYG
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LFILATSSLSVYSILWSGWASNSKYSLFGALRAVAQTISYEVTMAIILLSVLLMSGSF
SLQMLITTQEHIWLLIPAWPMAMMWYISTLAETNRAPFDLTEGESELVSGFNVEYAAG
PFALFFMAEYTNIILMNALTSIVFLGPLYHINYPELYSTSFMTETLLLSTTFLWIRAS
YPRFRYDQLMHLLWKNFLPLTLAFCMWYISLPIFLAGIPPYT"

ORIGIN

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       1 gtgtacttta ttaatatcct aacactccta atcccaatct taattgccat ggccttcctc
      61 accctagtag aacggaaaat cctaggctac atacaactac gcaaaggccc caacatcgta
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      121 ggcccatatg gtattctaca accatttgca gatgccataa aactattcat aaaagaaccc
      181 atacgccccc taaccacctc aatatcacta tttattatcg ccccaaccct ctcccttaca
      241 ctagctctaa gcctatgaat ccccttacca atacctcacc cccttatcaa cctcaaccta
      301 ggcatactat ttattctagc cacatcaagt ctttcagtct actccattct atgatcagga
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      421 tcttacgaag tcacaatagc cattatcctc ttatccgtcc tcctaataag cggctccttc
      481 tccctacaaa tacttatcac tacacaagaa catatctgac tattaatccc cgcctgacca
      541 atagccataa tatgatacat ttcaacccta gcagaaacaa atcgagctcc cttcgactta
      601 acagaaggag aatcagaatt agtctcaggc tttaacgttg aatacgccgc aggaccattc
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      841 cgatatgacc aactaatgca cctcctatga aaaaatttcc tcccactaac actagcattc
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