Introduction to applied bioinformatics

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2024/2025

5/10

„Nucleotide bioinformatics I“

Retrieving nucleotide sequences from databases (Genbank/NCBI)

Feature analysis: statistics, reverse complement, restriction analysis

Translation, identifying open reading frame

PCR primer design, rt-PCR

Secondary structure prediction

Sequence comparison

Single Nucleotide Polymorphisms

DNA sequencing

Gene expression

microRNA

Genomes….

….

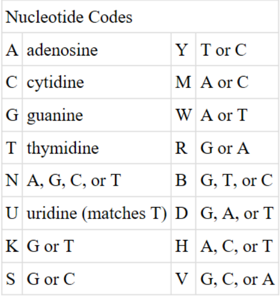
DNA/RNA

4 nucleotides: Adenin, Guanin, Thymidin (Uracil), Cytosin : 5´→ 3´

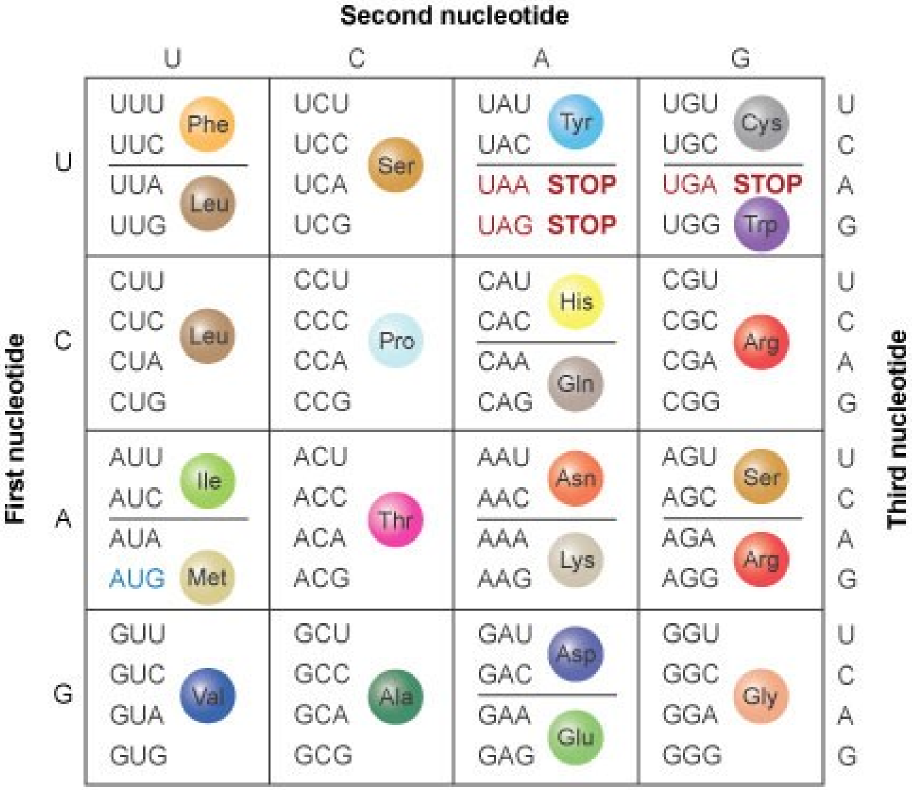
(Frederick Sanger/Walter Gilbert 1980 Nobel price for DNA sequencing)

Genetic code/ triplets:

A, C, T (U), G
N any nucleotide
R A/G purine
Y C/T pyrimidine



Nucleotide Codes			
A	adenosine	Y	T or C
C	cytidine	M	A or C
G	guanine	W	A or T
T	thymidine	R	G or A
N	A, G, C, or T	B	G, T, or C
U	uridine (matches T)	D	G, A, or T
K	G or T	H	A, C, or T
S	G or C	V	G, C, or A



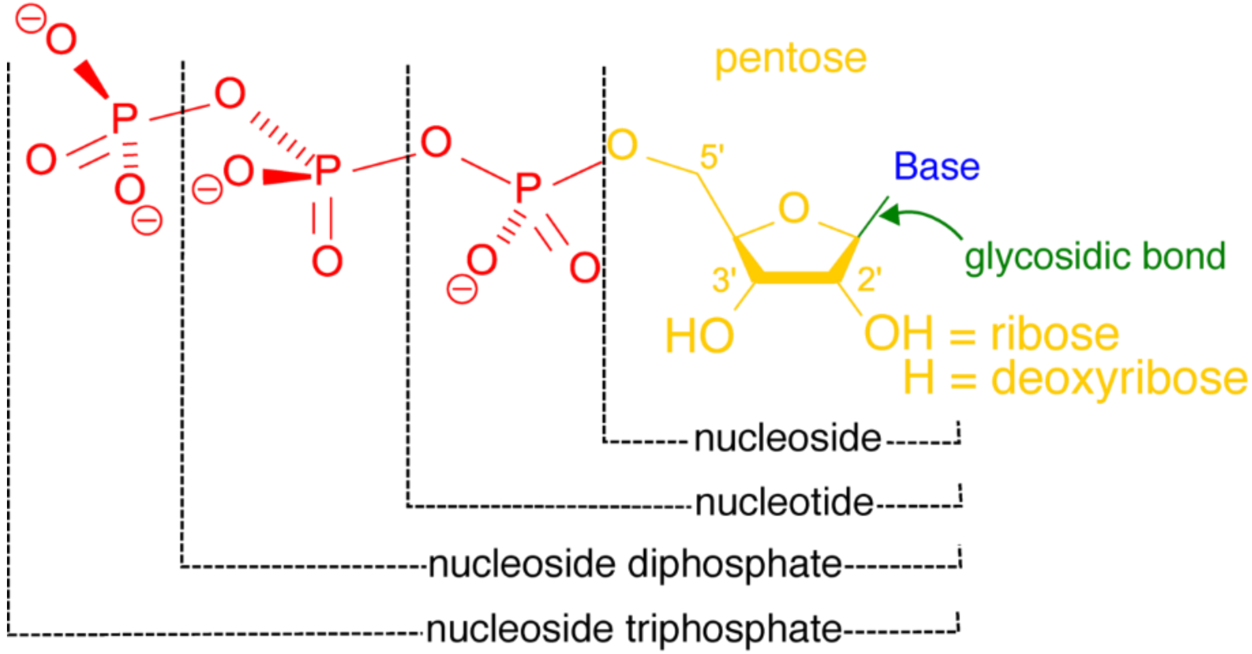
	Second nucleotide								
First nucleotide	U		C		A		G		Third nucleotide
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC		UCC		UAC		UGC		C
	UUA	Leu	UCA		UAA	STOP	UGA	STOP	A
	UUG		UCG		UAG	STOP	UGG	Trp	G
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U
	CUC		CCC		CAC		CGC		C
	CUA		CCA		CAA	Gln	CGA		A
	CUG		CCG		CAG		CGG		G
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	U
	AUC		ACC		AAC		AGC		C
	AUA		ACA		AAA	Lys	AGA	Arg	A
	AUG	Met	ACG		AAG		AGG		G
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	U
	GUC		GCC		GAC		GGC		C
	GUA		GCA		GAA	Glu	GGA		A
	GUG		GCG		GAG		GGG		G

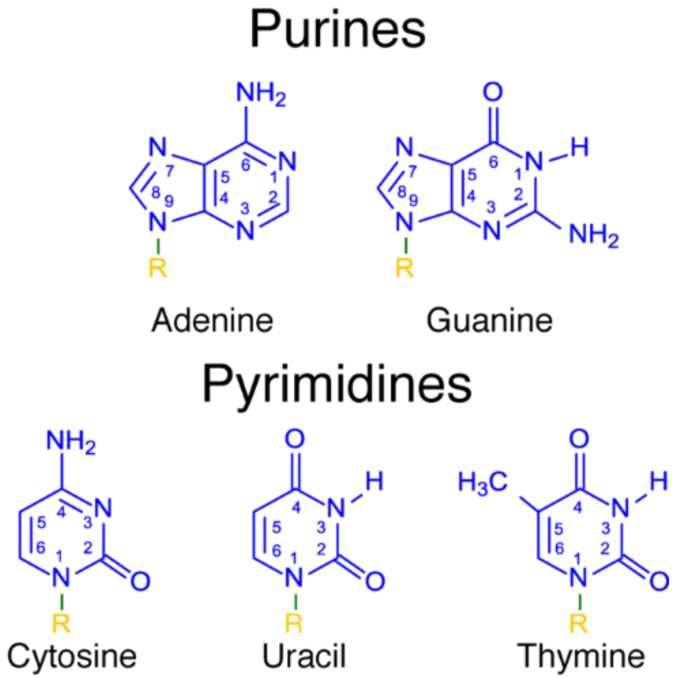
Complementarity: A=T, C≡G

Double strand DNA: 5´-ATGCCATAAAA-3´
3´-TACGGTATTTT-5´

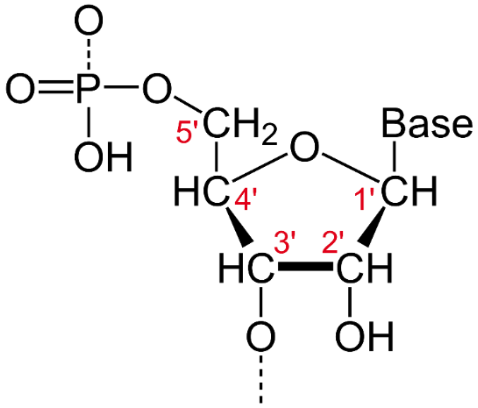
400-nt (nucleotides) = 400 bp (base pairs)…kbp, Mbp

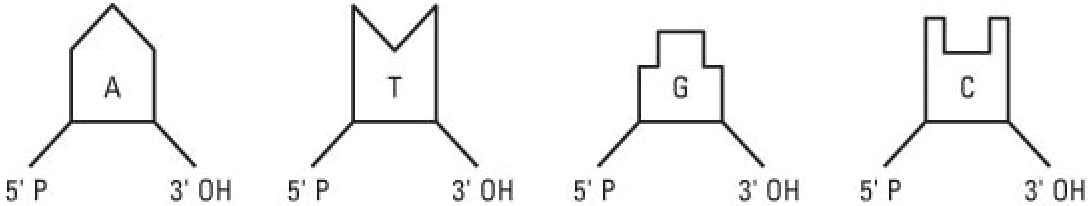
DNA/RNA

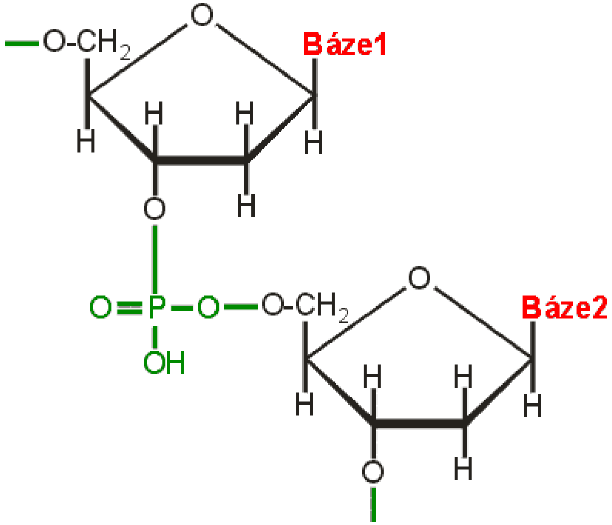

pentose
Base
glycosidic bond
5'
3'
2'
HO
OH = ribose
H = deoxyribose
nucleoside
nucleotide
nucleoside diphosphate
nucleoside triphosphate

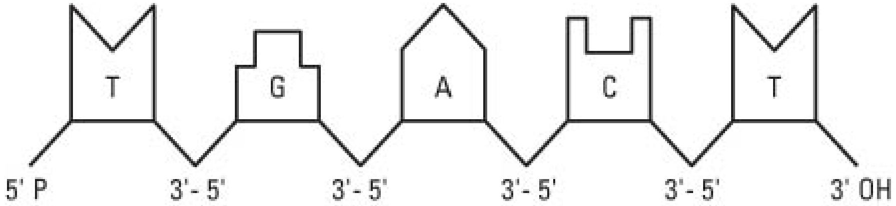

Purines
Adenine
Guanine
Pyrimidines
Cytosine
Uracil
Thymine

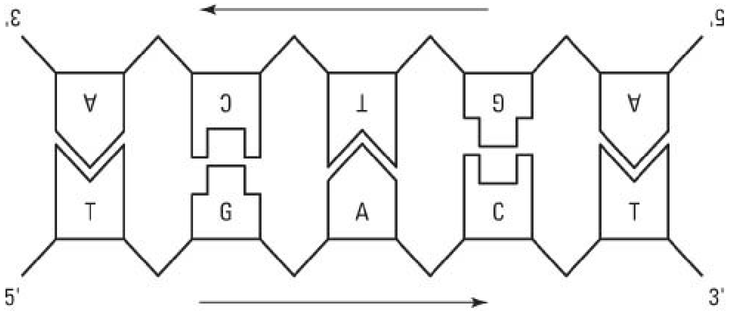
DNA/RNA


O
O=P—O
OH
5'
CH2
O
Base
HC
4'
1'
CH
3'
2'
HC
CH
O
OH


A
5' P
3' OH
T
5' P
3' OH
G
5' P
3' OH
C
5' P
3' OH


O-CH2
O
Báze1
H
H
H
H
O
H
O=P-O—O-CH2
OH
O
Báze2
H
H
H
H
O
H


T
G
A
C
T
5' P
3'- 5'
3'- 5'
3'- 5'
3'- 5'
3' OH


3'
5'
A
C
T
G
A
T
G
A
C
T
5'
3'

Prokaryotes

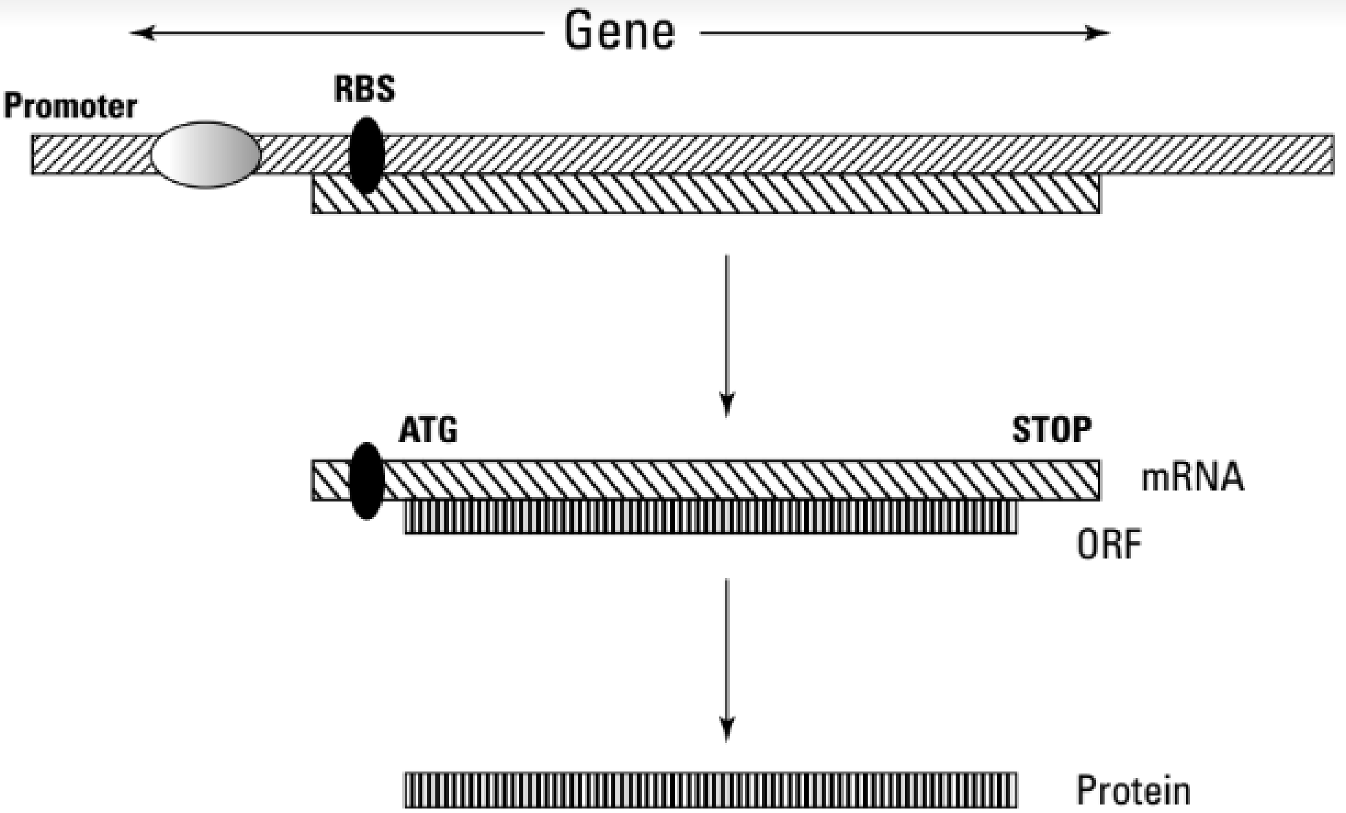
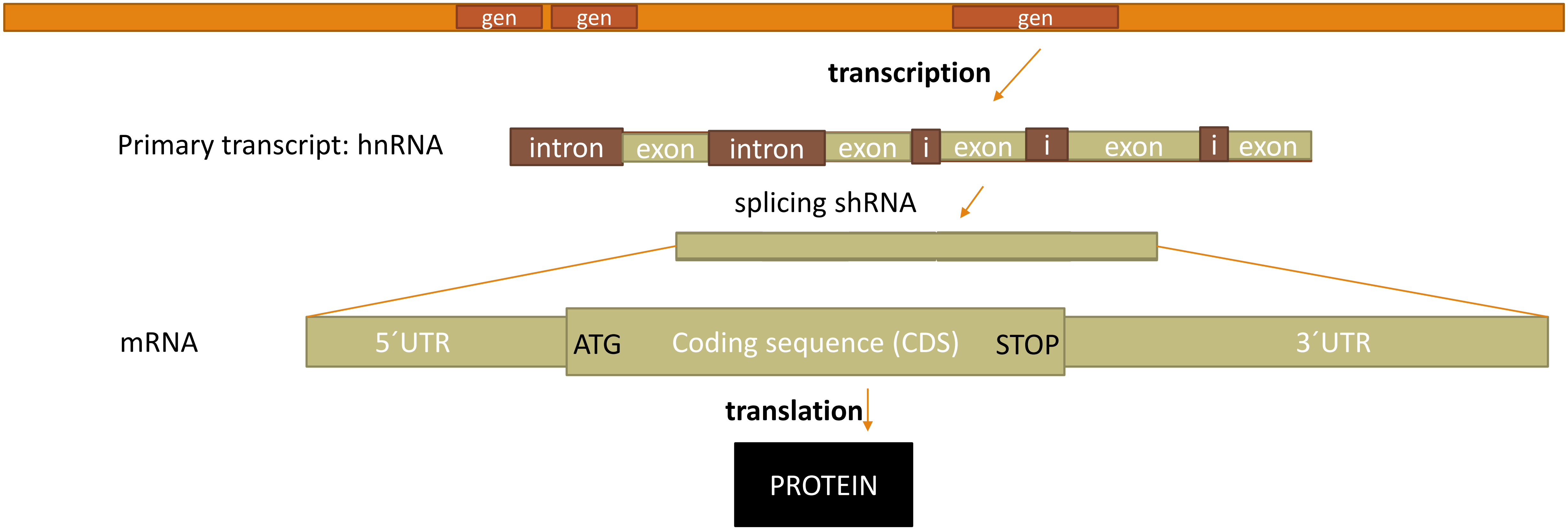


Figure 3-1: Relationship between gene, mRNA, and protein sequence for prokaryotes.

Eukaryotes

Genomic DNA / chromozomes



gen gen gen

transcription

Primary transcript: hnRNA

intron exon intron exon i exon i exon i exon

splicing shRNA

mRNA

5´UTR ATG Coding sequence (CDS) STOP 3´UTR

translation

PROTEIN

DNA sequence/GenBank

GenBank the leading nucleotide sequence repository maintained as a consortium:

http://www.ncbi.nlm.nih.gov/nuccore/

U.S. National Center for Biotechnology Information (**NCBI**)

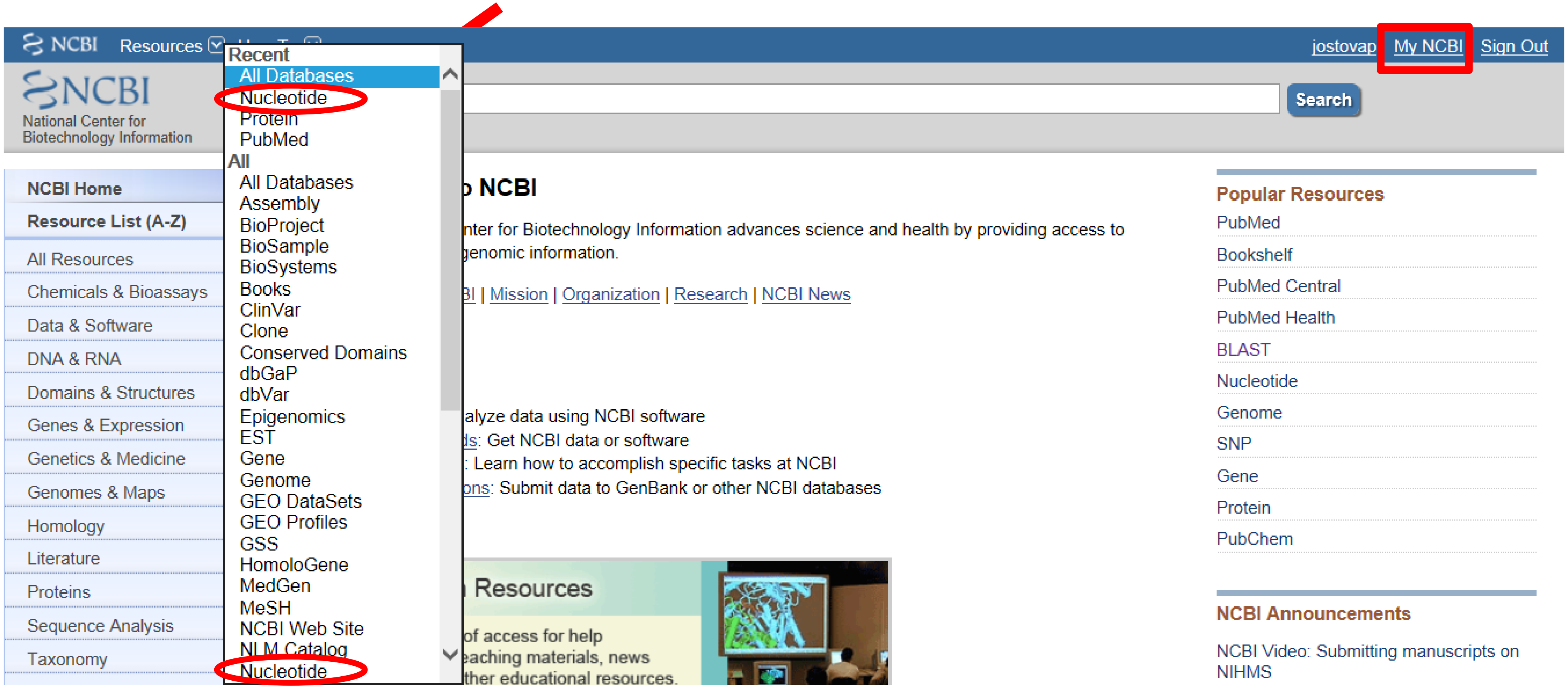
European Molecular Biology Laboratory (EMBL)

http://www.ebi.ac.uk/ena/

DNA Data Bank of Japan (DDBJ)

http://www.ddbj.nig.ac.jp/

DNA databases NCBI



o NCBI

nter for Biotechnology Information advances science and health by providing access to genomic information.

BI | Mission | Organization | Research | NCBI News

alyze data using NCBI software

ds: Get NCBI data or software

: Learn how to accomplish specific tasks at NCBI

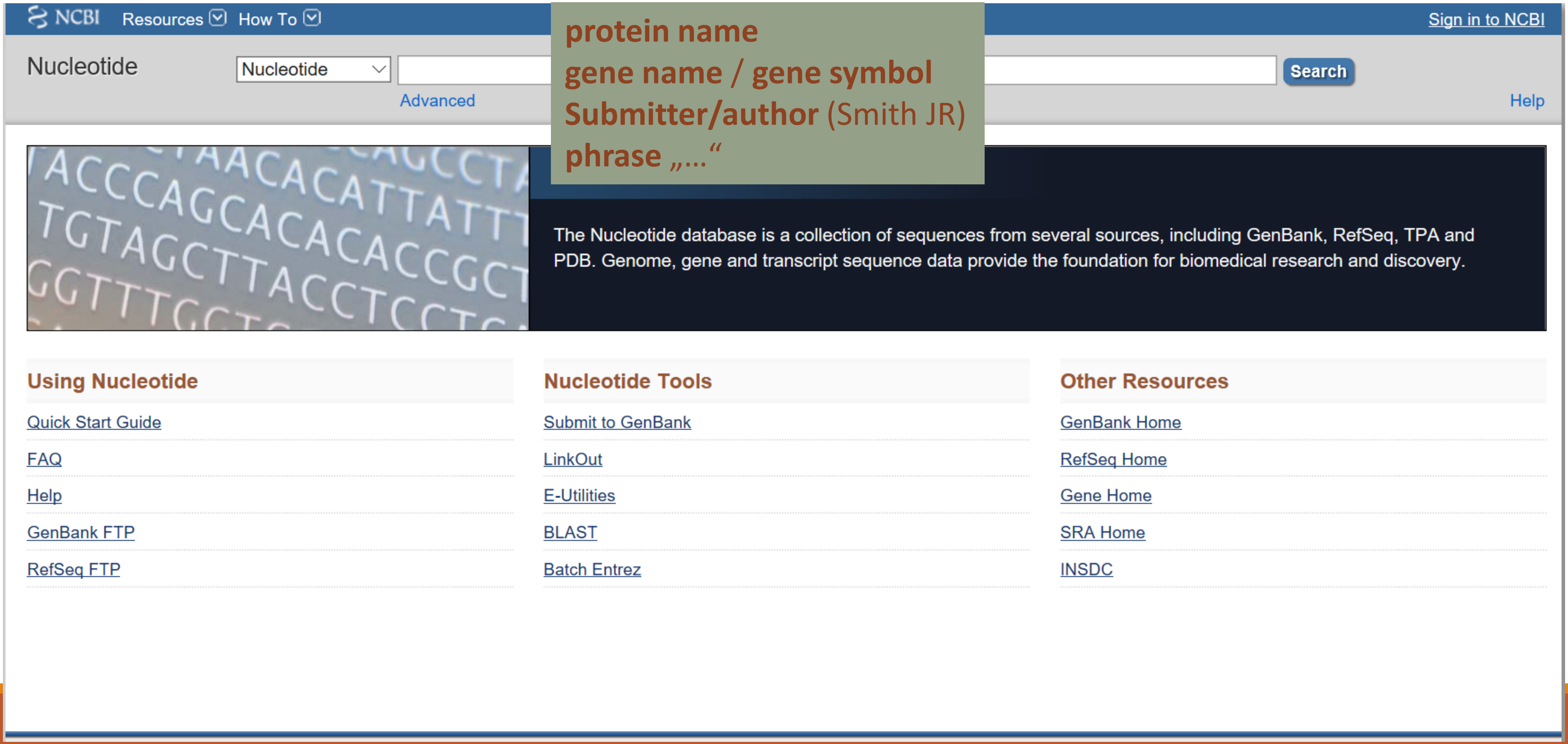
ons: Submit data to GenBank or other NCBI databases

Resources

of access for help
eaching materials, news
ther educational resources.

NCBI Video: Submitting manuscripts on NIHMS

DNA databases NCBI



protein name
gene name / gene symbol
Submitter/author (Smith JR)
phrase „…“

The Nucleotide database is a collection of sequences from several sources, including GenBank, RefSeq, TPA and PDB. Genome, gene and transcript sequence data provide the foundation for biomedical research and discovery.

Using Nucleotide

- Quick Start Guide
- FAQ
- Help
- GenBank FTP
- RefSeq FTP

Nucleotide Tools

- Submit to GenBank
- LinkOut
- E-Utilities
- BLAST
- Batch Entrez

Other Resources

- GenBank Home
- RefSeq Home
- Gene Home
- SRA Home
- INSDC

DNA databases NCBI

Nucleotide: nqo1

Species
Animals (826)
Fungi (3)
Protists (3)
Bacteria (8,564)
Customize ...

Molecule types
genomic DNA/RNA (8,907)
mRNA (455)
Customize ...

Source databases
INSDC (GenBank) (8,754)
RefSeq (668)
Customize ...

Sequence Type
Nucleotide (9,417)
EST (4)
GSS (3)

Genetic compartments
Plasmid (2)

Sequence length
Custom range...

Release date

GENE

NQO1 – NAD(P)H quinone dehydrogenase 1

Homo sapiens (human)

Also known as: DHQU, DIA4, DTD, NMOR1, NMORI, QR1

Gene ID: 1728

transcript = without introns (mRNA)

RefSeq transcripts (4) RefSeq proteins (4) RefSeqGene (1) PubMed (580)

RefSeq Sequences

Items: 1 to 20 of 9424

<< First < Prev Page 1 of 472 Next > Last >>

Filter your results:
All (9424)
Bacteria (8564)
INSDC (GenBank) (8754)
mRNA (455)
RefSeq (668)
Manage Filters

Results by taxon

Top Organisms [Tree]

Mycobacteroides abscessus	*(2510)*
Clostridioides difficile	*(2236)*
Neisseria meningitidis	*(995)*
Legionella pneumophila	*(716)*
Neisseria gonorrhoeae	*(551)*
All other taxa	*(2416)*

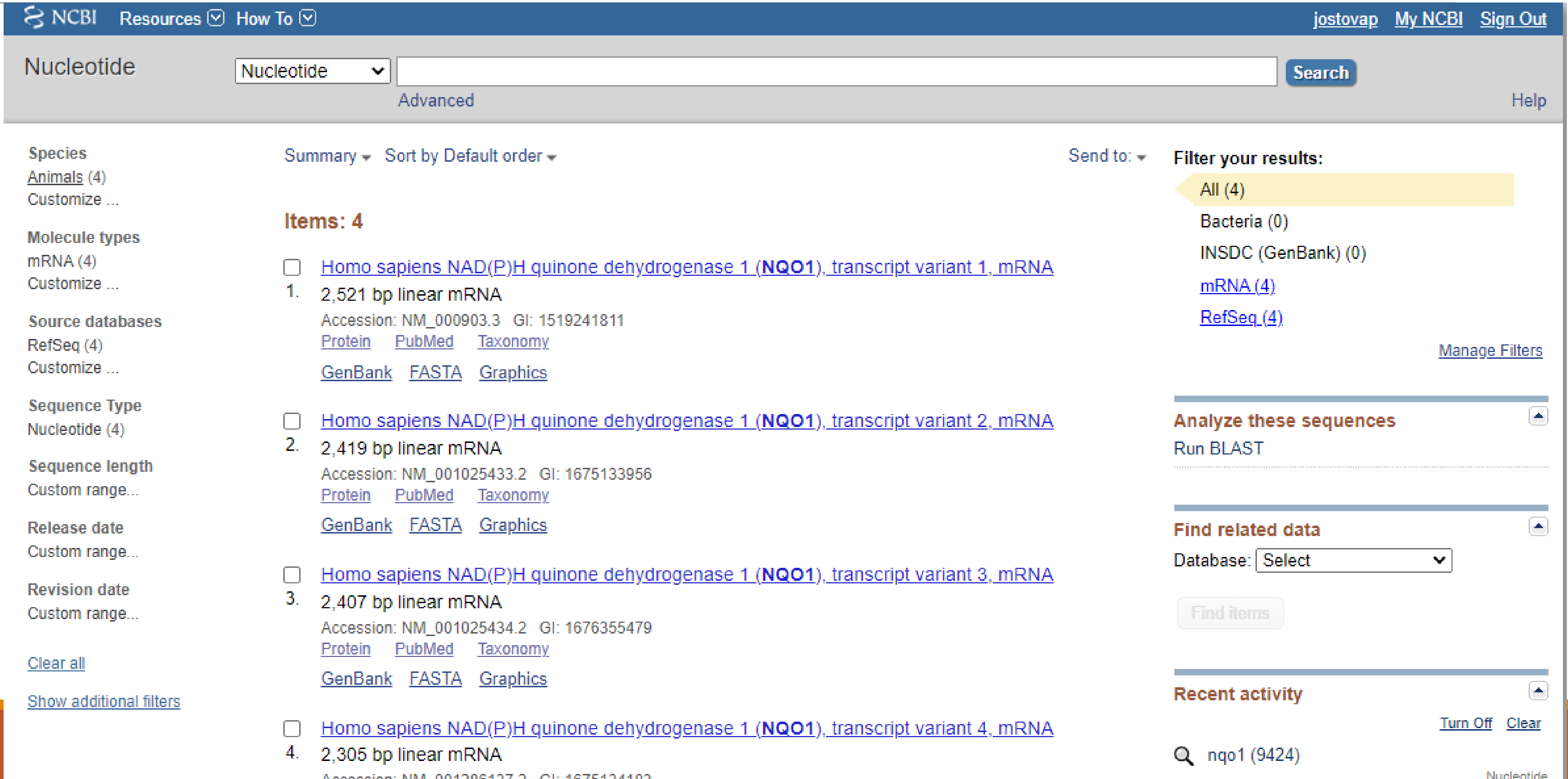
More...

Find related data

Database: Select

Find items

DNA databasesNCBI



Nucleotide: Nucleotide

Species
Animals (4)
Customize ...

Molecule types
mRNA (4)
Customize ...

Source databases
RefSeq (4)
Customize ...

Sequence Type
Nucleotide (4)

Sequence length
Custom range...

Release date
Custom range...

Revision date
Custom range...

Clear all

Show additional filters

Items: 4

☐ 1. Homo sapiens NAD(P)H quinone dehydrogenase 1 (**NQO1**), transcript variant 1, mRNA
2,521 bp linear mRNA
Accession: NM_000903.3 GI: 1519241811
Protein PubMed Taxonomy
GenBank FASTA Graphics

☐ 2. Homo sapiens NAD(P)H quinone dehydrogenase 1 (**NQO1**), transcript variant 2, mRNA
2,419 bp linear mRNA
Accession: NM_001025433.2 GI: 1675133956
Protein PubMed Taxonomy
GenBank FASTA Graphics

☐ 3. Homo sapiens NAD(P)H quinone dehydrogenase 1 (**NQO1**), transcript variant 3, mRNA
2,407 bp linear mRNA
Accession: NM_001025434.2 GI: 1676355479
Protein PubMed Taxonomy
GenBank FASTA Graphics

☐ 4. Homo sapiens NAD(P)H quinone dehydrogenase 1 (**NQO1**), transcript variant 4, mRNA
2,305 bp linear mRNA

Filter your results:
All (4)
Bacteria (0)
INSDC (GenBank) (0)
mRNA (4)
RefSeq (4)
Manage Filters

Analyze these sequences
Run BLAST

Find related data
Database: Select
Find items

Recent activity
Turn Off Clear
nqo1 (9424)

DNA databases NCBI

Nucleotide

Nucleotide ▾ | nqo1 | **Search**

Species
- Animals (509)
- Fungi (3)
- Protists (3)
- Bacteria (3,070)
- Customize ...

Molecule types
- genomic DNA/RNA (3,288)
- mRNA (279)
- Customize ...

Source databases
- INSDC (GenBank) (3,193)
- RefSeq (412)
- Customize ...

Genetic compartments
- Plasmid (1)

Sequence length
- Custom range...

Release date
- Custom range...

Revision date
- Custom range...

refinement:

Summary ▾ 20 per page ▾ Sort by Default order ▾ Send to: ▾

See NQO1 NAD(P)H quinone dehydrogenase 1 in the Gene database
nqo1 reference sequences Genomic (1) Transcript (4) Protein (4)

Items: 1 to 20 of 3607

<< First < Prev Page 1 of 181 Next > Last >>

Found 3616 nucleotide sequences. Nucleotide (3607) EST (6) GSS (3)

☐ 1. Mus musculus full open reading frame cDNA clone RZPDo836H0851D for gene **Nqo1**, NAD(P)H dehydrogenase, quinone 1; complete cds, incl. stopcodon
825 bp linear mRNA
Accession: CT010284.1 GI: 71059896
Protein Taxonomy
GenBank FASTA Graphics

☐ 2. Rhodothermus marinus strain PRQ 62B putative adenylosuccinate lyase gene, partial cds; and Nqo7, Nqo6, Nqo5, Nqo4, Nqo2, **Nqo1**, Nqo3, putative malate synthase, and putative transcriptional regulator genes, complete cds
12,551 bp linear DNA
Accession: AY972100.1 GI: 66219960
Protein PubMed Taxonomy
GenBank FASTA Graphics

Filters: Manage Filters

Results by taxon
Top Organisms [Tree]
- Mycobacterium abscessus *(1253)*
- Neisseria meningitidis *(490)*
- Legionella pneumophila *(345)*
- Neisseria gonorrhoeae *(267)*
- Clostridioides difficile *(256)*
- All other taxa *(996)*

More...

Find related data
Database: Select ▾
Find items

Search details
```
nqo1[All Fields]
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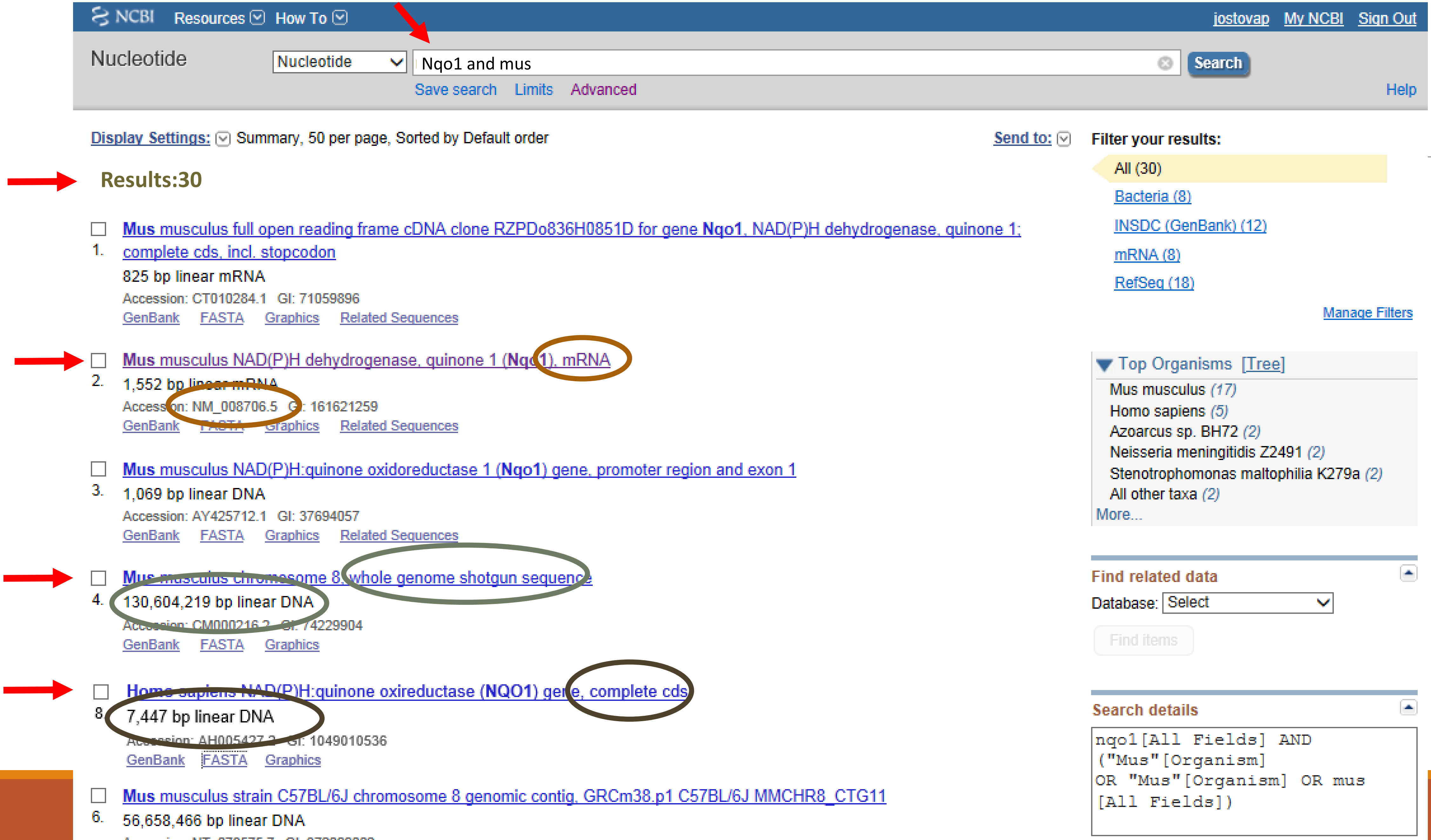

Nucleotide

Nucleotide

Nqo1 and mus

Display Settings: Summary, 50 per page, Sorted by Default order

Results:30

☐ 1. Mus musculus full open reading frame cDNA clone RZPDo836H0851D for gene **Nqo1**, NAD(P)H dehydrogenase, quinone 1; complete cds, incl. stopcodon
825 bp linear mRNA
Accession: CT010284.1 GI: 71059896
GenBank FASTA Graphics Related Sequences

☐ 2. Mus musculus NAD(P)H dehydrogenase, quinone 1 (**Nqo1**), mRNA
1,552 bp linear mRNA
Accession: NM_008706.5 GI: 161621259
GenBank FASTA Graphics Related Sequences

☐ 3. Mus musculus NAD(P)H:quinone oxidoreductase 1 (**Nqo1**) gene, promoter region and exon 1
1,069 bp linear DNA
Accession: AY425712.1 GI: 37694057
GenBank FASTA Graphics Related Sequences

☐ 4. Mus musculus chromosome 8, whole genome shotgun sequence
130,604,219 bp linear DNA
Accession: CM000216.2 GI: 74229904
GenBank FASTA Graphics

☐ 8. Homo sapiens NAD(P)H:quinone oxireductase (**NQO1**) gene, complete cds
7,447 bp linear DNA
Accession: AH005427.2 GI: 1049010536
GenBank FASTA Graphics

☐ 6. Mus musculus strain C57BL/6J chromosome 8 genomic contig, GRCm38.p1 C57BL/6J MMCHR8_CTG11
56,658,466 bp linear DNA

Filter your results:

All (30)
Bacteria (8)
INSDC (GenBank) (12)
mRNA (8)
RefSeq (18)

Top Organisms [Tree]

Mus musculus	(17)
Homo sapiens	(5)
Azoarcus sp. BH72	(2)
Neisseria meningitidis Z2491	(2)
Stenotrophomonas maltophilia K279a	(2)
All other taxa	(2)

More...

Find related data

Database: Select

Search details

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nqo1[All Fields] AND
("Mus"[Organism]
OR "Mus"[Organism] OR mus
[All Fields])
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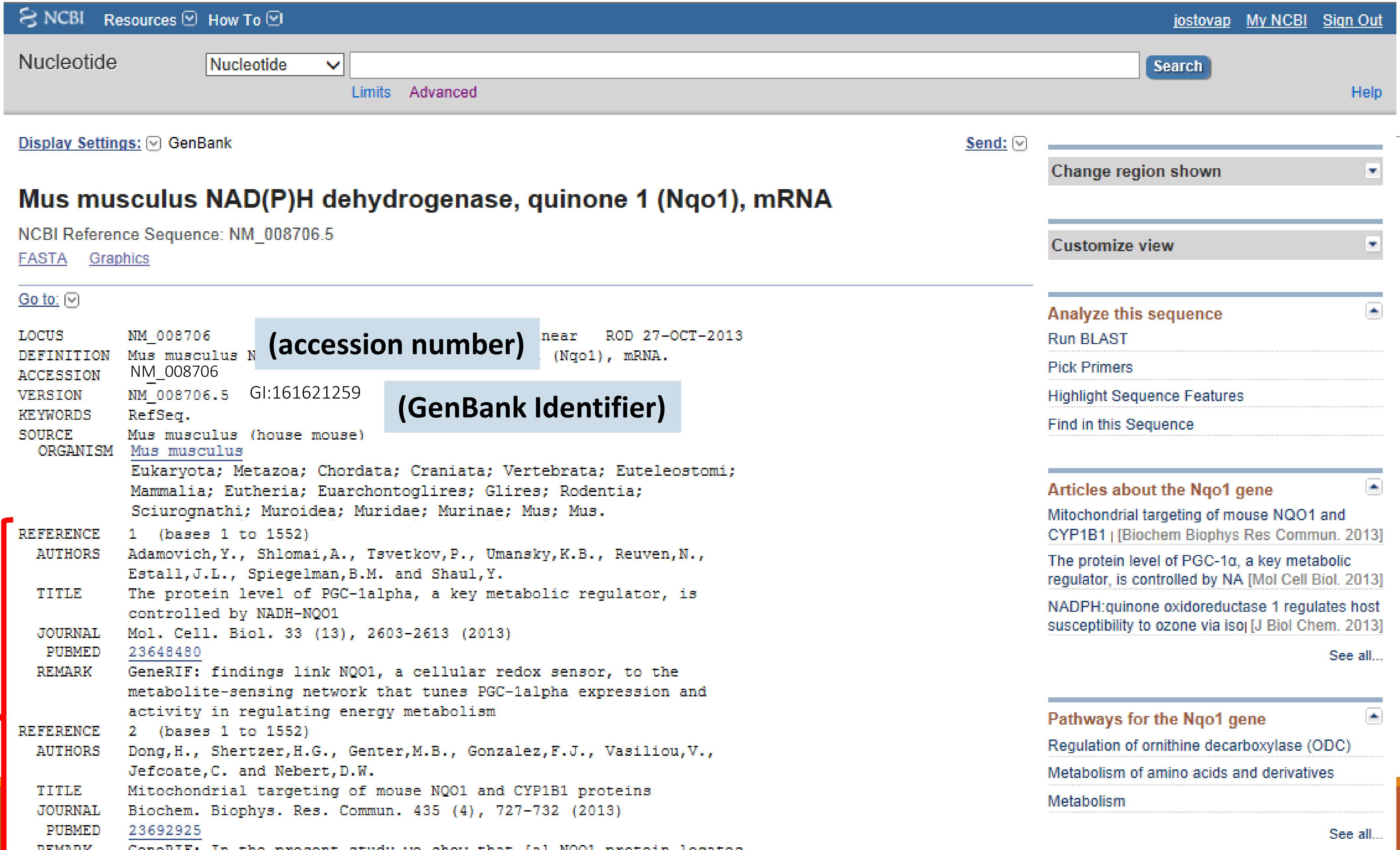
„GenBank flatfile“



Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA

NCBI Reference Sequence: NM_008706.5

(accession number)

(GenBank Identifier)

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DEFINITION  Mus musculus N                           (Nqo1), mRNA.
ACCESSION   NM_008706
VERSION     NM_008706.5   GI:161621259
KEYWORDS    RefSeq.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus; Mus.
REFERENCE   1  (bases 1 to 1552)
  AUTHORS   Adamovich,Y., Shlomai,A., Tsvetkov,P., Umansky,K.B., Reuven,N.,
            Estall,J.L., Spiegelman,B.M. and Shaul,Y.
  TITLE     The protein level of PGC-1alpha, a key metabolic regulator, is
            controlled by NADH-NQO1
  JOURNAL   Mol. Cell. Biol. 33 (13), 2603-2613 (2013)
   PUBMED   23648480
  REMARK    GeneRIF: findings link NQO1, a cellular redox sensor, to the
            metabolite-sensing network that tunes PGC-1alpha expression and
            activity in regulating energy metabolism
REFERENCE   2  (bases 1 to 1552)
  AUTHORS   Dong,H., Shertzer,H.G., Genter,M.B., Gonzalez,F.J., Vasiliou,V.,
            Jefcoate,C. and Nebert,D.W.
  TITLE     Mitochondrial targeting of mouse NQO1 and CYP1B1 proteins
  JOURNAL   Biochem. Biophys. Res. Commun. 435 (4), 727-732 (2013)
   PUBMED   23692925
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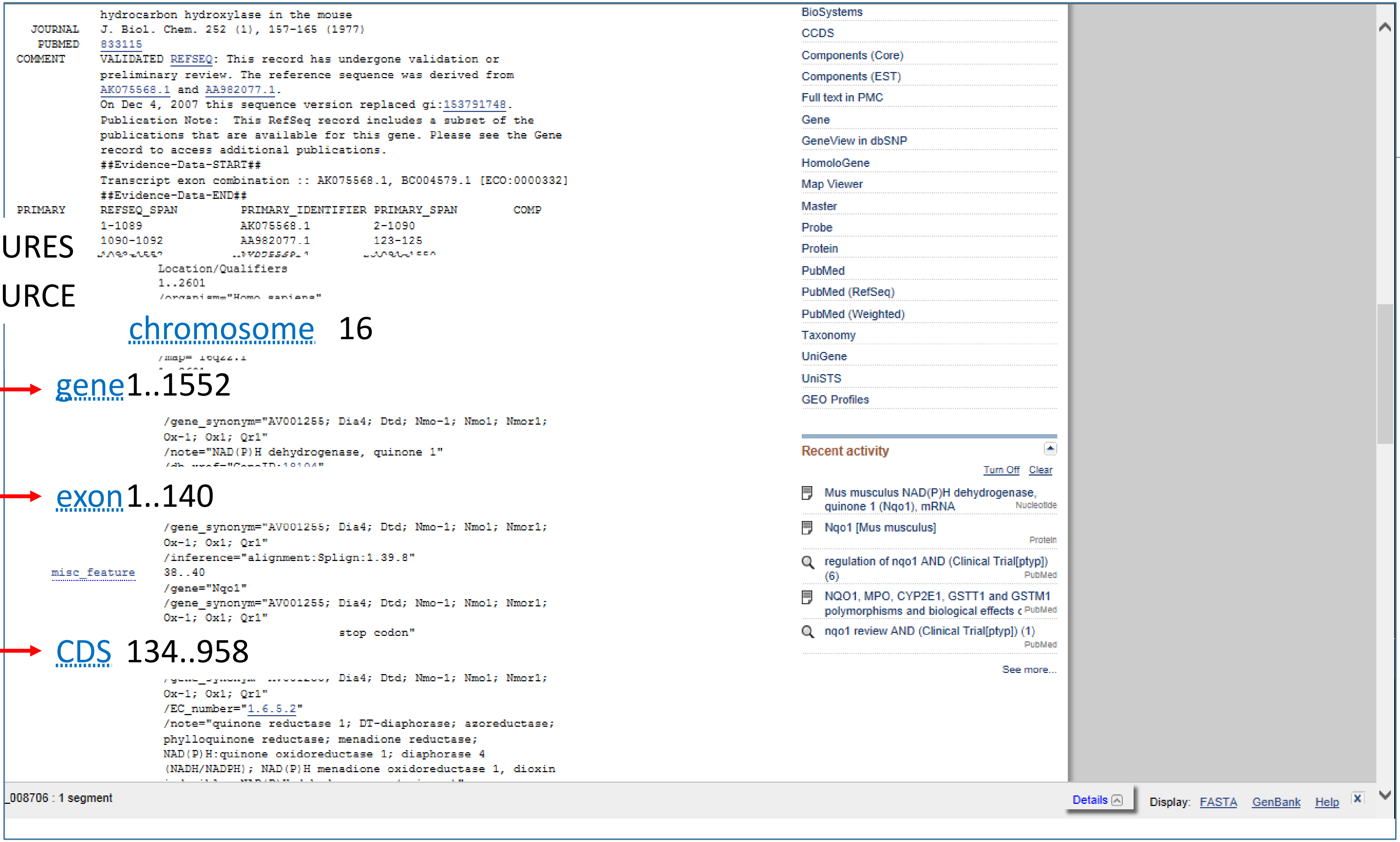

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            hydrocarbon hydroxylase in the mouse
  JOURNAL   J. Biol. Chem. 252 (1), 157-165 (1977)
   PUBMED   833115
COMMENT     VALIDATED REFSEQ: This record has undergone validation or
            preliminary review. The reference sequence was derived from
            AK075568.1 and AA982077.1.
            On Dec 4, 2007 this sequence version replaced gi:153791748.
            Publication Note:  This RefSeq record includes a subset of the
            publications that are available for this gene. Please see the Gene
            record to access additional publications.
            ##Evidence-Data-START##
            Transcript exon combination :: AK075568.1, BC004579.1 [ECO:0000332]
            ##Evidence-Data-END##
PRIMARY     REFSEQ_SPAN         PRIMARY_IDENTIFIER PRIMARY_SPAN        COMP
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            1090-1092           AA982077.1         123-125
                    Location/Qualifiers
                    1..2601
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FEATURES

SOURCE

chromosome 16

gene1..1552

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exon1..140

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CDS 134..958

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                     Ox-1; Ox1; Qr1"
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                     /note="quinone reductase 1; DT-diaphorase; azoreductase;
                     phylloquinone reductase; menadione reductase;
                     NAD(P)H:quinone oxidoreductase 1; diaphorase 4
                     (NADH/NADPH); NAD(P)H menadione oxidoreductase 1, dioxin
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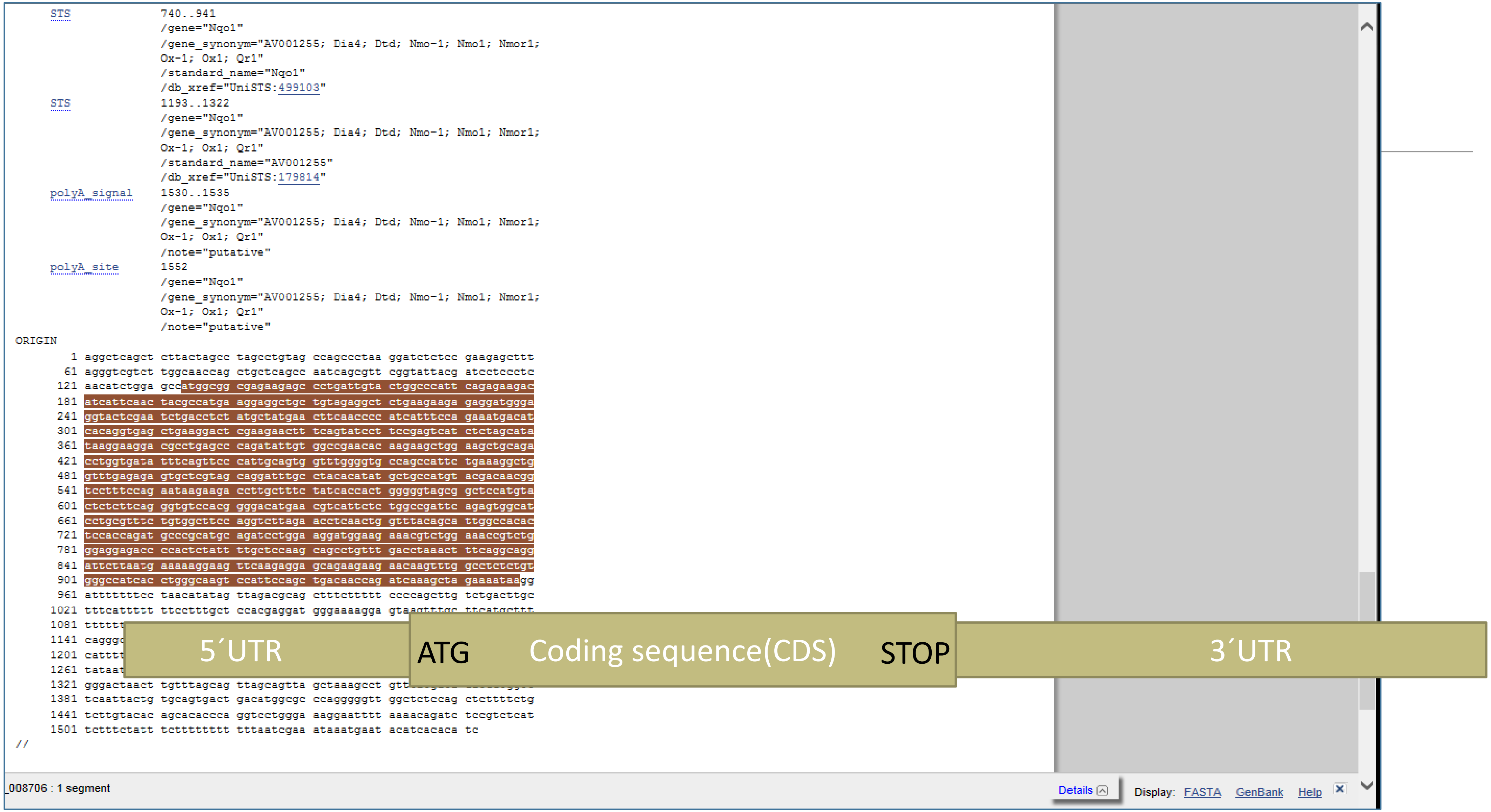

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                     /db_xref="UniSTS:499103"
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                     /gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmo1; Nmor1;
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     polyA_site      1552
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                     Ox-1; Ox1; Qr1"
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ORIGIN
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       61 agggtcgtct tggcaaccag ctgctcagcc aatcagcgtt cggtattacg atcctccctc
      121 aacatctgga gccatggcgg cgagaagagc cctgattgta ctggcccatt cagagaagac
      181 atcattcaac tacgccatga aggaggctgc tgtagaggct ctgaagaaga gaggatggga
      241 ggtactcgaa tctgacctct atgctatgaa cttcaacccc atcatttcca gaaatgacat
      301 cacaggtgag ctgaaggact cgaagaactt tcagtatcct tccgagtcat ctctagcata
      361 taaggaagga cgcctgagcc cagatattgt ggccgaacac aagaagctgg aagctgcaga
      421 cctggtgata tttcagttcc cattgcagtg gtttggggtg ccagccattc tgaaaggctg
      481 gtttgagaga gtgctcgtag caggatttgc ctacacatat gctgccatgt acgacaacgg
      541 tcctttccag aataagaaga ccttgctttc tatcaccact gggggtagcg gctccatgta
      601 ctctcttcag ggtgtccacg gggacatgaa cgtcattctc tggccgattc agagtggcat
      661 cctgcgtttc tgtggcttcc aggtcttaga acctcaactg gtttacagca ttggccacac
      721 tccaccagat gcccgcatgc agatcctgga aggatggaag aaacgtctgg aaaccgtctg
      781 ggaggagacc ccactctatt ttgctccaag cagcctgttt gacctaaact ttcaggcagg
      841 attcttaatg aaaaaggaag ttcaagagga gcagaagaag aacaagtttg gcctctctgt
      901 gggccatcac ctgggcaagt ccattccagc tgacaaccag atcaaagcta gaaaataagg
      961 attttttcc taacatatag ttagacgcag ctttcttttt ccccagcttg tctgacttgc
     1021 tttcattttt ttcctttgct ccacgaggat gggaaaagga gtaagtttgc ttcatgcttt
     1081 tttttt
     1141 cagggc
     1201 catttt
     1261 tataat
     1321 gggactaact tgtttagcag ttagcagtta gctaaagcct gtt
     1381 tcaattactg tgcagtgact gacatggcgc ccaggggggtt ggctctccag ctcttttctg
     1441 tcttgtacac agcacaccca ggtcctggga aaggaatttt aaaacagatc tccgtctcat
     1501 tctttctatt tctttttttt tttaatcgaa ataaatgaat acatcacaca tc
//
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_008706 : 1 segment

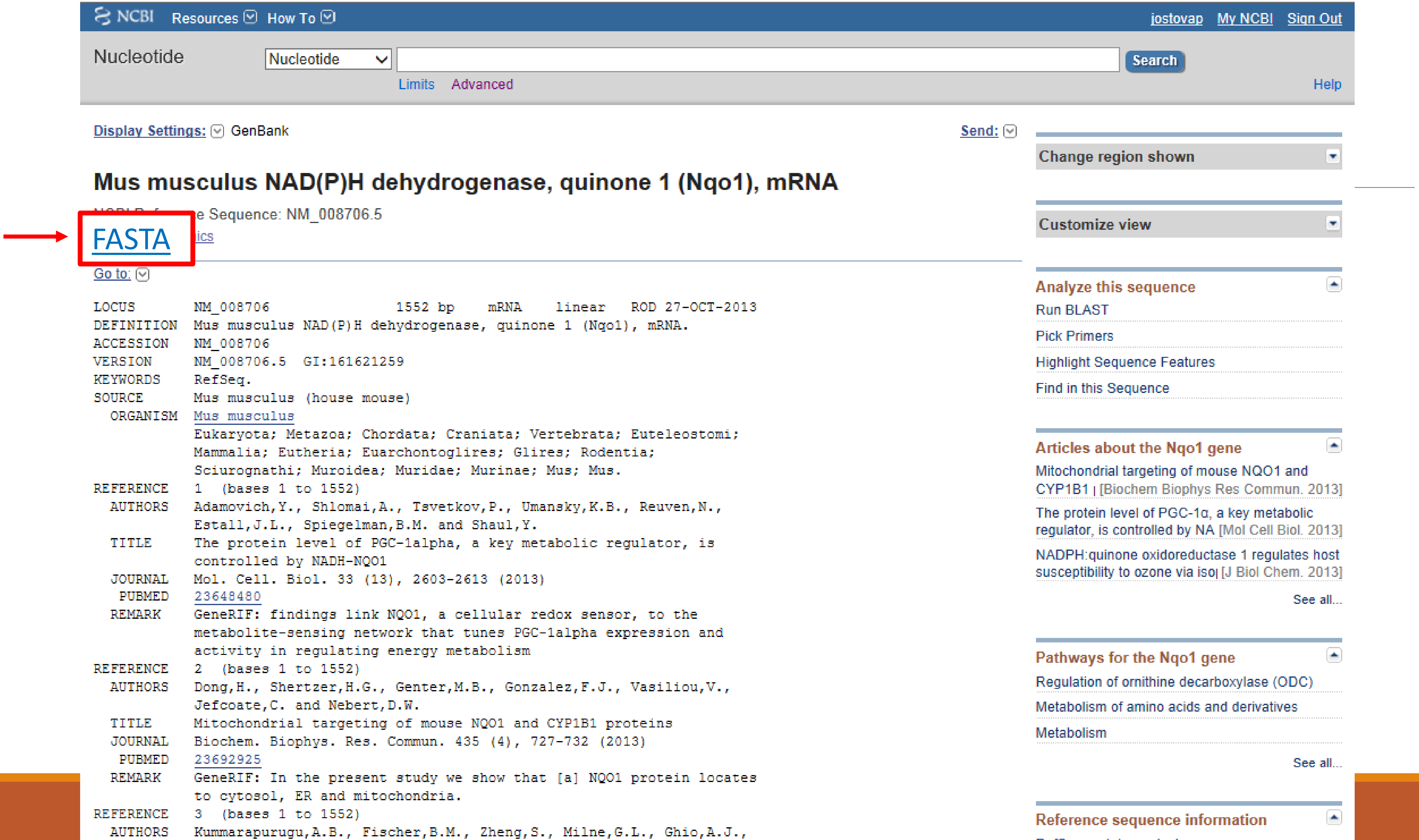
5´UTR

ATG

Coding sequence(CDS)

STOP

3´UTR



Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA

e Sequence: NM_008706.5

FASTA

ics

Go to:

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DEFINITION  Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA.
ACCESSION   NM_008706
VERSION     NM_008706.5  GI:161621259
KEYWORDS    RefSeq.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus; Mus.
REFERENCE   1  (bases 1 to 1552)
  AUTHORS   Adamovich,Y., Shlomai,A., Tsvetkov,P., Umansky,K.B., Reuven,N.,
            Estall,J.L., Spiegelman,B.M. and Shaul,Y.
  TITLE     The protein level of PGC-1alpha, a key metabolic regulator, is
            controlled by NADH-NQO1
  JOURNAL   Mol. Cell. Biol. 33 (13), 2603-2613 (2013)
   PUBMED   23648480
  REMARK    GeneRIF: findings link NQO1, a cellular redox sensor, to the
            metabolite-sensing network that tunes PGC-1alpha expression and
            activity in regulating energy metabolism
REFERENCE   2  (bases 1 to 1552)
  AUTHORS   Dong,H., Shertzer,H.G., Genter,M.B., Gonzalez,F.J., Vasiliou,V.,
            Jefcoate,C. and Nebert,D.W.
  TITLE     Mitochondrial targeting of mouse NQO1 and CYP1B1 proteins
  JOURNAL   Biochem. Biophys. Res. Commun. 435 (4), 727-732 (2013)
   PUBMED   23692925
  REMARK    GeneRIF: In the present study we show that [a] NQO1 protein locates
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REFERENCE   3  (bases 1 to 1552)
  AUTHORS   Kummarapurugu,A.B., Fischer,B.M., Zheng,S., Milne,G.L., Ghio,A.J.,
```

Analyze this sequence

- Run BLAST
- Pick Primers
- Highlight Sequence Features
- Find in this Sequence

Articles about the Nqo1 gene

- Mitochondrial targeting of mouse NQO1 and CYP1B1 | [Biochem Biophys Res Commun. 2013]
- The protein level of PGC-1α, a key metabolic regulator, is controlled by NA [Mol Cell Biol. 2013]
- NADPH:quinone oxidoreductase 1 regulates host susceptibility to ozone via iso| [J Biol Chem. 2013]

See all...

Pathways for the Nqo1 gene

- Regulation of ornithine decarboxylase (ODC)
- Metabolism of amino acids and derivatives
- Metabolism

See all...

Reference sequence information

FASTA (and RAW) format

FASTA is the name of a popular sequence alignment-and-database-scanning program created by

W.R. Pearson and D.J. Lipman in 1988

The sequences used by FASTA have to obey the following format:

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>NQO1_mus
AGGCTCAGCTCTTACTAGCCTAGCCTGTA
GCCAGCCCTAAGGATCTCTCCGAAGAGCT
AATGTCGG
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```
AGGCTCAGCTCTTACTAGCCTAGCCTGTA
GCCAGCCCTAAGGATCTCTCCGAAGAGCT
AATGTCGG
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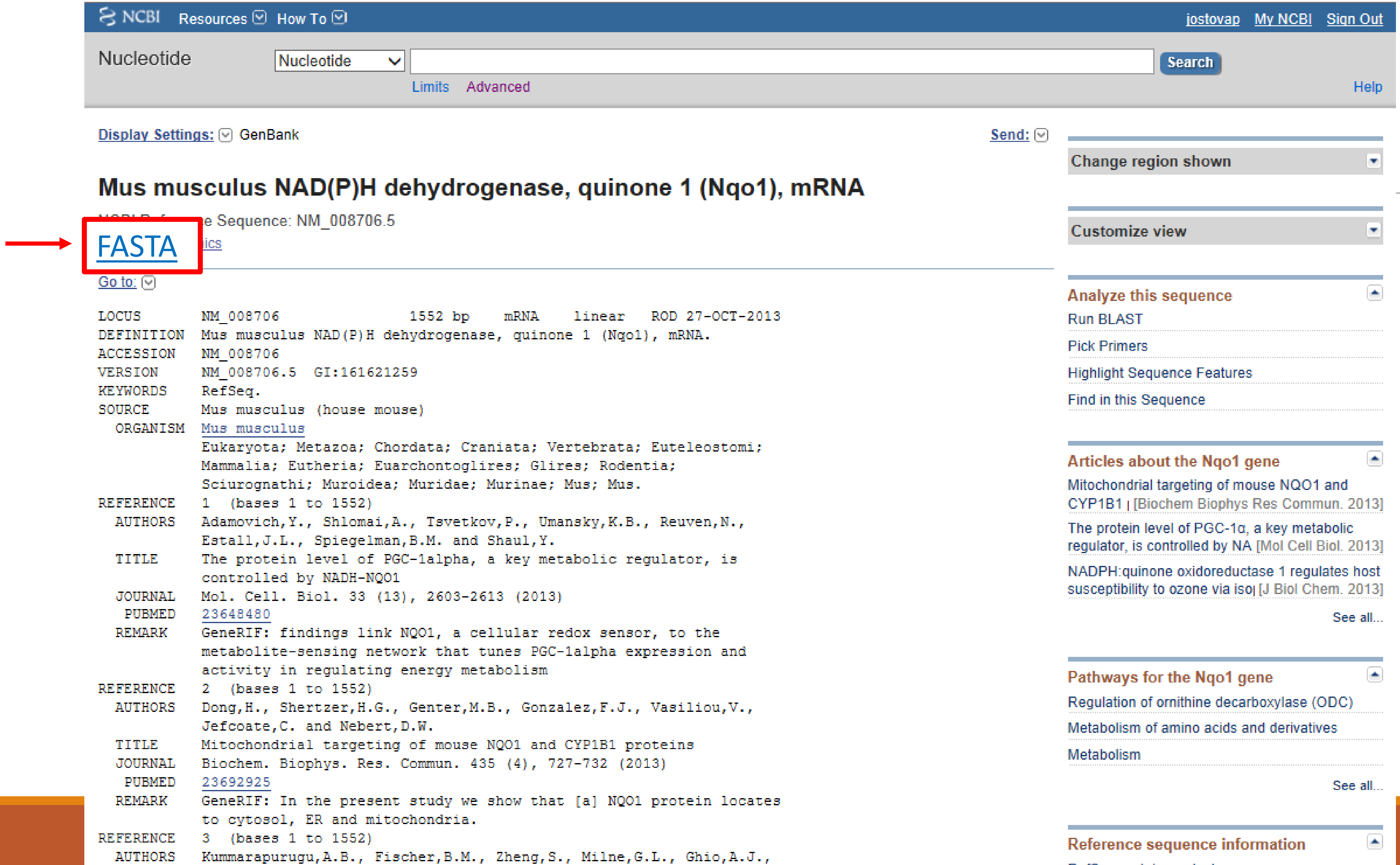
The line starting with **>** (the definition line) contains a unique identifier followed by an optional short definition.

The lines that follow it contain the DNA or protein sequence (in one-letter code) until the next > character in the file indicates the beginning of a new sequence.



Display Settings: GenBank

Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA

e Sequence: NM_008706.5

FASTA

ics

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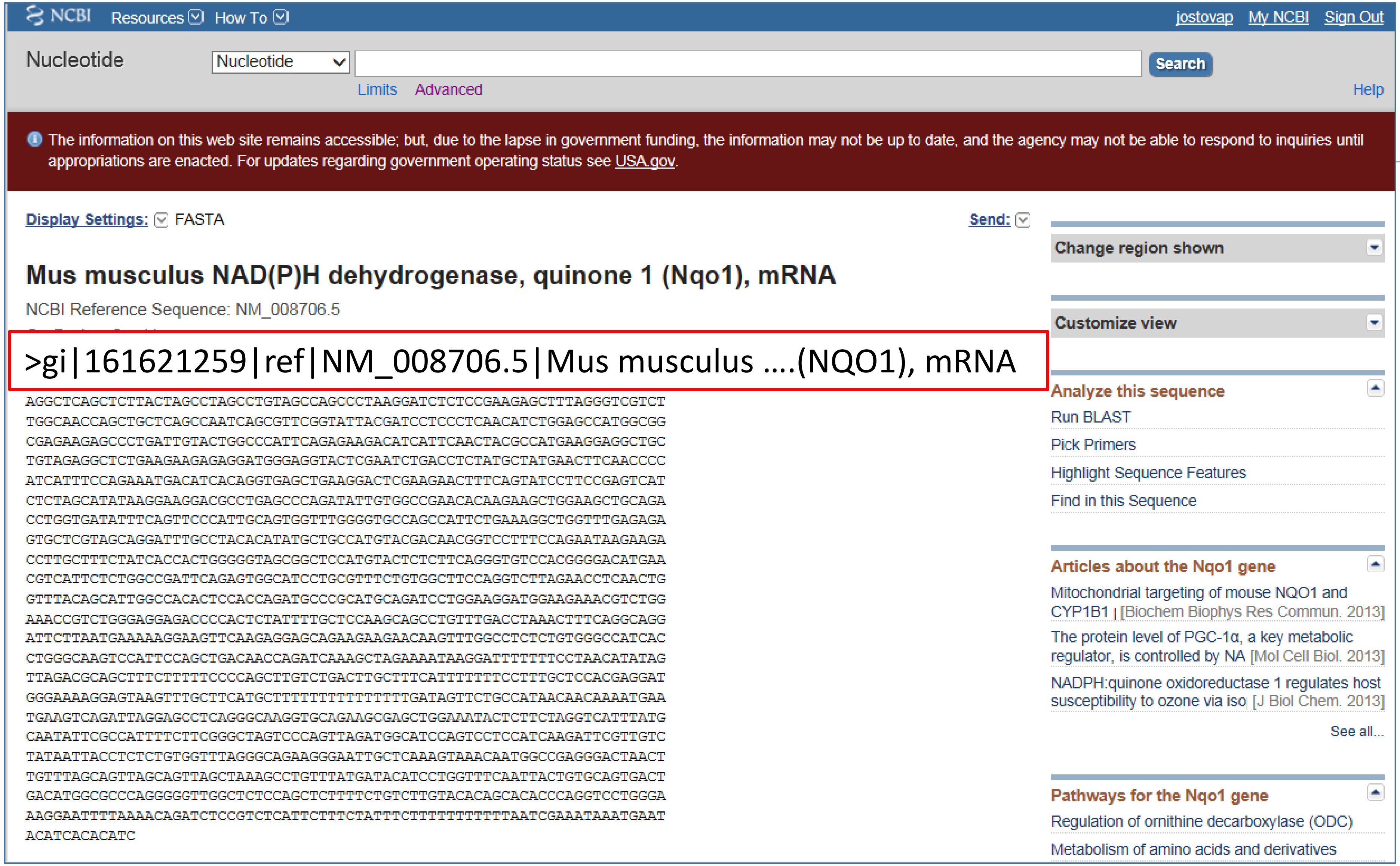

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Display Settings: FASTA

Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA

NCBI Reference Sequence: NM_008706.5

fasta

>gi|161621259|ref|NM_008706.5|Mus musculus ….(NQO1), mRNA

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```

Analyze this sequence

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Find in this Sequence

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See all...

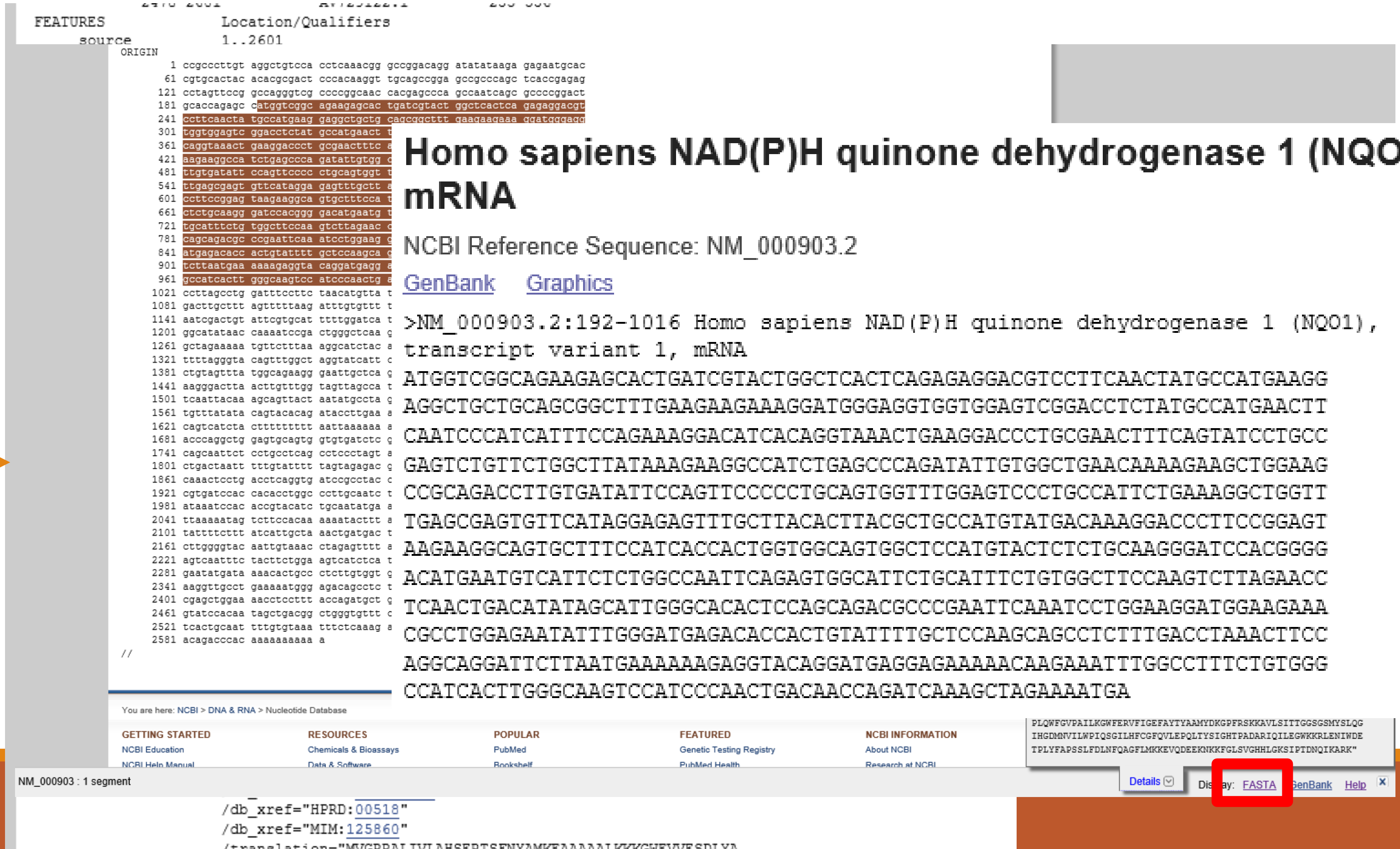
Pathways for the Nqo1 gene

Regulation of ornithine decarboxylase (ODC)

Metabolism of amino acids and derivatives

NCBI/coding sequence (CDS)

Select CDS → in brown (FASTA bottom right corner)



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Homo sapiens NAD(P)H quinone dehydrogenase 1 (NQO1), transcript variant 1, mRNA

NCBI Reference Sequence: NM_000903.2

GenBank Graphics

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transcript variant 1, mRNA
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You are here: NCBI > DNA & RNA > Nucleotide Database

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Data & Software

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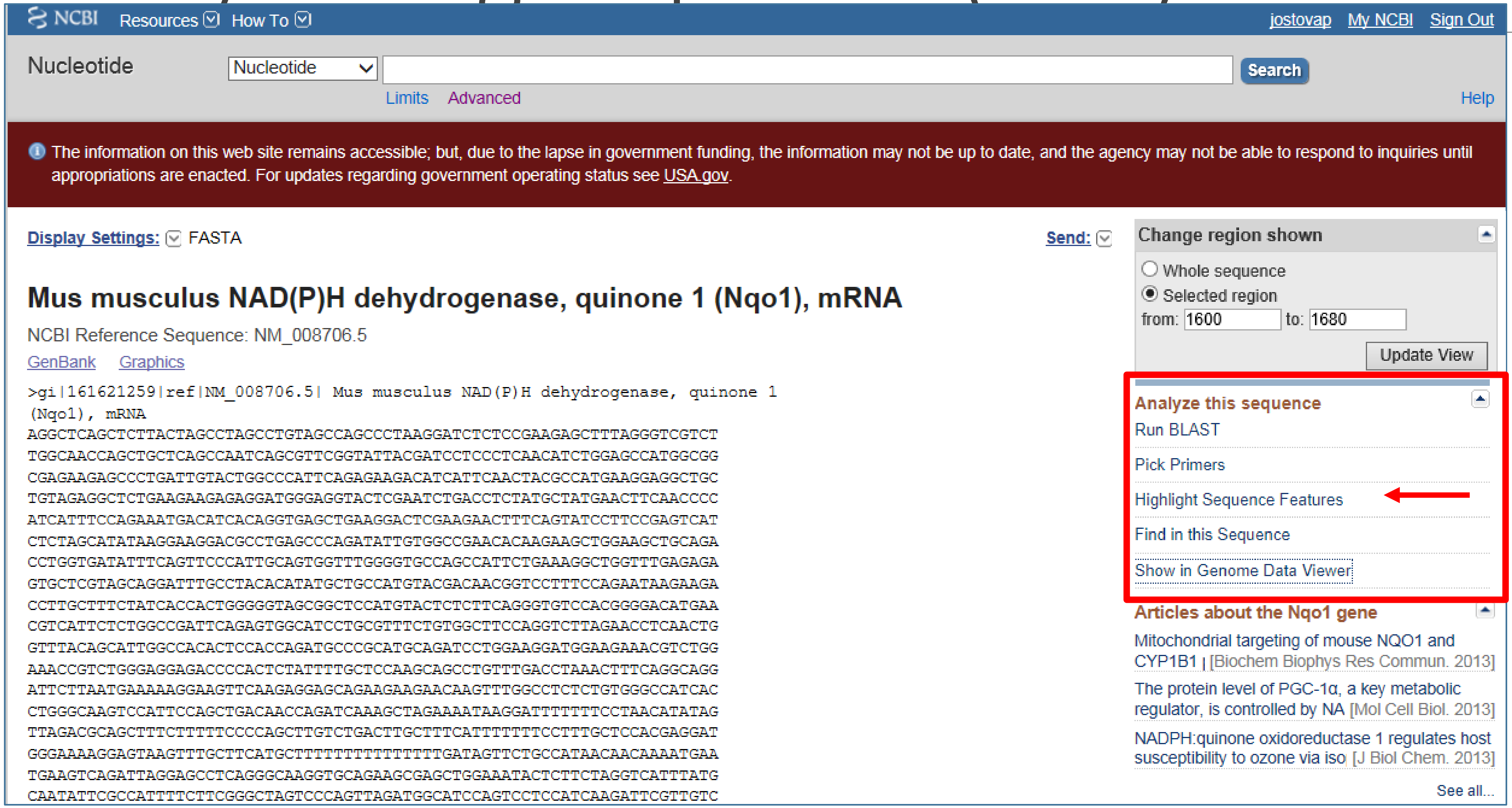
NCBI/coding sequence (CDS)



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Send:

Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA

NCBI Reference Sequence: NM_008706.5

GenBank Graphics

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(Nqo1), mRNA
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Change region shown

○ Whole sequence
● Selected region
from: 1600 to: 1680

Update View

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Run BLAST

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Show in Genome Data Viewer

Articles about the Nqo1 gene

Mitochondrial targeting of mouse NQO1 and CYP1B1 [Biochem Biophys Res Commun. 2013]

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See all...

In the bottom line:

COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: https://www.coronavirus.gov .
Get the latest research from NIH: https://www.nih.gov/coronavirus.

Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA

NCBI Reference Sequence: NM_008706.5

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>NM_008706.5:141-305 Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA
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ATCATTTCCAGAAATGACATCACAG
```

Change region shown

○ Whole sequence
● Selected region
from: 141 to: 305

Analyze this sequence

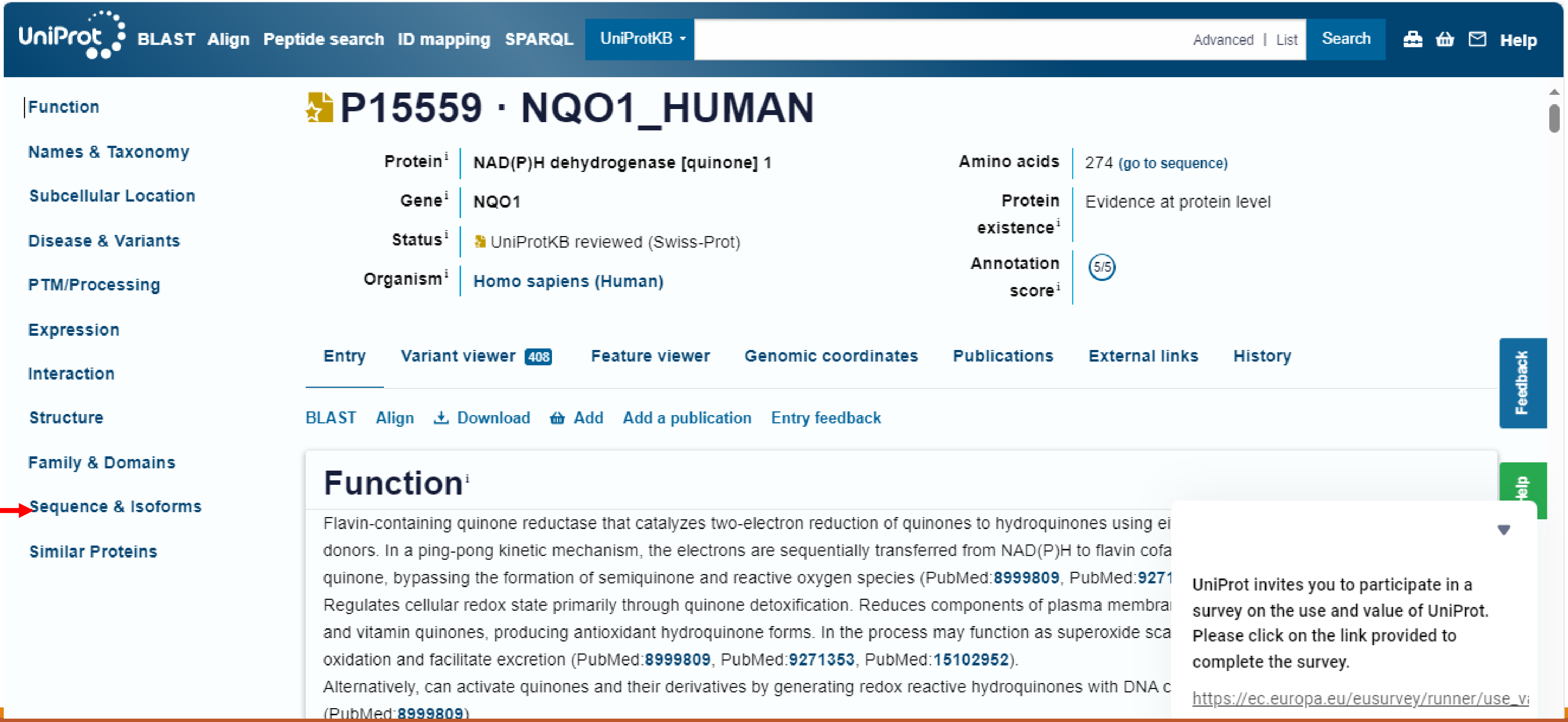
Articles about the Nqo1 gene

Practical part

Find „your“ nucleotide sequence.

look for CDS

Link to nucleotides from UniProt



P15559 · NQO1_HUMAN

Protein	NAD(P)H dehydrogenase [quinone] 1
Gene	NQO1
Status	UniProtKB reviewed (Swiss-Prot)
Organism	Homo sapiens (Human)
Amino acids	274 (go to sequence)
Protein existence	Evidence at protein level
Annotation score	5/5

Function

Flavin-containing quinone reductase that catalyzes two-electron reduction of quinones to hydroquinones using ei
donors. In a ping-pong kinetic mechanism, the electrons are sequentially transferred from NAD(P)H to flavin cofa
quinone, bypassing the formation of semiquinone and reactive oxygen species (PubMed:8999809, PubMed:9271
Regulates cellular redox state primarily through quinone detoxification. Reduces components of plasma membra
and vitamin quinones, producing antioxidant hydroquinone forms. In the process may function as superoxide sca
oxidation and facilitate excretion (PubMed:8999809, PubMed:9271353, PubMed:15102952).
Alternatively, can activate quinones and their derivatives by generating redox reactive hydroquinones with DNA c
(PubMed:8999809)

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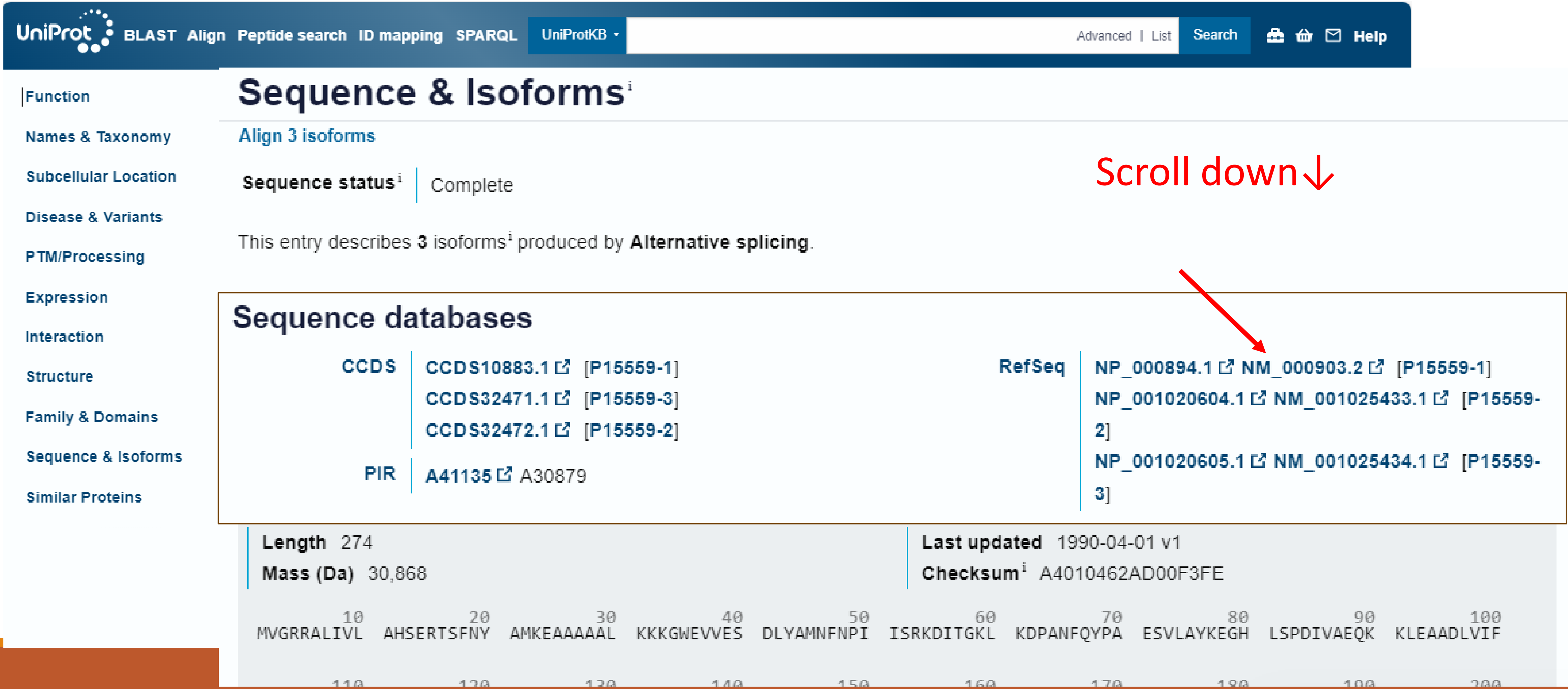
https://ec.europa.eu/eusurvey/runner/use_v

Link to nucleotides from UniProt



Sequence & Isoforms

Align 3 isoforms

Sequence status Complete

This entry describes **3** isoforms produced by **Alternative splicing**.

Sequence databases

CCDS	CCDS10883.1 [P15559-1] CCDS32471.1 [P15559-3] CCDS32472.1 [P15559-2]	**RefSeq**	NP_000894.1 NM_000903.2 [P15559-1] NP_001020604.1 NM_001025433.1 [P15559-2] NP_001020605.1 NM_001025434.1 [P15559-3]
PIR	A41135 A30879		

Length 274

Mass (Da) 30,868

Last updated 1990-04-01 v1

Checksum A4010462AD00F3FE

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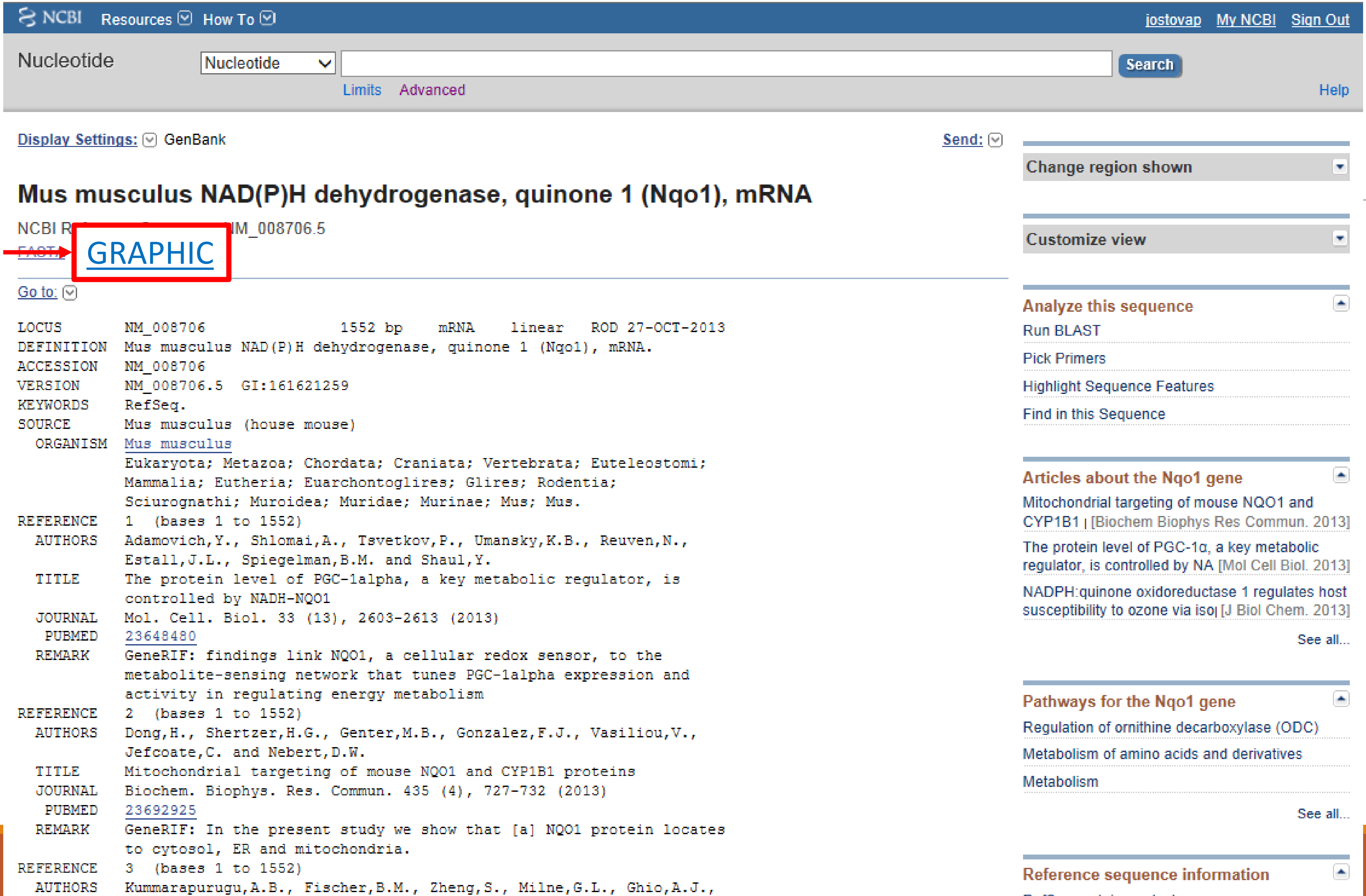
Scroll down↓

Practical part

Find „your“ nucleotide sequence.

Try to link through Uniprot

and check if the accession number you found is the same here



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NCBI R IM_008706.5

FASTA

GRAPHIC

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KEYWORDS    RefSeq.
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  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 1552)
  AUTHORS   Adamovich,Y., Shlomai,A., Tsvetkov,P., Umansky,K.B., Reuven,N.,
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            to cytosol, ER and mitochondria.
REFERENCE   3  (bases 1 to 1552)
  AUTHORS   Kummarapurugu,A.B., Fischer,B.M., Zheng,S., Milne,G.L., Ghio,A.J.,
```

Analyze this sequence
- Run BLAST
- Pick Primers
- Highlight Sequence Features
- Find in this Sequence

Articles about the Nqo1 gene
- Mitochondrial targeting of mouse NQO1 and CYP1B1 [Biochem Biophys Res Commun. 2013]
- The protein level of PGC-1α, a key metabolic regulator, is controlled by NA [Mol Cell Biol. 2013]
- NADPH:quinone oxidoreductase 1 regulates host susceptibility to ozone via iso [J Biol Chem. 2013]

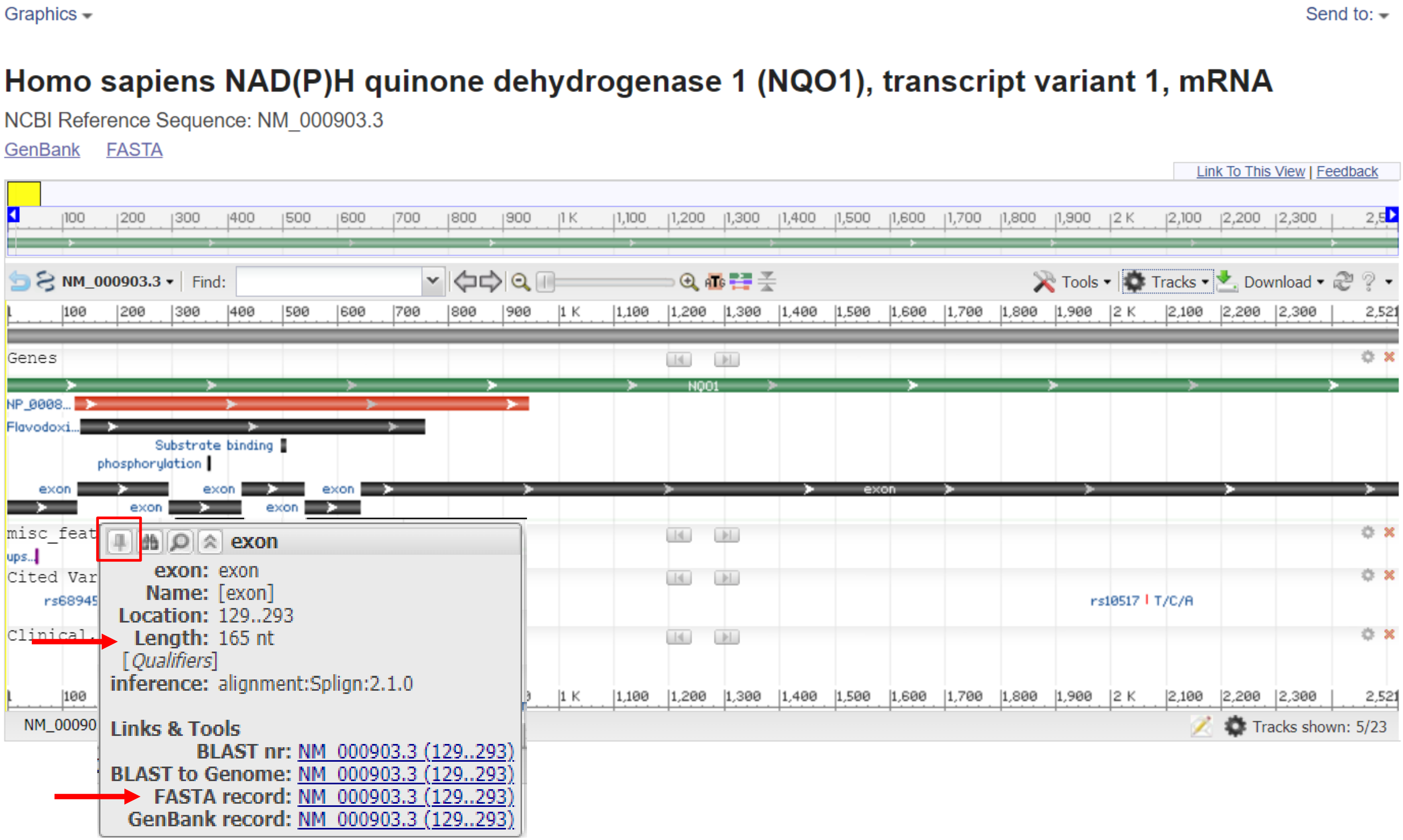
See all...

Pathways for the Nqo1 gene
- Regulation of ornithine decarboxylase (ODC)
- Metabolism of amino acids and derivatives
- Metabolism

See all...

Reference sequence information

NCBI/Graphic



Homo sapiens NAD(P)H quinone dehydrogenase 1 (NQO1), transcript variant 1, mRNA

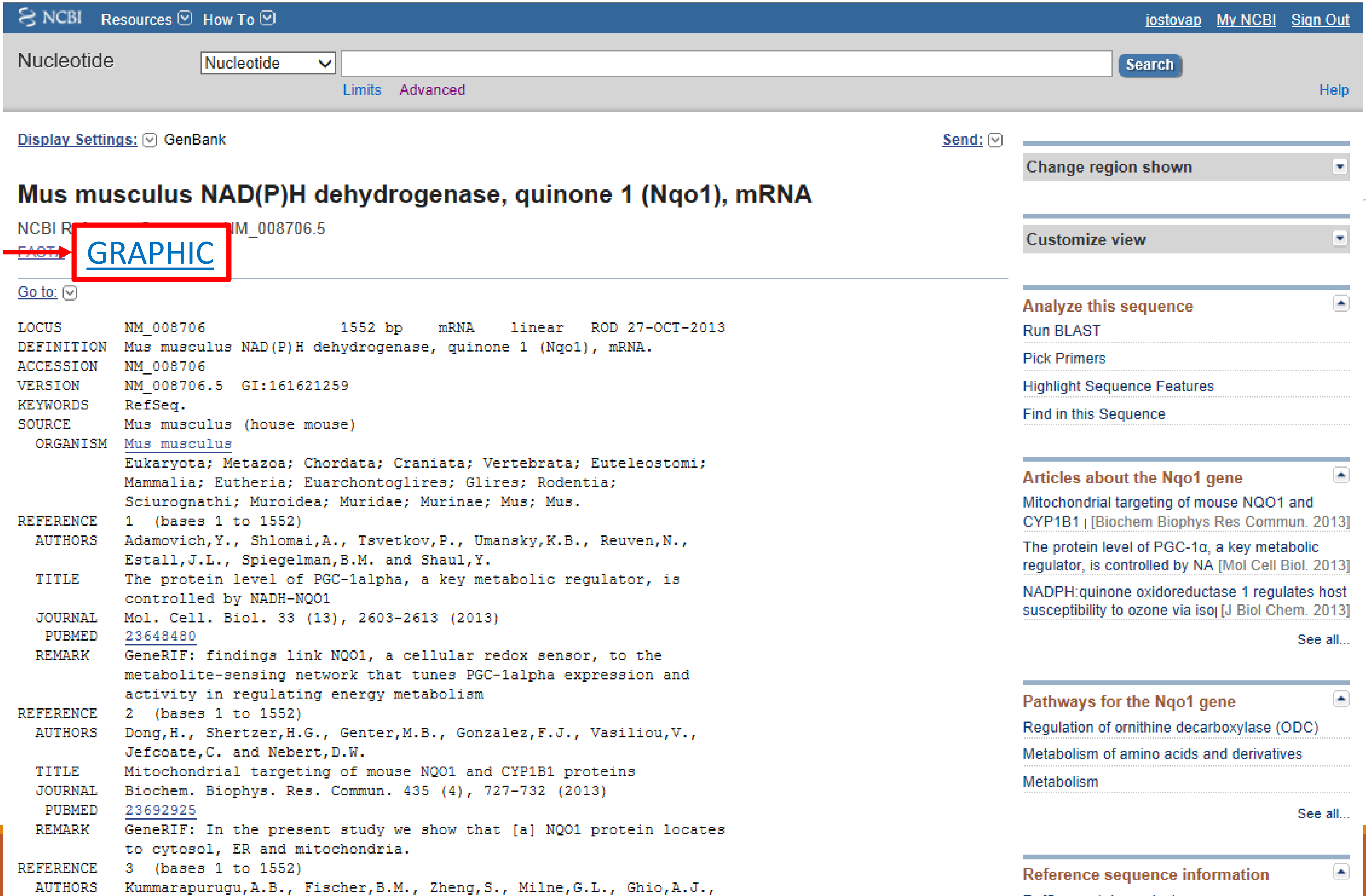
NCBI Reference Sequence: NM_000903.3

GenBank FASTA

exon

exon: exon
Name: [exon]
Location: 129..293
Length: 165 nt
[*Qualifiers*]
inference: alignment:Splign:2.1.0

Links & Tools
BLAST nr: NM_000903.3 (129..293)
BLAST to Genome: NM_000903.3 (129..293)
FASTA record: NM_000903.3 (129..293)
GenBank record: NM_000903.3 (129..293)



Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA

NCBI R… NM_008706.5

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LOCUS       NM_008706               1552 bp    mRNA    linear   ROD 27-OCT-2013
DEFINITION  Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA.
ACCESSION   NM_008706
VERSION     NM_008706.5  GI:161621259
KEYWORDS    RefSeq.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus; Mus.
REFERENCE   1  (bases 1 to 1552)
  AUTHORS   Adamovich,Y., Shlomai,A., Tsvetkov,P., Umansky,K.B., Reuven,N.,
            Estall,J.L., Spiegelman,B.M. and Shaul,Y.
  TITLE     The protein level of PGC-1alpha, a key metabolic regulator, is
            controlled by NADH-NQO1
  JOURNAL   Mol. Cell. Biol. 33 (13), 2603-2613 (2013)
   PUBMED   23648480
  REMARK    GeneRIF: findings link NQO1, a cellular redox sensor, to the
            metabolite-sensing network that tunes PGC-1alpha expression and
            activity in regulating energy metabolism
REFERENCE   2  (bases 1 to 1552)
  AUTHORS   Dong,H., Shertzer,H.G., Genter,M.B., Gonzalez,F.J., Vasiliou,V.,
            Jefcoate,C. and Nebert,D.W.
  TITLE     Mitochondrial targeting of mouse NQO1 and CYP1B1 proteins
  JOURNAL   Biochem. Biophys. Res. Commun. 435 (4), 727-732 (2013)
   PUBMED   23692925
  REMARK    GeneRIF: In the present study we show that [a] NQO1 protein locates
            to cytosol, ER and mitochondria.
REFERENCE   3  (bases 1 to 1552)
  AUTHORS   Kummarapurugu,A.B., Fischer,B.M., Zheng,S., Milne,G.L., Ghio,A.J.,
```

Analyze this sequence
- Run BLAST
- Pick Primers
- Highlight Sequence Features
- Find in this Sequence

Articles about the Nqo1 gene
- Mitochondrial targeting of mouse NQO1 and CYP1B1 [Biochem Biophys Res Commun. 2013]
- The protein level of PGC-1α, a key metabolic regulator, is controlled by NA [Mol Cell Biol. 2013]
- NADPH:quinone oxidoreductase 1 regulates host susceptibility to ozone via iso [J Biol Chem. 2013]

See all...

Pathways for the Nqo1 gene
- Regulation of ornithine decarboxylase (ODC)
- Metabolism of amino acids and derivatives
- Metabolism

See all...

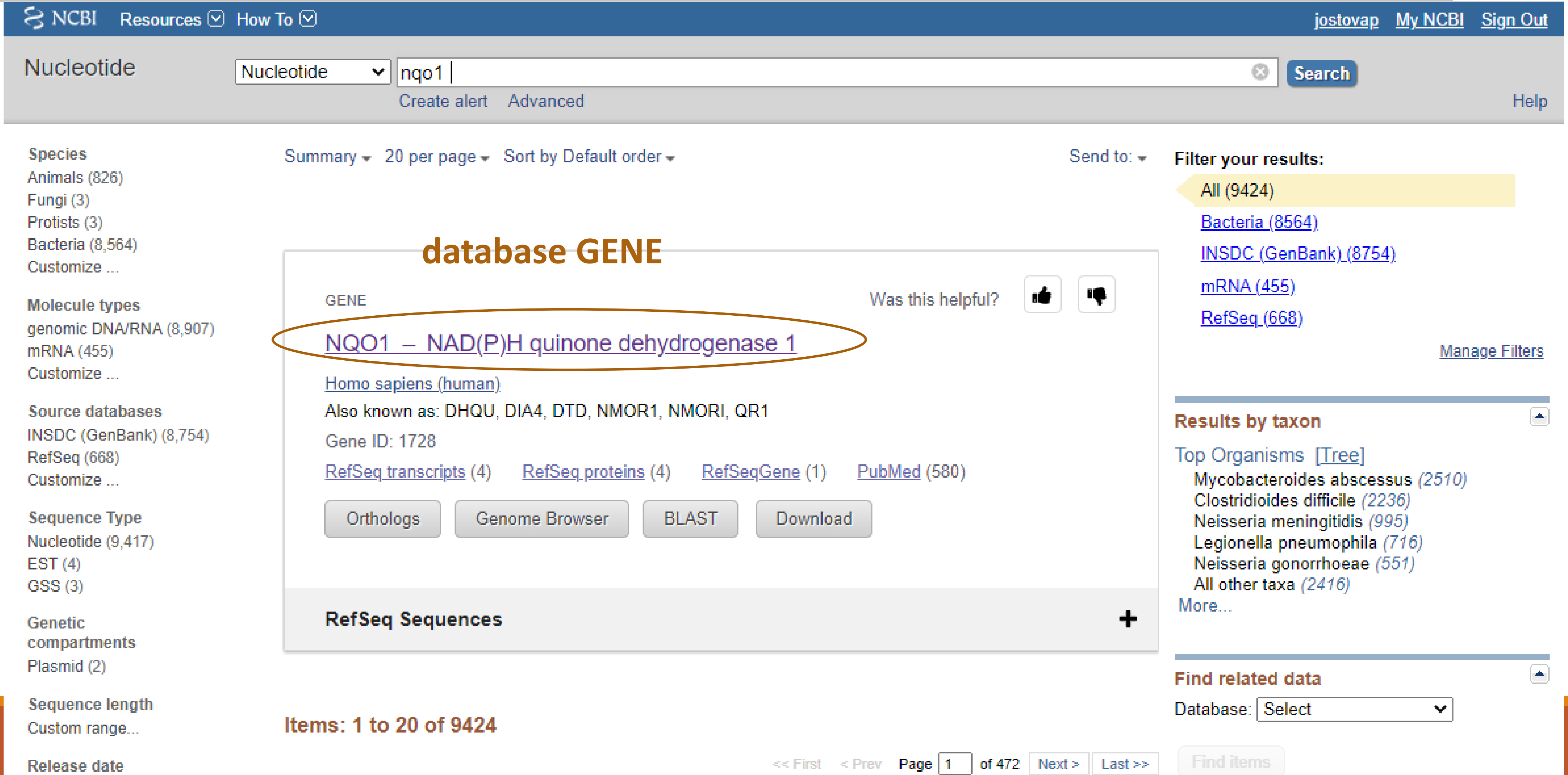
Reference sequence information

Practical part

Find „your“ nucleotide sequence.

Explore the graphic view

NCBI/Gene (secondary database)



Species
Animals (826)
Fungi (3)
Protists (3)
Bacteria (8,564)
Customize ...

Molecule types
genomic DNA/RNA (8,907)
mRNA (455)
Customize ...

Source databases
INSDC (GenBank) (8,754)
RefSeq (668)
Customize ...

Sequence Type
Nucleotide (9,417)
EST (4)
GSS (3)

Genetic compartments
Plasmid (2)

Sequence length
Custom range...

Release date

Summary 20 per page Sort by Default order Send to:

database GENE

GENE

Was this helpful?

NQO1 – NAD(P)H quinone dehydrogenase 1

Homo sapiens (human)
Also known as: DHQU, DIA4, DTD, NMOR1, NMORI, QR1
Gene ID: 1728
RefSeq transcripts (4) RefSeq proteins (4) RefSeqGene (1) PubMed (580)

RefSeq Sequences

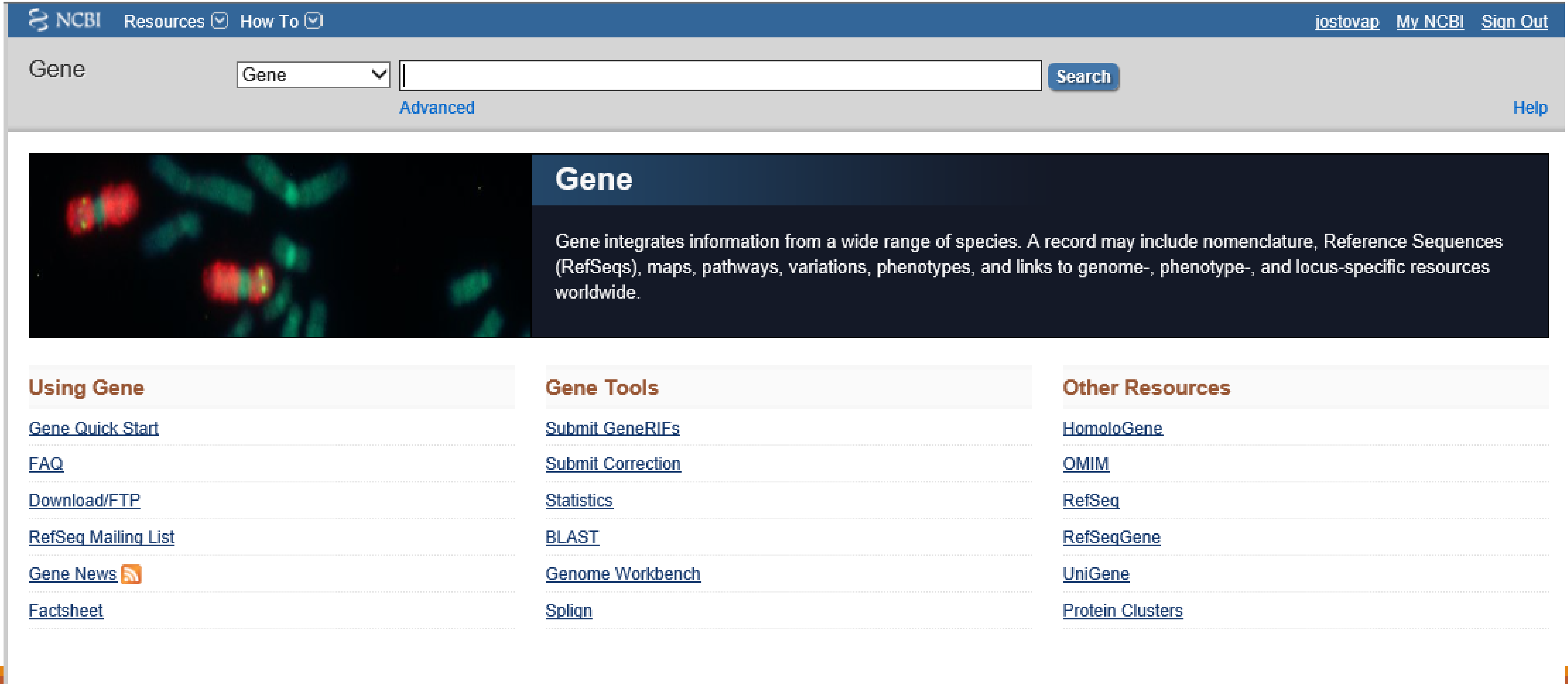
Items: 1 to 20 of 9424

Filter your results:
All (9424)
Bacteria (8564)
INSDC (GenBank) (8754)
mRNA (455)
RefSeq (668)
Manage Filters

Results by taxon
Top Organisms [Tree]
Mycobacteroides abscessus (2510)
Clostridioides difficile (2236)
Neisseria meningitidis (995)
Legionella pneumophila (716)
Neisseria gonorrhoeae (551)
All other taxa (2416)
More...

Find related data
Database: Select

NCBI/Gene (secondary database)



Gene

Gene integrates information from a wide range of species. A record may include nomenclature, Reference Sequences (RefSeqs), maps, pathways, variations, phenotypes, and links to genome-, phenotype-, and locus-specific resources worldwide.

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- BLAST
- Genome Workbench
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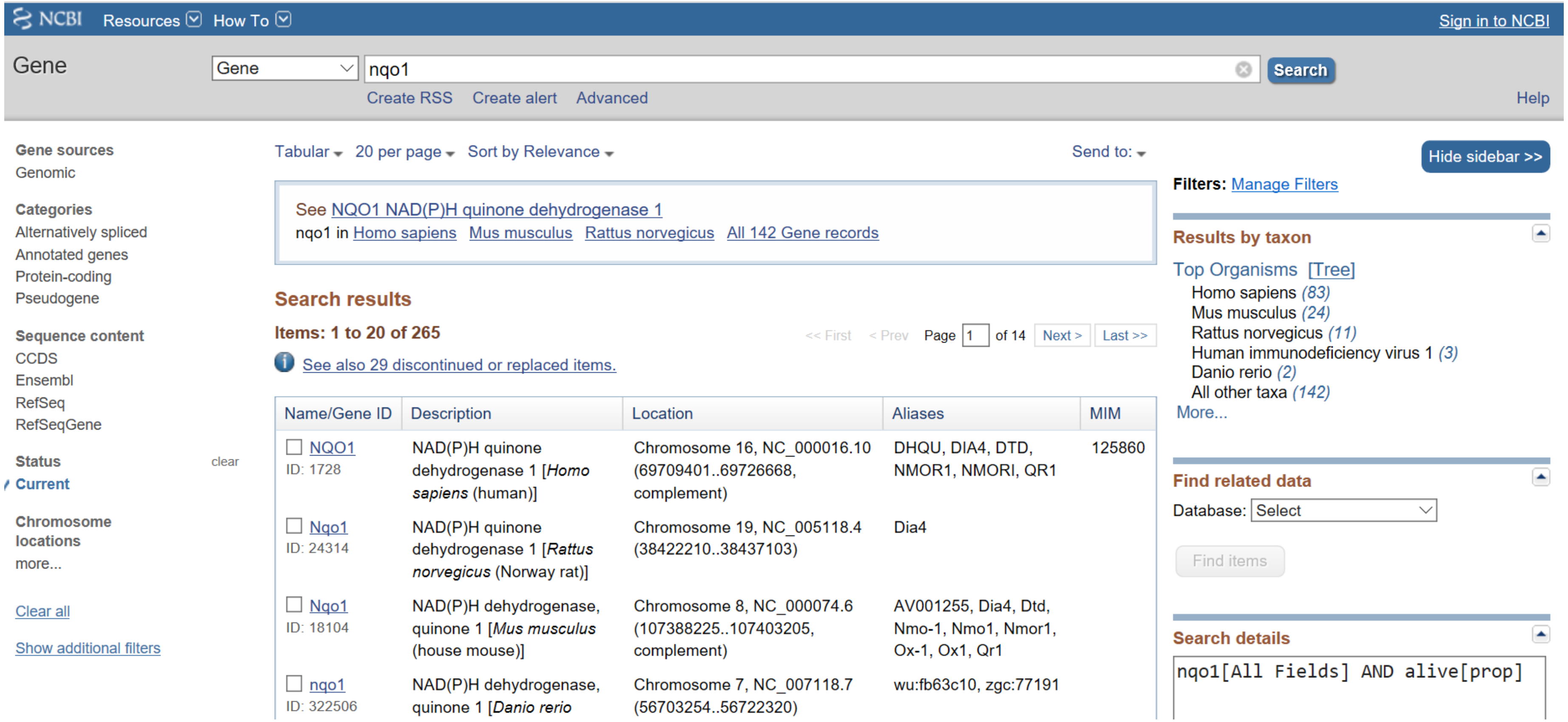
Other Resources
- HomoloGene
- OMIM
- RefSeq
- RefSeqGene
- UniGene
- Protein Clusters

NCBI/Gene



Gene: nqo1

Gene sources
Genomic

Categories
Alternatively spliced
Annotated genes
Protein-coding
Pseudogene

Sequence content
CCDS
Ensembl
RefSeq
RefSeqGene

Status
Current

Chromosome locations
more...

See NQO1 NAD(P)H quinone dehydrogenase 1
nqo1 in Homo sapiens Mus musculus Rattus norvegicus All 142 Gene records

Search results

Items: 1 to 20 of 265

Page 1 of 14

See also 29 discontinued or replaced items.

Name/Gene ID	Description	Location	Aliases	MIM
☐ NQO1 ID: 1728	NAD(P)H quinone dehydrogenase 1 [*Homo sapiens* (human)]	Chromosome 16, NC_000016.10 (69709401..69726668, complement)	DHQU, DIA4, DTD, NMOR1, NMORI, QR1	125860
☐ Nqo1 ID: 24314	NAD(P)H quinone dehydrogenase 1 [*Rattus norvegicus* (Norway rat)]	Chromosome 19, NC_005118.4 (38422210..38437103)	Dia4	
☐ Nqo1 ID: 18104	NAD(P)H dehydrogenase, quinone 1 [*Mus musculus* (house mouse)]	Chromosome 8, NC_000074.6 (107388225..107403205, complement)	AV001255, Dia4, Dtd, Nmo-1, Nmo1, Nmor1, Ox-1, Ox1, Qr1	
☐ nqo1 ID: 322506	NAD(P)H dehydrogenase, quinone 1 [*Danio rerio*	Chromosome 7, NC_007118.7 (56703254..56722320)	wu:fb63c10, zgc:77191	

Filters: Manage Filters

Results by taxon

Top Organisms [Tree]
Homo sapiens (83)
Mus musculus (24)
Rattus norvegicus (11)
Human immunodeficiency virus 1 (3)
Danio rerio (2)
All other taxa (142)
More...

Find related data

Database: Select

Search details

```
nqo1[All Fields] AND alive[prop]
```

NCBI/Gene

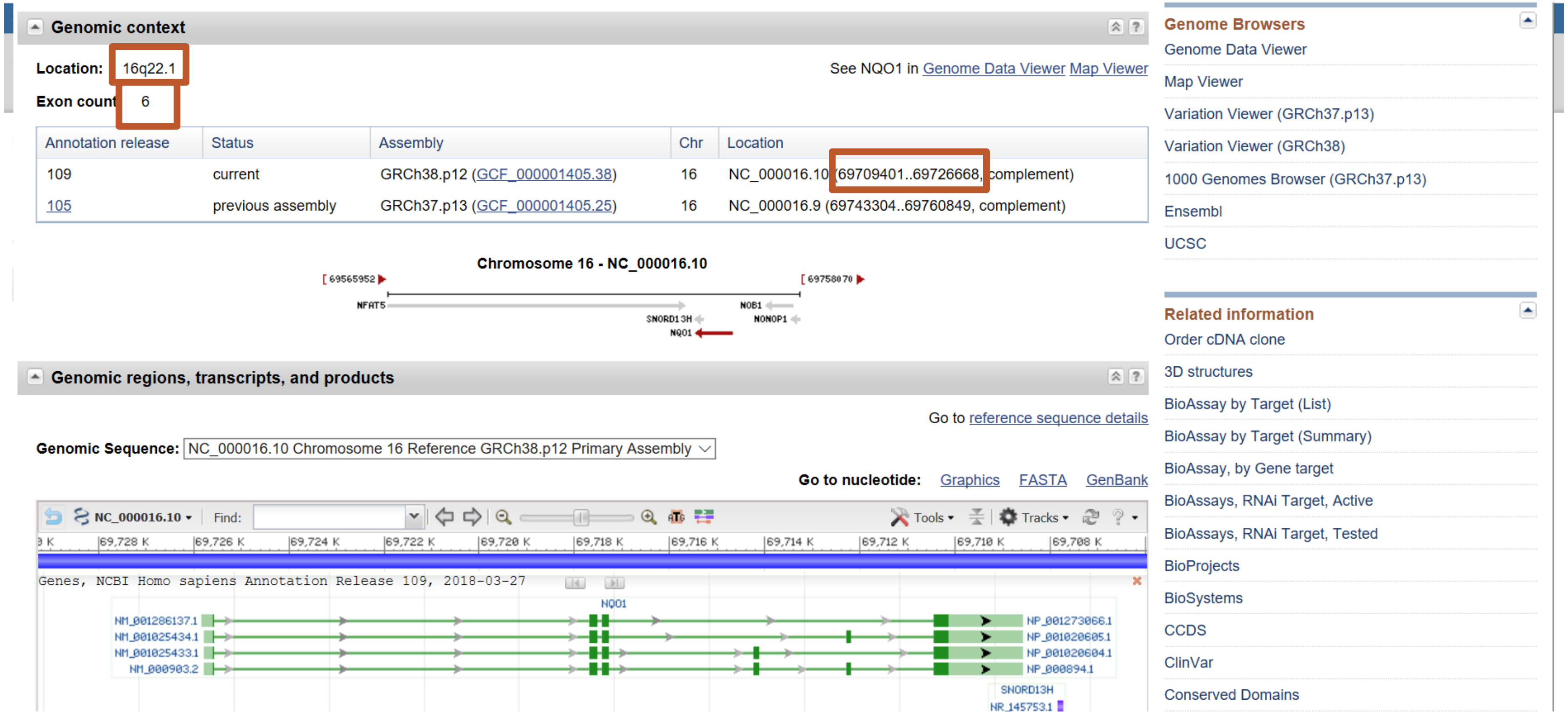
NQO1 NAD(P)H quinone dehydrogenase 1 [*Homo sapiens* (human)]

Gene ID: 1728, updated on 29-Mar-2018

Summary

Official Symbol	NQO1 provided by HGNC
Official Full Name	NAD(P)H quinone dehydrogenase 1 provided by HGNC
Primary source	HGNC:HGNC:2874
See related	Ensembl:ENSG00000181019 MIM:125860; Vega:OTTHUMG00000137575
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as	DTD; QR1; DHQU; DIA4; NMOR1; NMORI
Summary	This gene is a member of the NAD(P)H dehydrogenase (quinone) family and encodes a cytoplasmic 2-electron reductase. This FAD-binding protein forms homodimers and reduces quinones to hydroquinones. This protein's enzymatic activity prevents the one electron reduction of quinones that results in the production of radical species. Mutations in this gene have been associated with tardive dyskinesia (TD), an increased risk of hematotoxicity after exposure to benzene, and susceptibility to various forms of cancer. Altered expression of this protein has been seen in many tumors and is also associated with Alzheimer's disease (AD). Alternate transcriptional splice variants, encoding different isoforms, have been characterized. [provided by RefSeq, Jul 2008]
Expression	Biased expression in stomach (RPKM 136.7), gall bladder (RPKM 67.3) and 11 other tissues See more

NCBI/Gene



Genomic context

Location: 16q22.1

Exon count 6

See NQO1 in Genome Data Viewer Map Viewer

Annotation release	Status	Assembly	Chr	Location
109	current	GRCh38.p12 (GCF_000001405.38)	16	NC_000016.10 (69709401..69726668, complement)
105	previous assembly	GRCh37.p13 (GCF_000001405.25)	16	NC_000016.9 (69743304..69760849, complement)

Chromosome 16 - NC_000016.10

Genomic regions, transcripts, and products

Go to reference sequence details

Genomic Sequence: NC_000016.10 Chromosome 16 Reference GRCh38.p12 Primary Assembly

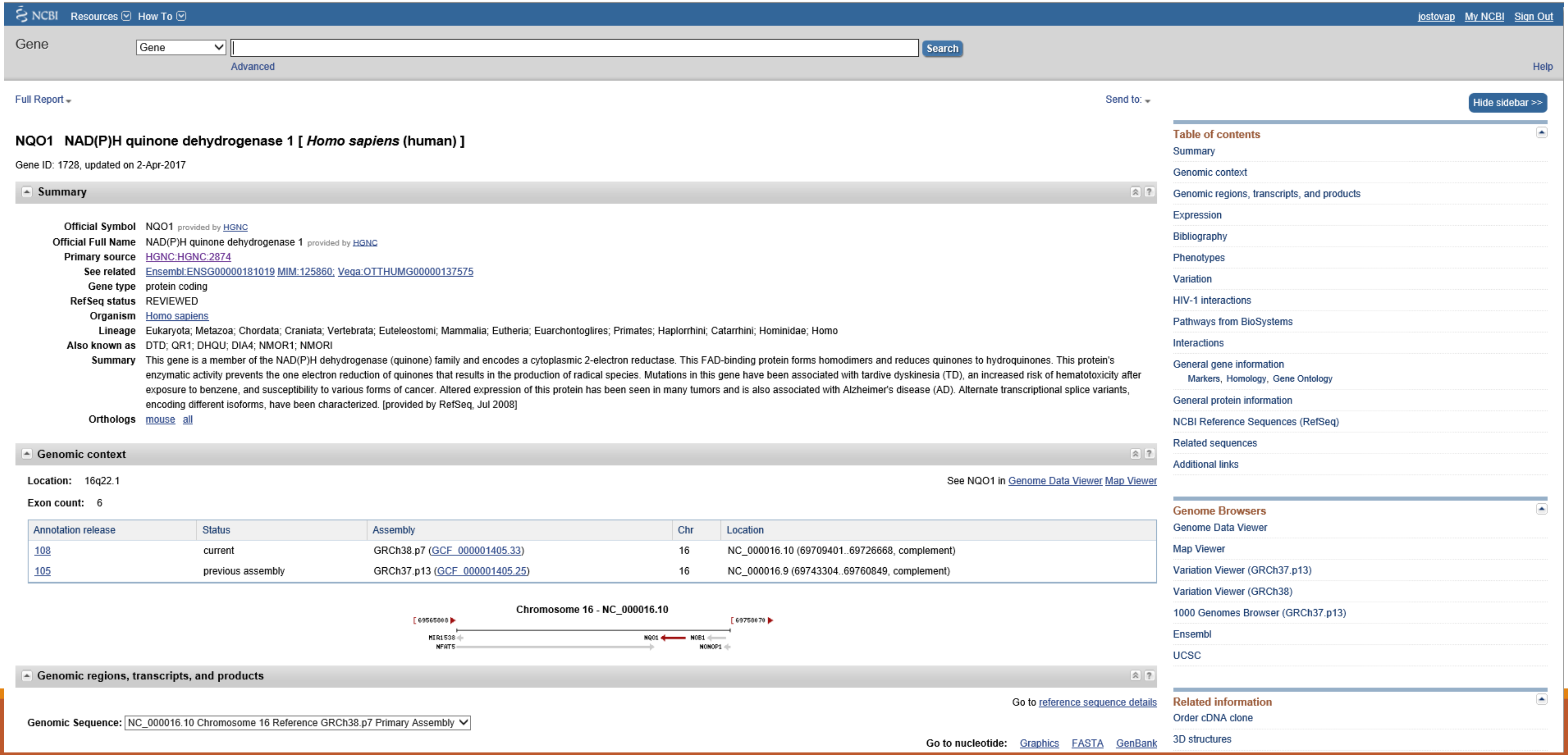
Go to nucleotide: Graphics FASTA GenBank

Genes, NCBI Homo sapiens Annotation Release 109, 2018-03-27

Genome Browsers
- Genome Data Viewer
- Map Viewer
- Variation Viewer (GRCh37.p13)
- Variation Viewer (GRCh38)
- 1000 Genomes Browser (GRCh37.p13)
- Ensembl
- UCSC

Related information
- Order cDNA clone
- 3D structures
- BioAssay by Target (List)
- BioAssay by Target (Summary)
- BioAssay, by Gene target
- BioAssays, RNAi Target, Active
- BioAssays, RNAi Target, Tested
- BioProjects
- BioSystems
- CCDS
- ClinVar
- Conserved Domains

NCBI/Gene



NQO1 NAD(P)H quinone dehydrogenase 1 [*Homo sapiens* (human)]

Gene ID: 1728, updated on 2-Apr-2017

Summary

Official Symbol	NQO1 provided by HGNC
Official Full Name	NAD(P)H quinone dehydrogenase 1 provided by HGNC
Primary source	HGNC:HGNC:2874
See related	Ensembl:ENSG00000181019 MIM:125860; Vega:OTTHUMG00000137575
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as	DTD; QR1; DHQU; DIA4; NMOR1; NMORI
Summary	This gene is a member of the NAD(P)H dehydrogenase (quinone) family and encodes a cytoplasmic 2-electron reductase. This FAD-binding protein forms homodimers and reduces quinones to hydroquinones. This protein's enzymatic activity prevents the one electron reduction of quinones that results in the production of radical species. Mutations in this gene have been associated with tardive dyskinesia (TD), an increased risk of hematotoxicity after exposure to benzene, and susceptibility to various forms of cancer. Altered expression of this protein has been seen in many tumors and is also associated with Alzheimer's disease (AD). Alternate transcriptional splice variants, encoding different isoforms, have been characterized. [provided by RefSeq, Jul 2008]
Orthologs	mouse all

Genomic context

Location: 16q22.1

See NQO1 in Genome Data Viewer Map Viewer

Exon count: 6

Annotation release	Status	Assembly	Chr	Location
108	current	GRCh38.p7 (GCF_000001405.33)	16	NC_000016.10 (69709401..69726668, complement)
105	previous assembly	GRCh37.p13 (GCF_000001405.25)	16	NC_000016.9 (69743304..69760849, complement)

Genomic regions, transcripts, and products

Go to reference sequence details

Genomic Sequence: NC_000016.10 Chromosome 16 Reference GRCh38.p7 Primary Assembly

Table of contents

- Summary
- Genomic context
- Genomic regions, transcripts, and products
- Expression
- Bibliography
- Phenotypes
- Variation
- HIV-1 interactions
- Pathways from BioSystems
- Interactions
- General gene information
  - Markers, Homology, Gene Ontology
- General protein information
- NCBI Reference Sequences (RefSeq)
- Related sequences
- Additional links

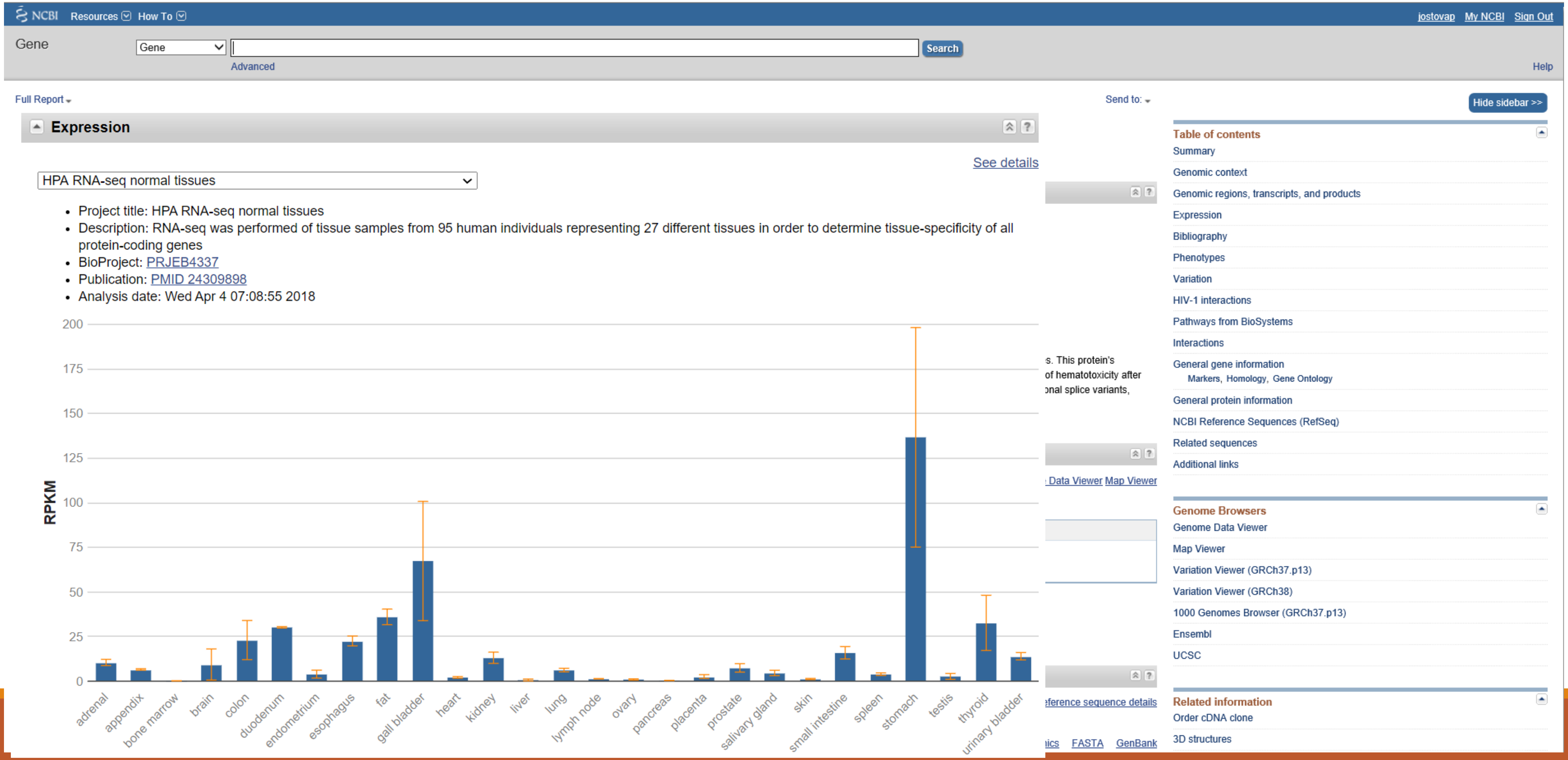
Genome Browsers

- Genome Data Viewer
- Map Viewer
- Variation Viewer (GRCh37.p13)
- Variation Viewer (GRCh38)
- 1000 Genomes Browser (GRCh37.p13)
- Ensembl
- UCSC

Related information

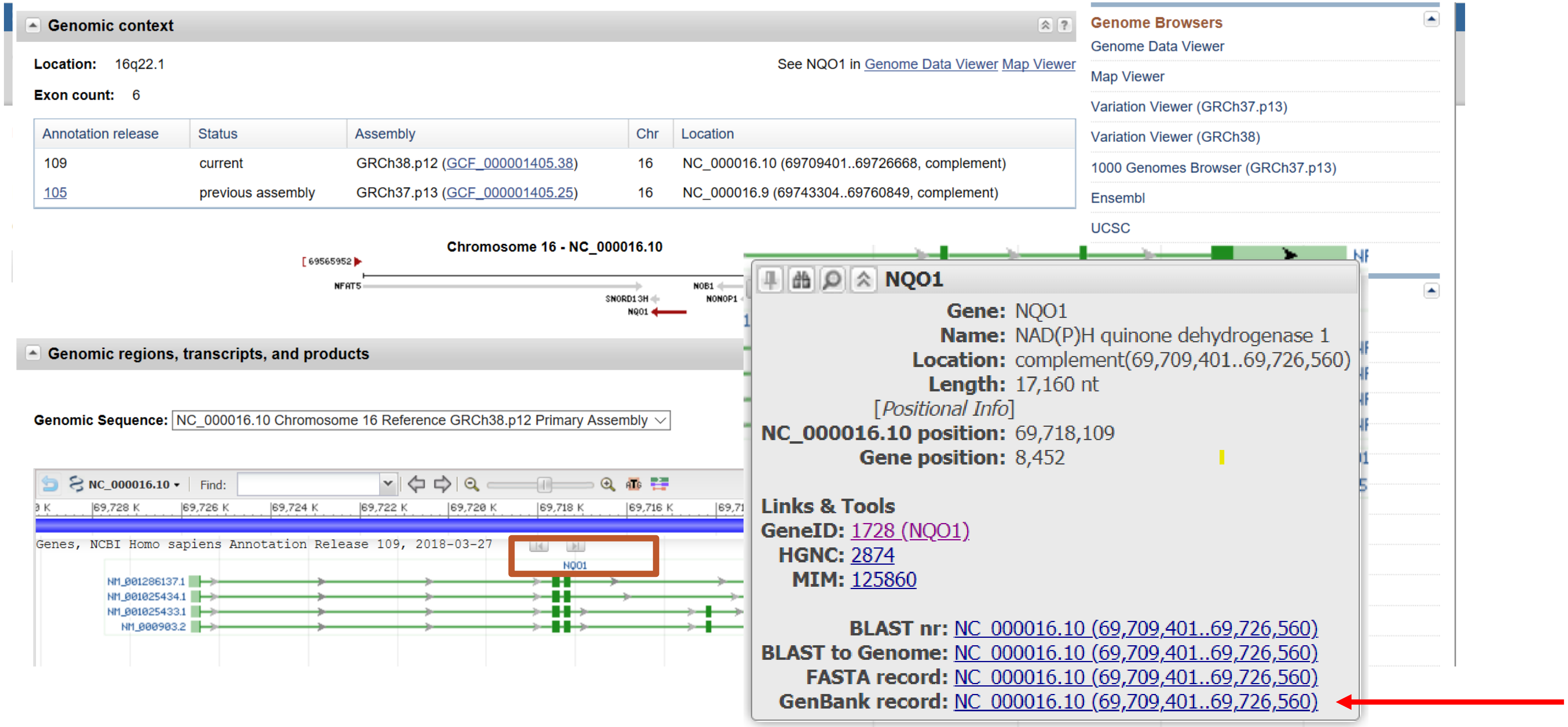
- Order cDNA clone
- 3D structures

NCBI/Gene - expression



- Project title: HPA RNA-seq normal tissues
- Description: RNA-seq was performed of tissue samples from 95 human individuals representing 27 different tissues in order to determine tissue-specificity of all protein-coding genes
- BioProject: PRJEB4337
- Publication: PMID 24309898
- Analysis date: Wed Apr 4 07:08:55 2018

NCBI/Gene – whole gene sequence



Genomic context

Location: 16q22.1

See NQO1 in Genome Data Viewer Map Viewer

Exon count: 6

Annotation release	Status	Assembly	Chr	Location
109	current	GRCh38.p12 (GCF_000001405.38)	16	NC_000016.10 (69709401..69726668, complement)
105	previous assembly	GRCh37.p13 (GCF_000001405.25)	16	NC_000016.9 (69743304..69760849, complement)

Chromosome 16 - NC_000016.10

Genomic regions, transcripts, and products

Genomic Sequence: NC_000016.10 Chromosome 16 Reference GRCh38.p12 Primary Assembly

Genes, NCBI Homo sapiens Annotation Release 109, 2018-03-27

NQO1

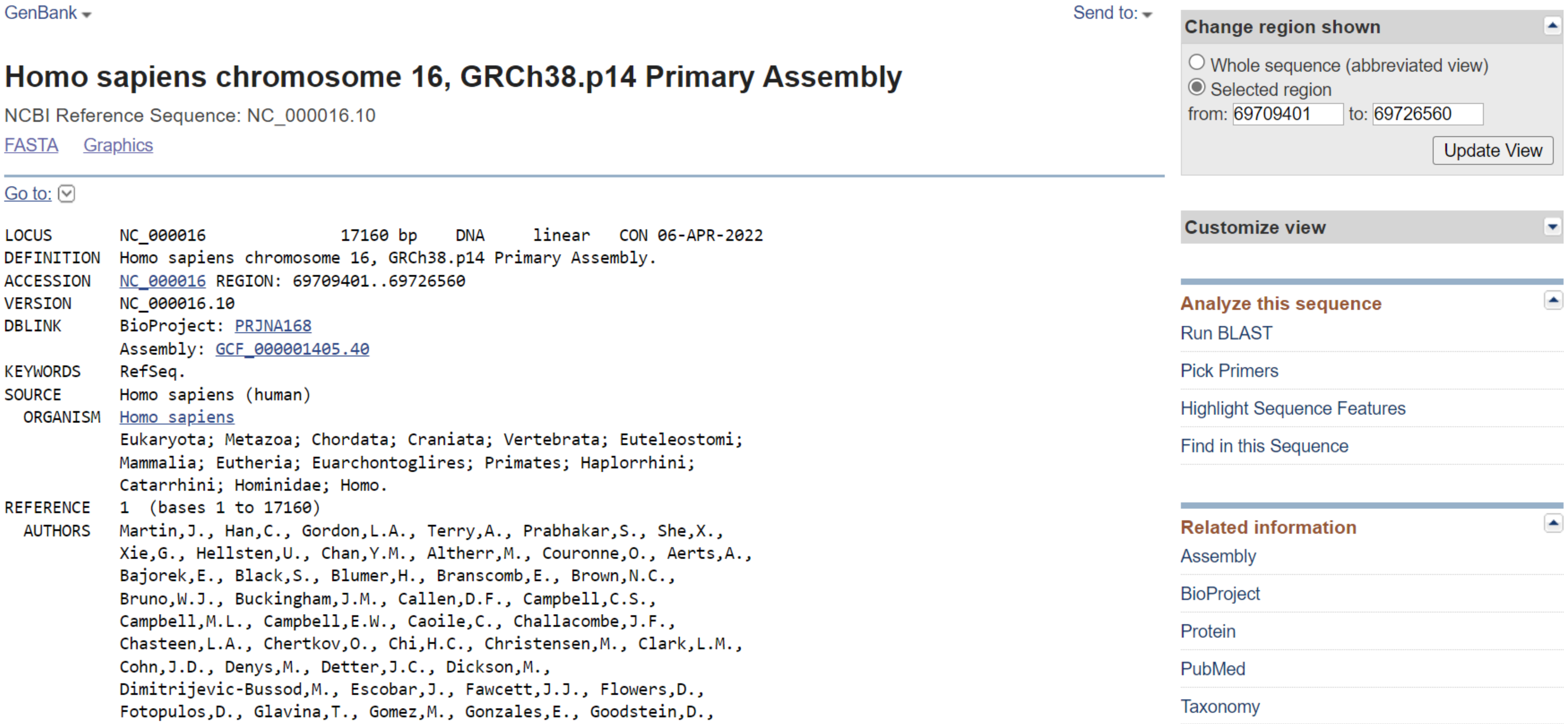
Gene: NQO1
Name: NAD(P)H quinone dehydrogenase 1
Location: complement(69,709,401..69,726,560)
Length: 17,160 nt
[Positional Info]
NC_000016.10 position: 69,718,109
Gene position: 8,452

Links & Tools
GeneID: 1728 (NQO1)
HGNC: 2874
MIM: 125860

BLAST nr: NC_000016.10 (69,709,401..69,726,560)
BLAST to Genome: NC_000016.10 (69,709,401..69,726,560)
FASTA record: NC_000016.10 (69,709,401..69,726,560)
GenBank record: NC_000016.10 (69,709,401..69,726,560)

Genome Browsers
Genome Data Viewer
Map Viewer
Variation Viewer (GRCh37.p13)
Variation Viewer (GRCh38)
1000 Genomes Browser (GRCh37.p13)
Ensembl
UCSC

NCBI/Gene – whole gene sequence



Homo sapiens chromosome 16, GRCh38.p14 Primary Assembly

NCBI Reference Sequence: NC_000016.10

Change region shown

○ Whole sequence (abbreviated view)
● Selected region
from: 69709401 to: 69726560

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VERSION     NC_000016.10
DBLINK      BioProject: PRJNA168
            Assembly: GCF_000001405.40
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17160)
  AUTHORS   Martin,J., Han,C., Gordon,L.A., Terry,A., Prabhakar,S., She,X.,
            Xie,G., Hellsten,U., Chan,Y.M., Altherr,M., Couronne,O., Aerts,A.,
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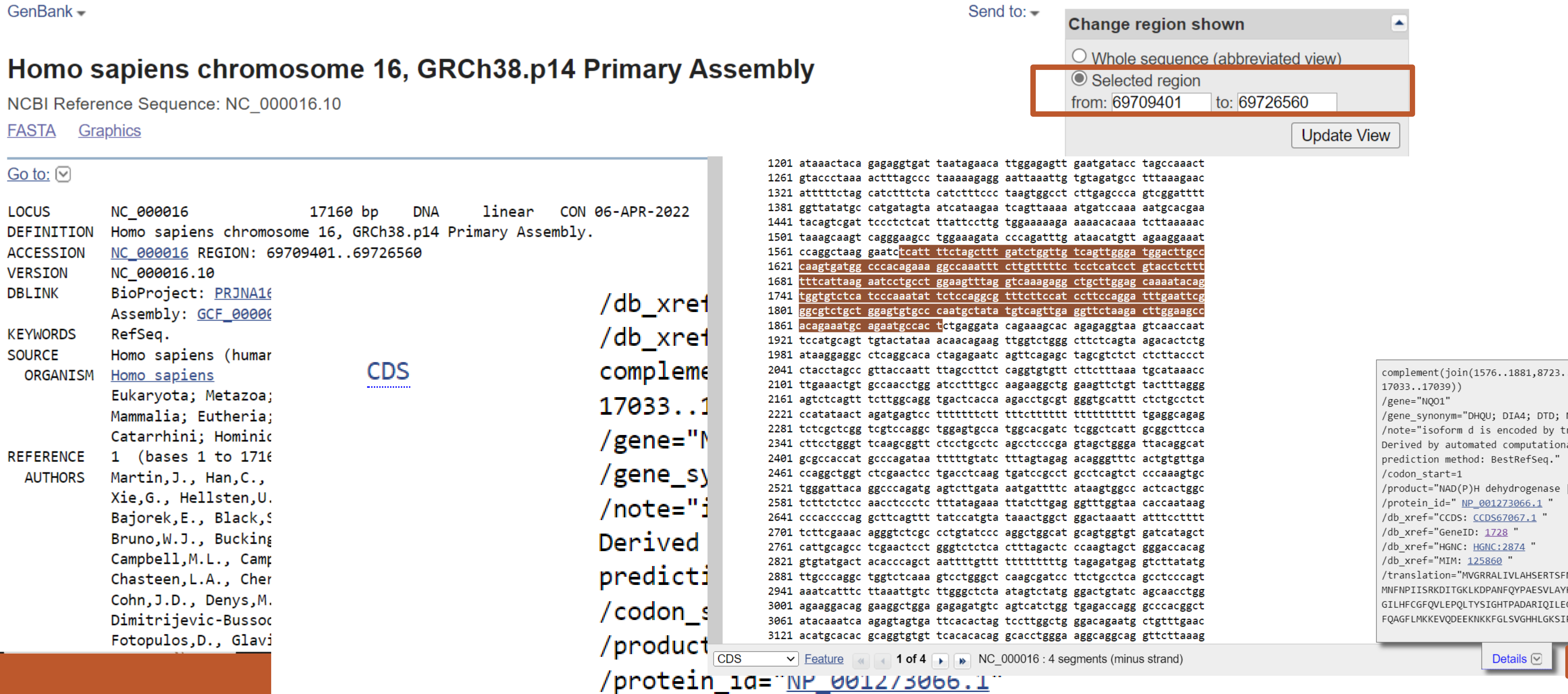
NCBI/Gene – whole gene sequence



Homo sapiens chromosome 16, GRCh38.p14 Primary Assembly

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            Catarrhini; Hominic
REFERENCE   1  (bases 1 to 1716
  AUTHORS   Martin,J., Han,C.,
            Xie,G., Hellsten,U.
            Bajorek,E., Black,S
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            Campbell,M.L., Camp
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NC_000016 : 4 segments (minus strand)

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/db_xref="CCDS: CCDS67067.1 "
/db_xref="GeneID: 1728 "
/db_xref="HGNC: HGNC:2874 "
/db_xref="MIM: 125860 "
/translation="MVGRRALIVLAHSERTSF
MNFNPIISRKDITGKLKDPANFQYPAESVLAY
GILHFCGFQVLEPQLTYSIGHTPADARIQILE
FQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSI
```
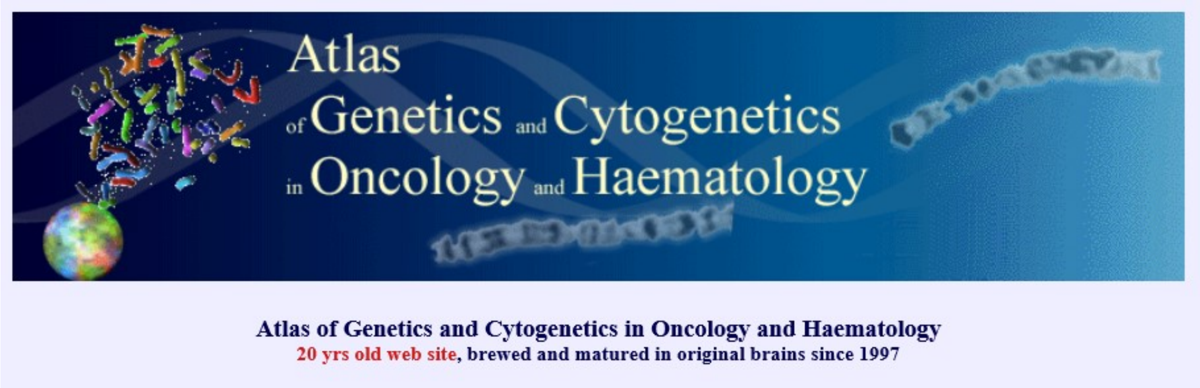

Practical part

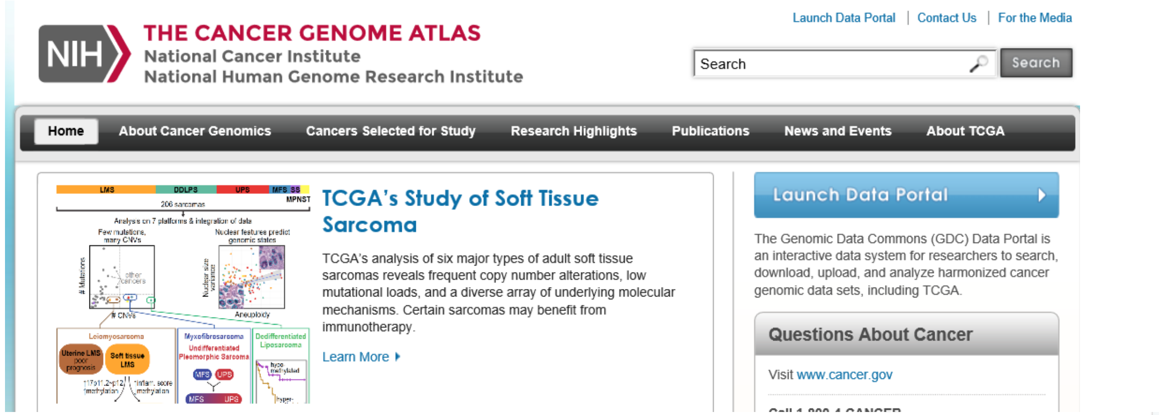
Explore „your“ nucleotide sequence in Gene.

Focused databases (secondary)



Atlas of Genetics and Cytogenetics in Oncology and Haematology

Atlas of Genetics and Cytogenetics in Oncology and Haematology
20 yrs old web site, brewed and matured in original brains since 1997



THE CANCER GENOME ATLAS
National Cancer Institute
National Human Genome Research Institute

TCGA's Study of Soft Tissue Sarcoma

TCGA's analysis of six major types of adult soft tissue sarcomas reveals frequent copy number alterations, low mutational loads, and a diverse array of underlying molecular mechanisms. Certain sarcomas may benefit from immunotherapy.

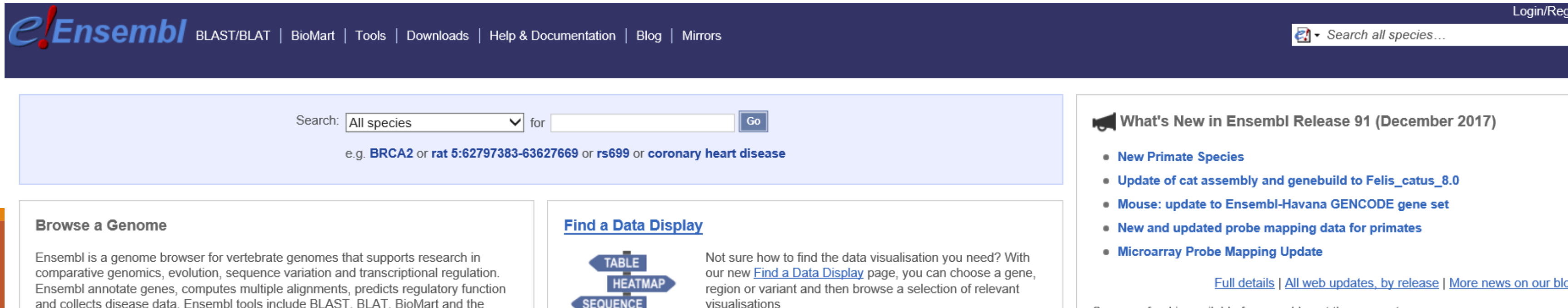
Learn More

The Genomic Data Commons (GDC) Data Portal is an interactive data system for researchers to search, download, upload, and analyze harmonized cancer genomic data sets, including TCGA.

Questions About Cancer

Visit www.cancer.gov

Free for academic non-profit institutions. Other users need a Commercial license



Search: All species for Go

e.g. BRCA2 or rat 5:62797383-63627669 or rs699 or coronary heart disease

Browse a Genome

Ensembl is a genome browser for vertebrate genomes that supports research in comparative genomics, evolution, sequence variation and transcriptional regulation. Ensembl annotate genes, computes multiple alignments, predicts regulatory function and collects disease data. Ensembl tools include BLAST, BLAT, BioMart and the

Find a Data Display

Not sure how to find the data visualisation you need? With our new Find a Data Display page, you can choose a gene, region or variant and then browse a selection of relevant visualisations

What's New in Ensembl Release 91 (December 2017)

- New Primate Species
- Update of cat assembly and genebuild to Felis_catus_8.0
- Mouse: update to Ensembl-Havana GENCODE gene set
- New and updated probe mapping data for primates
- Microarray Probe Mapping Update

Full details | All web updates, by release | More news on our blo

Practical part

Explore „your“ nucleotide sequence in database GeneCards.

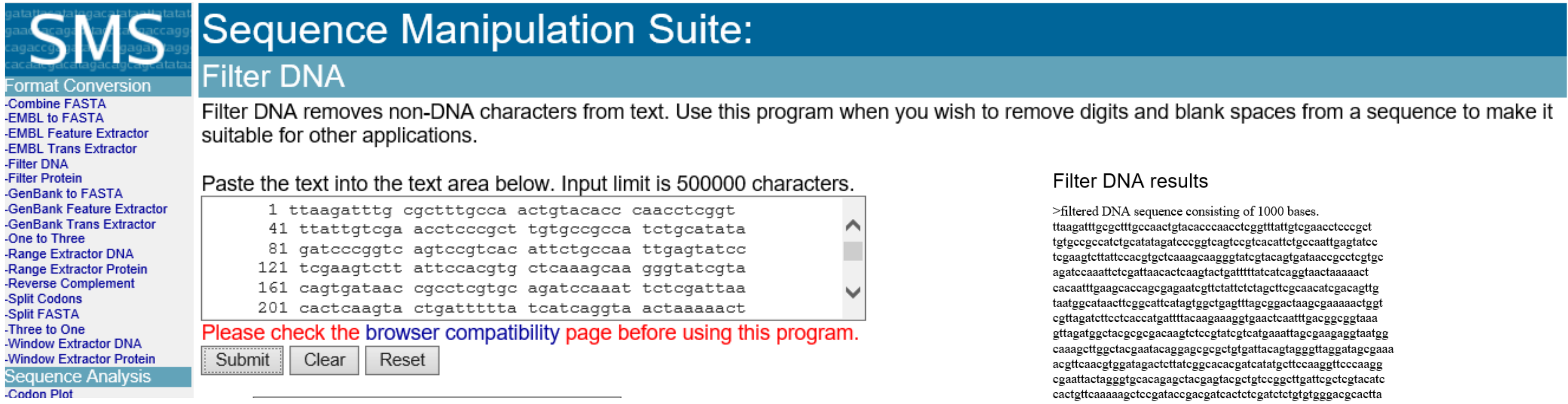
Sequence analysis

Filter DNA

DNA stats

Range Extractor DNA

Reverse complement



Sequence Manipulation Suite:

Filter DNA

Filter DNA removes non-DNA characters from text. Use this program when you wish to remove digits and blank spaces from a sequence to make it suitable for other applications.

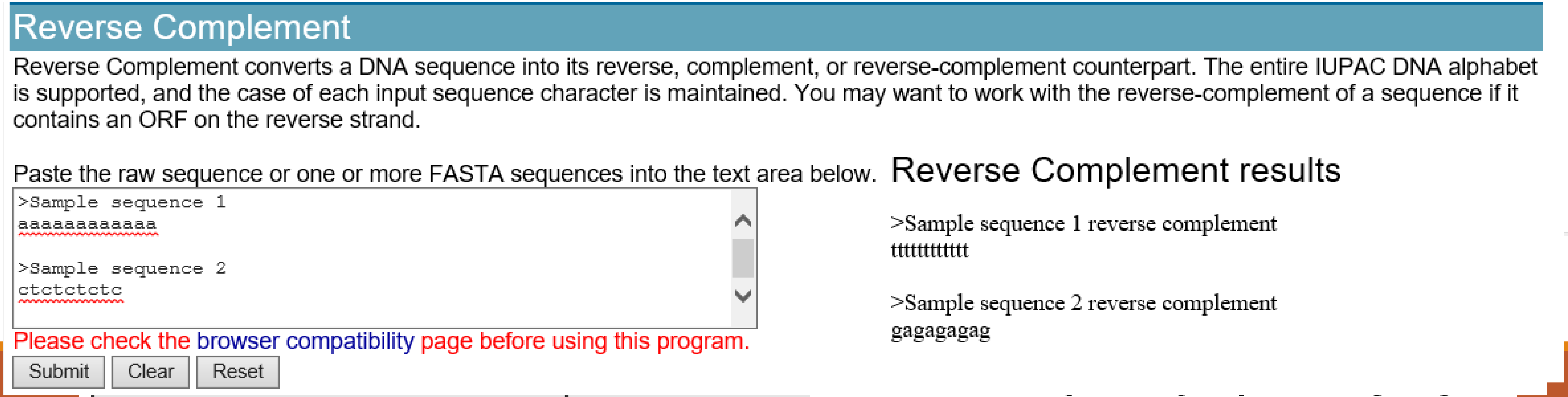
Paste the text into the text area below. Input limit is 500000 characters.

```
    1 ttaagatttg cgctttgcca actgtacacc caacctcggt
   41 ttattgtcga acctcccgct tgtgccgcca tctgcatata
   81 gatcccggtc agtccgtcac attctgccaa ttgagtatcc
  121 tcgaagtctt attccacgtg ctcaaagcaa gggtatcgta
  161 cagtgataac cgcctcgtgc agatccaaat tctcgattaa
  201 cactcaagta ctgattttta tcatcaggta actaaaaact
```

Please check the browser compatibility page before using this program.

Filter DNA results

```
>filtered DNA sequence consisting of 1000 bases.
ttaagatttgcgctttgccaactgtacacccaacctcggtttattgtcgaacctcccgct
tgtgccgccatctgcatatagatcccggtcagtccgtcacattctgccaattgagtatcc
tcgaagtcttattccacgtgctcaaagcaagggtatcgtacagtgataaccgcctcgtgc
agatccaaattctcgattaacactcaagtactgatttttatcatcaggtaactaaaaact
cacaatttgaagcaccagcgagaatcgttctattctctagcttcgcaacatcgacagttg
taatggcataacttcggcattcatagtggctgagtttagcggactaagcgaaaaactggt
cgttagatcttcctcaccatgattttacaagaaaggtgaactcaatttgacggcggtaaa
gttagatggctacgcgcgacaagtctccgtatcgtcatgaaattagcgaagaggtaatgg
caaagcttggctacgaatacaggagcgcgctgtgattacagtagggttaggatagcgaaa
acgttcaacgtggatagactcttatcggcacacgatcatatgcttccaaggttcccaagg
cgaattactagggtgcacagagctacgagtacgctgtccggcttgattcgctcgtacatc
cactgttcaaaaagctccgataccgacgatcactctcgatctctgtgtgggacgcactta
```



Reverse Complement

Reverse Complement converts a DNA sequence into its reverse, complement, or reverse-complement counterpart. The entire IUPAC DNA alphabet is supported, and the case of each input sequence character is maintained. You may want to work with the reverse-complement of a sequence if it contains an ORF on the reverse strand.

Paste the raw sequence or one or more FASTA sequences into the text area below.

```
>Sample sequence 1
aaaaaaaaaaaa

>Sample sequence 2
ctctctctc
```

Please check the browser compatibility page before using this program.

Reverse Complement results

```
>Sample sequence 1 reverse complement
tttttttttttt

>Sample sequence 2 reverse complement
gagagagag
```

atttttttttttc

Practical part

Analyze „your“ nucleotide sequence.

(HW: How many cytosins and contains 2. exon?)

Homework 5

Work with „your“ abbreviation.

1) Find your nucleotide sequence, what is your accession number?

2) Download the **CDS** of your sequence,and save it in FASTA format.

3) Which chromosome contains your sequence? How many exons does your sequence have?

4) How long is the second exon? How many cytosines have the second exon?

5) Where is your sequence mostly expressed?

E.g use „výstřižky“ „snipping tool“

- Compile in „one note“ (or word, or pdf)

Homework 5:example

DÚ5

1) NQO1:
Homo sapiens NAD(P)H quinone dehydrogenase 1 (NQO1), transcript variant 1, mRNA

NM_000903.2

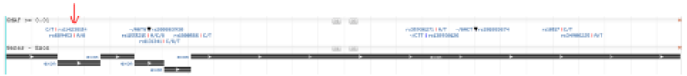
2) >CDS

```
ATGGTCGGCAGAAGAGCACTGATCGTACTGGCTCACTCAGAGAGGACGTCCTTCAACTATGCCATGAAGG
AGGCTGCTGCAGCGGCTTTGAAGAAGAAAGGATGGGAGGTGGTGGAGTCGGACCTCTATGCCATGAACTT
CAATCCCATCATTTCCAGAAAGGACATCACAGGTAAACTGAAGGACCCTGCGAACTTTCAGTATCCTGCC
GAGTCTGTTCTGGCTTATAAAGAAGGCCATCTGAGCCCAGATATTGTGGCTGAACAAAAGAAGCTGGAAG
CCGCAGACCTTGTGATATTCCAGTTCCCCCTGCAGTGGTTTGGAGTCCCTGCCATTCTGAAAGGCTGGTT
TGAGCGAGTGTTCATAGGAGAGTTTGCTTACACTTACGCTGCCATGTATGACAAAGGACCCTTCCGGAGT
AAGAAGGCAGTGCTTTCCATCACCACTGGTGGCAGTGGCTCCATGTACTCTCTGCAAGGGATCCACGGGG
ACATGAATGTCATTCTCTGGCCAATTCAGAGTGGCATTCTGCATTTCTGTGGCTTCCAAGTCTTAGAACC
TCAACTGACATATAGCATTGGGCACACTCCAGCAGACGCCCGAATTCAAATCCTGGAAGGATGGAAGAAA
CGCCTGGAGAATATTTGGGATGAGACACCACTGTATTTTGCTCCAAGCAGCCTCTTTGACCTAAACTTCC
AGGCAGGATTCTTAATGAAAAAAGAGGTACAGGATGAGGAGAAAAACAAGAAATTTGGCCTTTCTGTGGG
CCATCACTTGGGCAAGTCCATCCCAACTGACAACCAGATCAAAGCTAGAAAATGA
```

3) Chromozome 16 (map="16q22.1)
4) 6 exonů (2:164nt)
>NM_000903.2:199-363 Homo sapiens NAD(P)H quinone dehydrogenase 1 (NQO1), transcript variant 1, mRNA

```
GCAGAAGAGCACTGATCGTACTGGCTCACTCAGAGAGGACGTCCTTCAACTATGCCATGAAGGAGGCTGC
TGCAGCGGCTTTGAAGAAGAAAGGATGGGAGGTGGTGGAGTCGGACCTCTATGCCATGAACTTCAATCCC
ATCATTTCCAGAAAGGACATCACAG
```

ANO, jeden (rs689453)



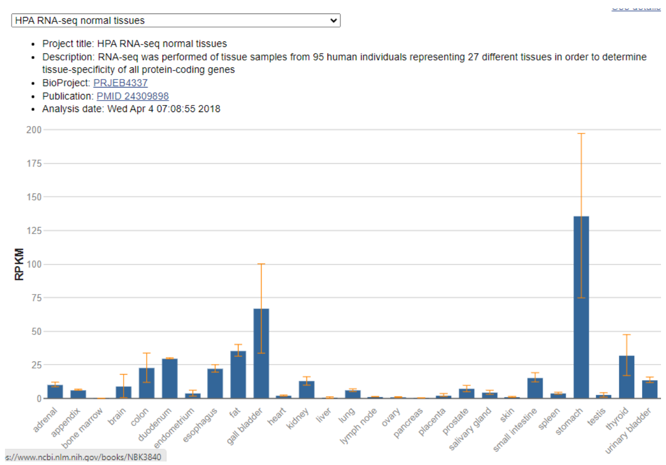
Exon obsahuje: 38 cytosinů a 4 dinukleotidy CG

DNA Stats results

Results for 165 residue sequence "Untitled" starting "GCAGAAGAGC"

Pattern:	Times found:	Percentage:
g	47	28.48
a	47	28.48
t	33	20.00
c	38	23.03
cg	4	2.44
ca	15	9.15

5)



HPA RNA-seq normal tissues

- Project title: HPA RNA-seq normal tissues
- Description: RNA-seq was performed of tissue samples from 95 human individuals representing 27 different tissues in order to determine tissue-specificity of all protein-coding genes
- BioProject: PRJEB4337
- Publication: PMID 24309898
- Analysis date: Wed Apr 4 07:08:55 2018