Home - NIH Genetic Testing Registry (GTR) - NCBI

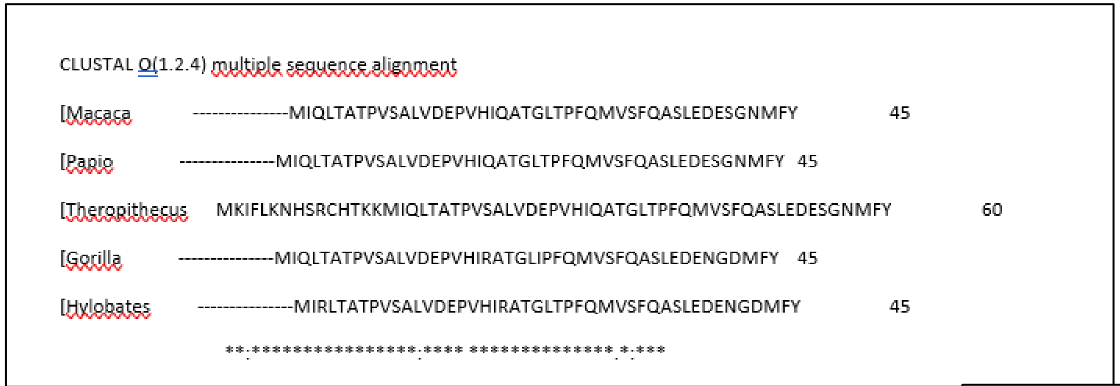
Základy praktické Bioinformatiky

PETRA MATOUŠKOVÁ

2023/2024

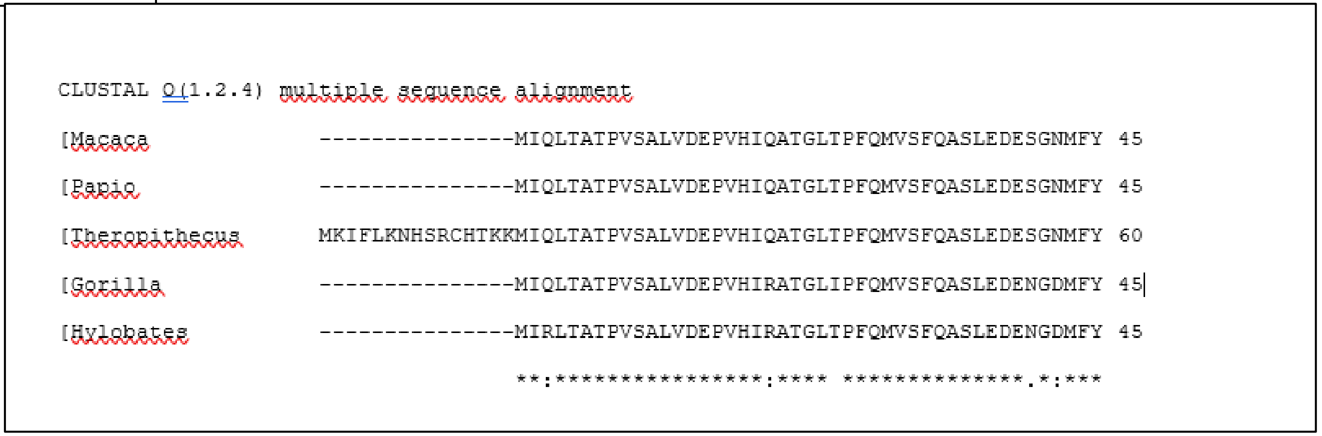
5/10

font:Courier new



```
CLUSTAL O(1.2.4) multiple sequence alignment

[Macaca         ---------------MIQLTATPVSALVDEPVHIQATGLTPFQMVSFQASLEDESGNMFY          45

[Papio          ---------------MIQLTATPVSALVDEPVHIQATGLTPFQMVSFQASLEDESGNMFY  45

[Theropithecus     MKIFLKNHSRCHTKKMIQLTATPVSALVDEPVHIQATGLTPFQMVSFQASLEDESGNMFY          60

[Gorilla        ---------------MIQLTATPVSALVDEPVHIRATGLIPFQMVSFQASLEDENGDMFY  45

[Hylobates      ---------------MIRLTATPVSALVDEPVHIRATGLTPFQMVSFQASLEDENGDMFY          45

                   **:****************:**** **************.*:***
```

Calibri → Courier new

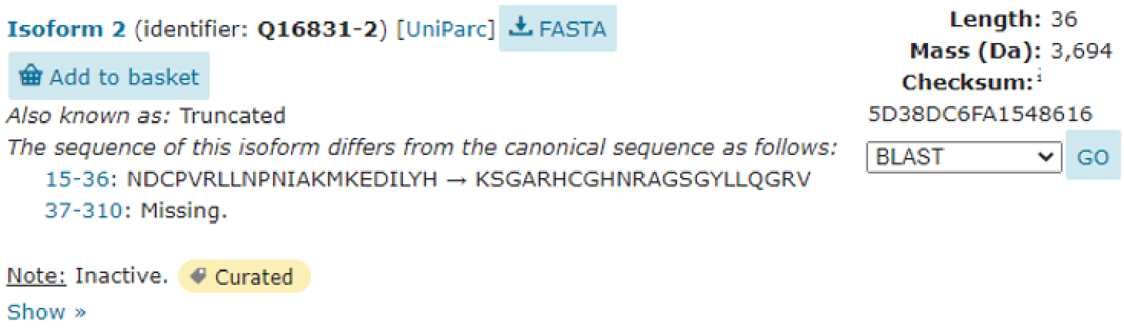


```
CLUSTAL O(1.2.4) multiple sequence alignment

[Macaca              ---------------MIQLTATPVSALVDEPVHIQATGLTPFQMVSFQASLEDESGNMFY 45

[Papio               ---------------MIQLTATPVSALVDEPVHIQATGLTPFQMVSFQASLEDESGNMFY 45

[Theropithecus       MKIFLKNHSRCHTKKMIQLTATPVSALVDEPVHIQATGLTPFQMVSFQASLEDESGNMFY 60

[Gorilla             ---------------MIQLTATPVSALVDEPVHIRATGLIPFQMVSFQASLEDENGDMFY 45

[Hylobates           ---------------MIRLTATPVSALVDEPVHIRATGLTPFQMVSFQASLEDENGDMFY 45

                                    **:****************:**** **************.*:***
```

isoformy?

3. **Má váš protein nějaké isoformy? Porovnejte je.**

- ano, UPP1 má ještě jednu isoformu



Isoform 2 (identifier: **Q16831-2**) [UniParc]

Also known as: Truncated

The sequence of this isoform differs from the canonical sequence as follows:

15-36: NDCPVRLLNPNIAKMKEDILYH → KSGARHCGHNRAGSGYLLQGRV

37-310: Missing.

Note: Inactive.

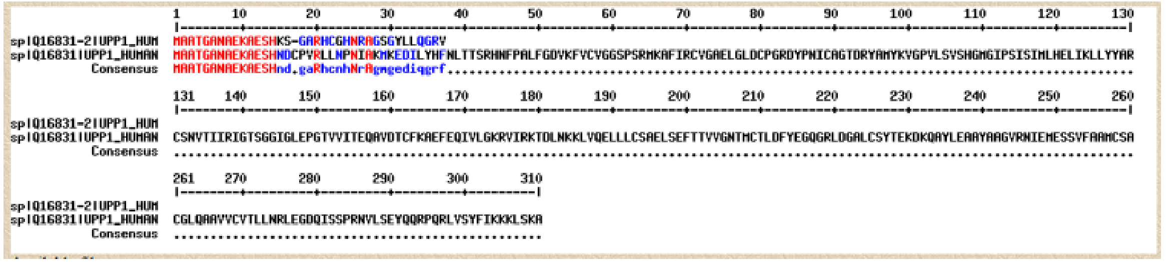
Length: 36

Mass (Da): 3,694

Checksum:

5D38DC6FA1548616

- porovnání isoforem



```
                      1       10        20        30        40        50        60        70        80        90        100       110       120       130
                      |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
sp|Q16831-2|UPP1_HUM  MAATGANAEKAESHKS-GARHCGHNRAGSGYLLQGRV
sp|Q16831|UPP1_HUMAN  MAATGANAEKAESHNDCPVRLLNPNIAKMKEDILYHFNLTTSRHNFPALFGDVKFVCVGGSPSRMKAFIRCVGAELGLDCPGRDYPNICAGTDRYAMYKVGPVLSVSHGMGIPSISIMLHELIKLLYYAR
           Consensus  MAATGANAEKAESHnd.gaRhcnhNrAgmgediqgrf.............................................................................................

                      131     140       150       160       170       180       190       200       210       220       230       240       250       260
                      |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
sp|Q16831-2|UPP1_HUM
sp|Q16831|UPP1_HUMAN  CSNVTIIRIGTSGGIGLEPGTVVITEQAVDTCFKAEFEQIVLGKRVIRKTDLNKKLVQELLLCSAELSEFTTVVGNTMCTLDFYEGQGRLDGALCSYTEKDKQAYLEAAYAAGVRNIEMESSVFAAMCSA
           Consensus  ..................................................................................................................................

                      261     270       280       290       300       310
                      |--------+---------+---------+---------+---------|
sp|Q16831-2|UPP1_HUM
sp|Q16831|UPP1_HUMAN  CGLQAAVVCVTLLNRLEGDQISSPRNVLSEYQQRPQRLVSYFIKKKLSKA
           Consensus  ..................................................
```

Základy praktické bioinformatiky

Téma 5/10

Nukleotidová bioinformatika I

Cíle:

Student bude schopen vyhledat a stáhnout nukleotidové sekvence vybraných genů a získat relevantní informace o těchto genech. Student bude schopen analyzovat základní vlastnosti vybraných nukleotidových sekvencí a porovnat vícero nukleotidových sekvencí.

„Bioinformatika nukleových kyselin“

Vyhledávání NK sekvencí

Analýza vlastností sekvencí-složení, reverse complement, identifikace restrikčních míst (Palindromy)

Práce s kódující DNA=práce s proteiny / překlad DNA sekvence-otvírání čtecího rámce

Návrh primerů pro PCR, rt-PCR

Předpověď sekundárních struktur

Porovnávání sekvencí

Vyhledání SNPs

„čtení“ sekvenačních dat a spojování fragmentů

Vyhledávání hladin expresí jednotlivých genů

mikroRNA

Celé genomy

….

„Bioinformatika nukleových kyselin“

Vyhledávání NK sekvencí

Analýza vlastností sekvencí-složení, reverse complement, identifikace restrikčních míst (Palindromy)

Práce s kódující DNA=práce s proteiny / překlad DNA sekvence-otvírání čtecího rámce

Návrh primerů pro PCR, rt-PCR

Předpověď sekundárních struktur

Porovnávání sekvencí

Vyhledání SNPs

„čtení“ sekvenačních dat a spojování fragmentů

Vyhledávání hladin expresí jednotlivých genů

mikroRNA

Celé genomy

….

DNA/RNA

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

(Frederick Sanger/Walter Gilbert 1980 Nobelova cena za určování DNA sekvence)

Genetický kód založený na tripletech:

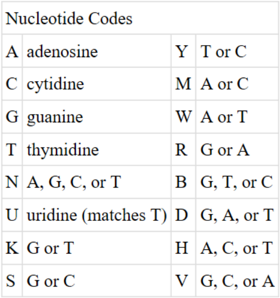
Zápis sekvence:

A, C, T (U), G

N cokoliv

R A/G purin

Y C/T pyrimidin

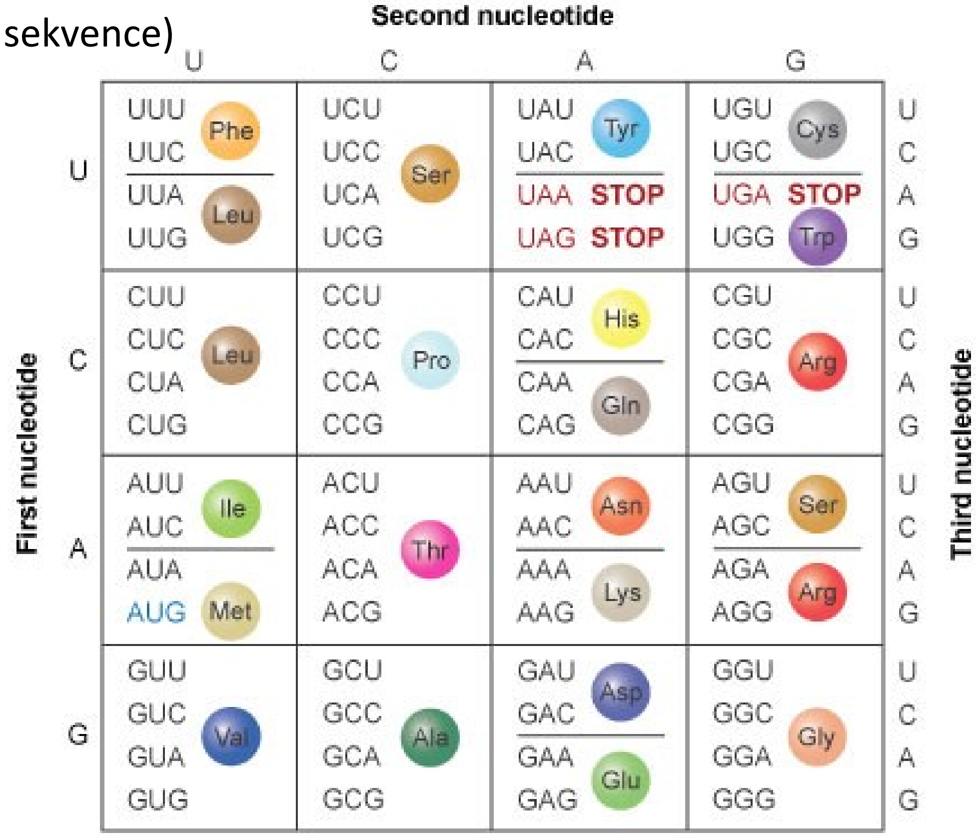


Nucleotide Codes			
A	adenosine	Y	T or C
C	cytidine	M	A or C
G	guanine	W	A or T
T	thymidine	R	G or A
N	A, G, C, or T	B	G, T, or C
U	uridine (matches T)	D	G, A, or T
K	G or T	H	A, C, or T
S	G or C	V	G, C, or A

Komplementarita: A=T, C≡G

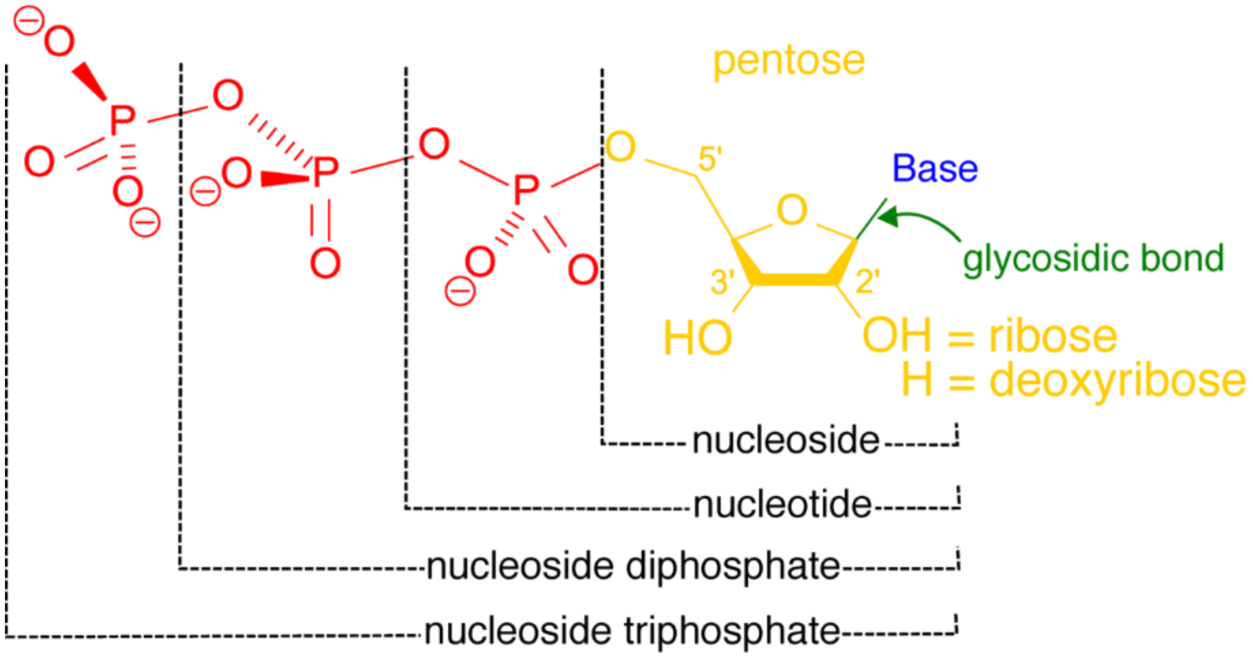
Dvojřetězcová DNA: 5´-ATGCCATAAAA-3´
3´-TACGGTATTTT-5´

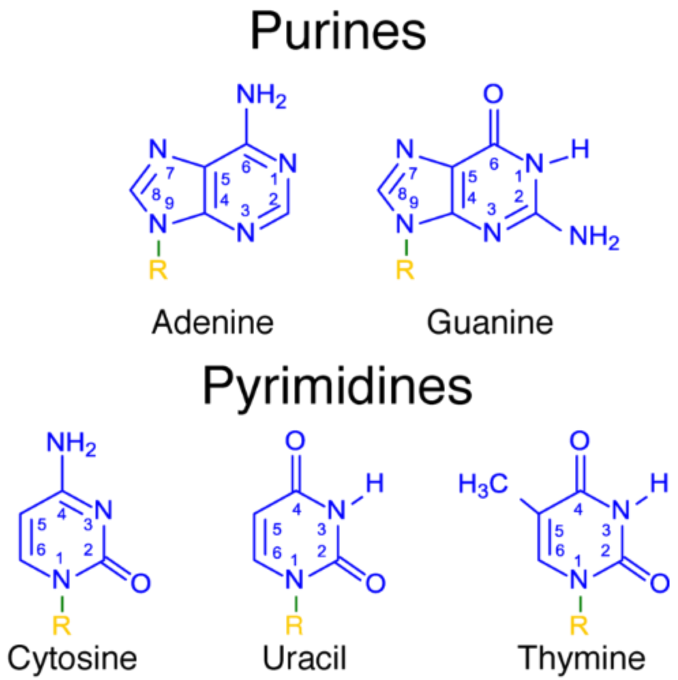
400-nt (nukleotidů) = 400 bp (base pairs/párů bazí)…kbp, Mbp



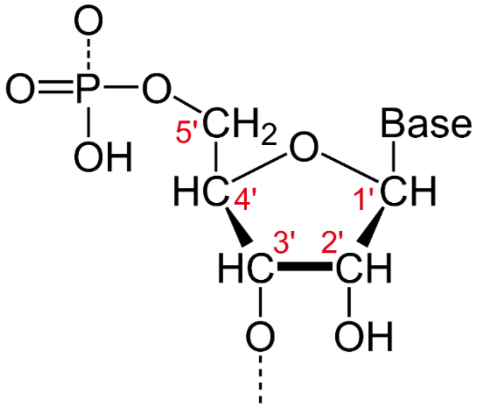
	Second nucleotide								
First nucleotide	U		C		A		G		Third nucleotide
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC		UCC		UAC		UGC		C
	UUA	Leu	UCA		UAA	STOP	UGA	STOP	A
	UUG		UCG		UAG	STOP	UGG	Trp	G
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U
	CUC		CCC		CAC		CGC		C
	CUA		CCA		CAA	Gln	CGA		A
	CUG		CCG		CAG		CGG		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

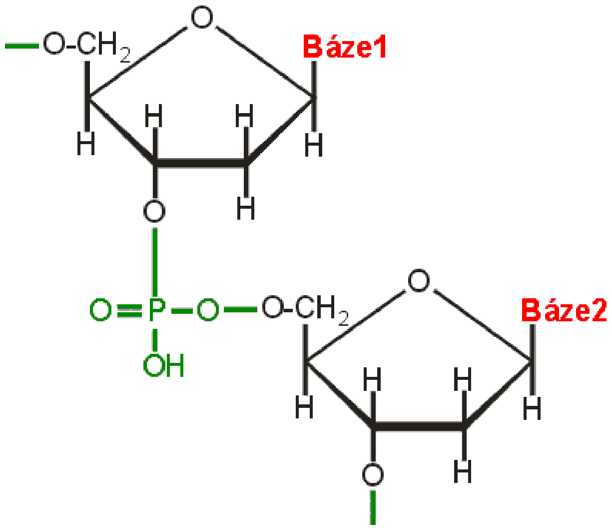
DNA/RNA

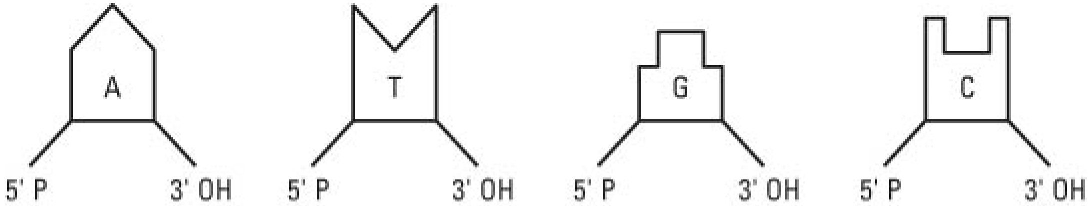

pentose
Base
glycosidic bond
5'
3'
2'
HO
OH = ribose
H = deoxyribose
nucleoside
nucleotide
nucleoside diphosphate
nucleoside triphosphate

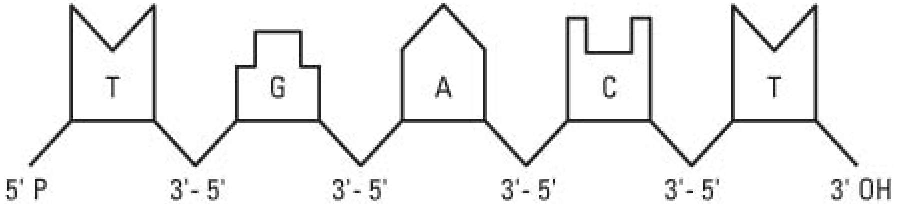

Purines
Adenine
Guanine
Pyrimidines
Cytosine
Uracil
Thymine

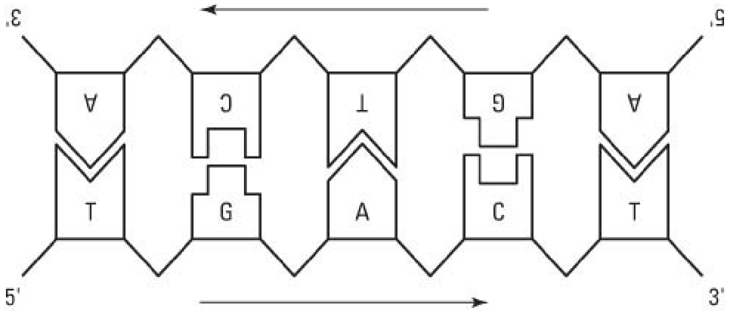
DNA/RNA


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


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


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


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'

DNA/RNA

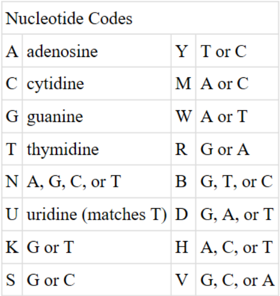
4 nukleotidy: Adenin, Guanin, Thymidin (Uracil), Cytosin : **5´→ 3´**

(Frederick Sanger/Walter Gilbert 1980 Nobelova cena za určování DNA sekvence)

Genetický kód založený na tripletech:

Zápis sekvence:

A, C, T (U), G
N cokoliv
R A/G purin
Y C/T pyrimidin

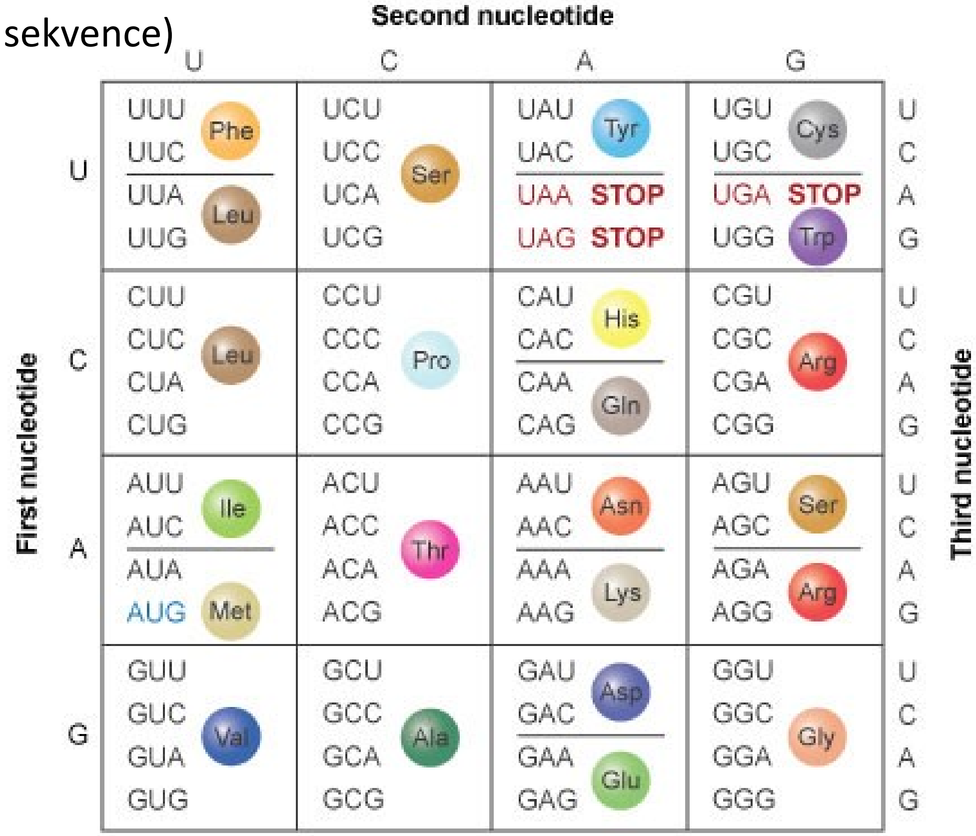


Nucleotide Codes			
A	adenosine	Y	T or C
C	cytidine	M	A or C
G	guanine	W	A or T
T	thymidine	R	G or A
N	A, G, C, or T	B	G, T, or C
U	uridine (matches T)	D	G, A, or T
K	G or T	H	A, C, or T
S	G or C	V	G, C, or A

Komplementarita: A=T, C≡G

Dvojřetězcová DNA: 5´-ATGCCATAAAA-3´
3´-TACGGTATTTT-5´

400-nt (nukleotidů) = 400 bp (base pairs/párů bazí)…kbp, Mbp



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

Prokaryota

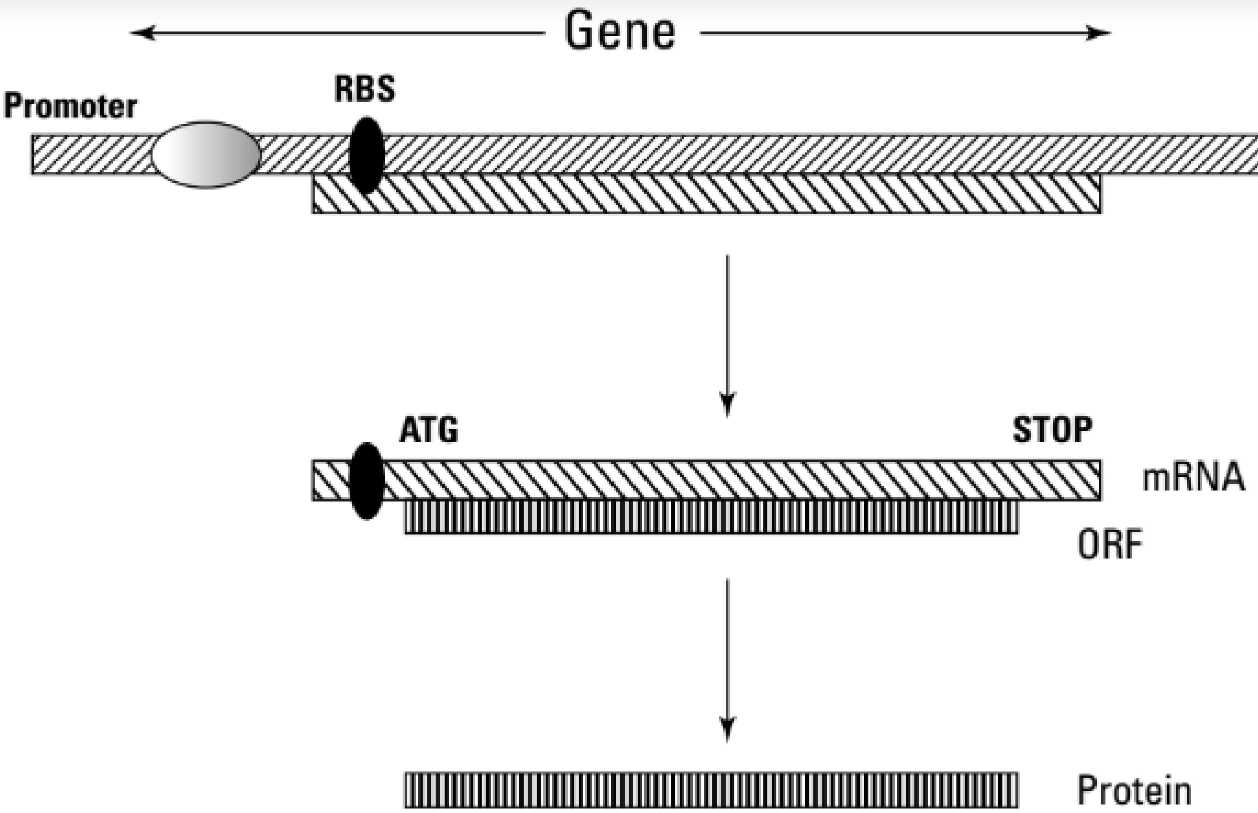
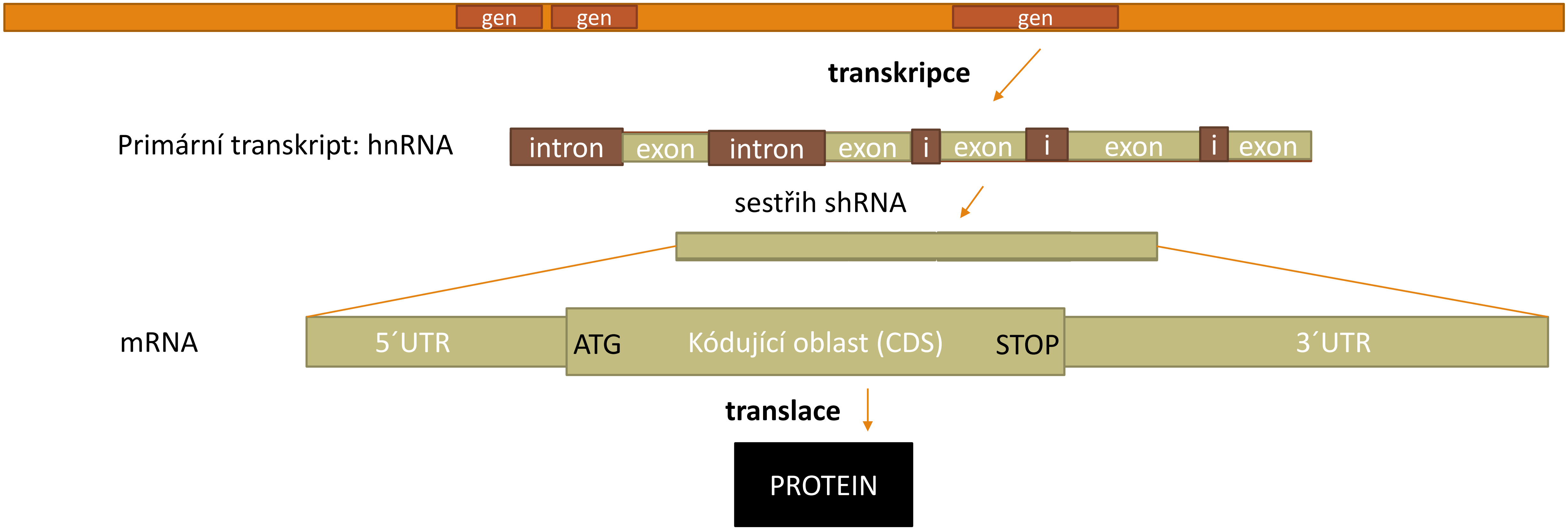


Figure 3-1: Relationship between gene, mRNA, and protein sequence for prokaryotes.

Eukaryota

Genomová DNA / chromozomy



gen gen gen

transkripce

Primární transkript: hnRNA

intron exon intron exon i exon i exon i exon

sestřih shRNA

mRNA

5´UTR ATG Kódující oblast (CDS) STOP 3´UTR

translace

PROTEIN

DNA sekvence / databáze (primární)

Hlavní databáze nukleotidových sekvencí (konsorcium):

Evropská **EMBL (EBI)** (1980) / **ENA**

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

European Molecular Biology Laboratory / European Nucleotide Archive

Americká **GenBank (NCBI)** 1982

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

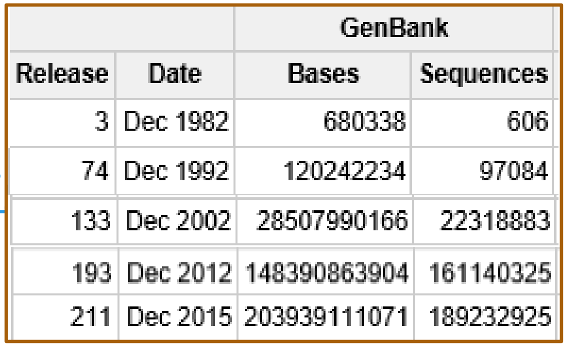
U.S. National Center for Biotechnology Information

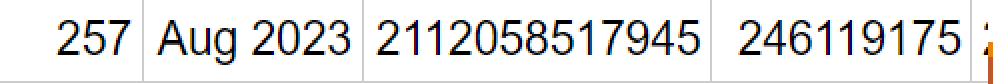
Japonská **DDBJ** (1984)

http://www.ddbj.ni

DNA Data Bank of Japan

X „nemoderované“ databáze (žádná záruka, že data jsou úplně kval



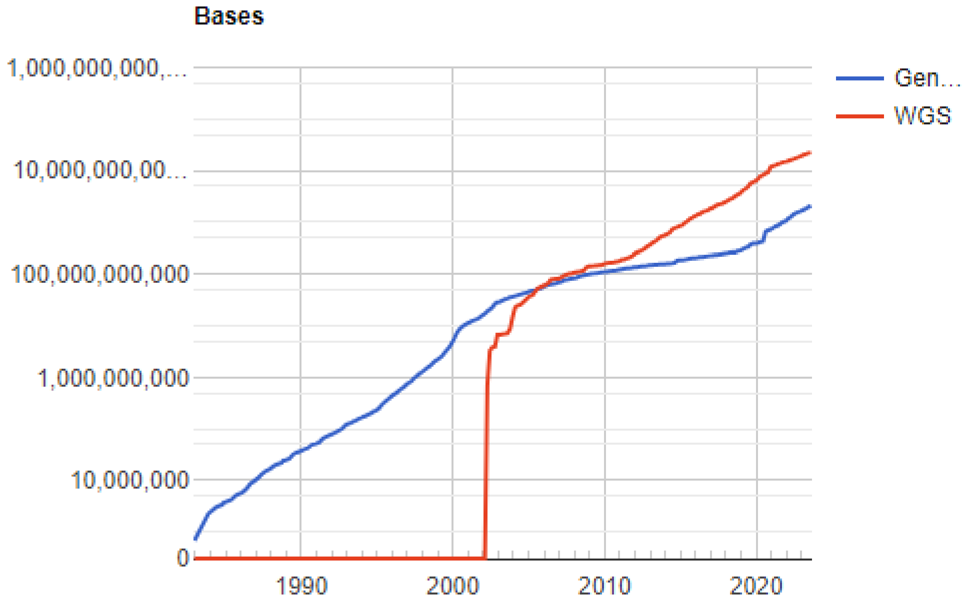


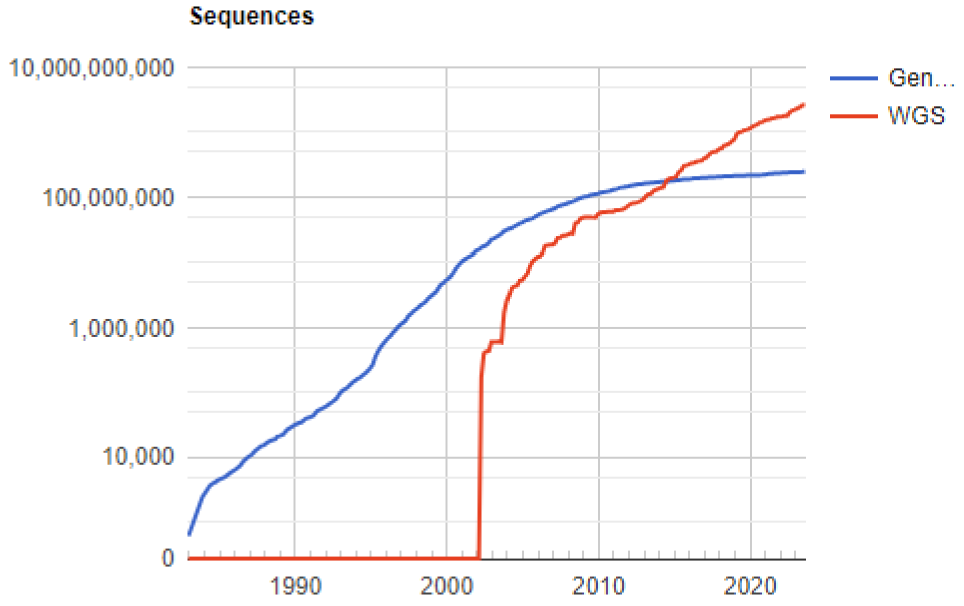
		GenBank	
Release	Date	Bases	Sequences
3	Dec 1982	680338	606
74	Dec 1992	120242234	97084
133	Dec 2002	28507990166	22318883
193	Dec 2012	148390863904	161140325
211	Dec 2015	203939111071	189232925
241	Dec 2020	723 003 822 007	221 467 827
257	Aug 2023	2112058517945	246119175

259 | Dec 2023| 2570711588044 | 249060436

GenBank/NCBI

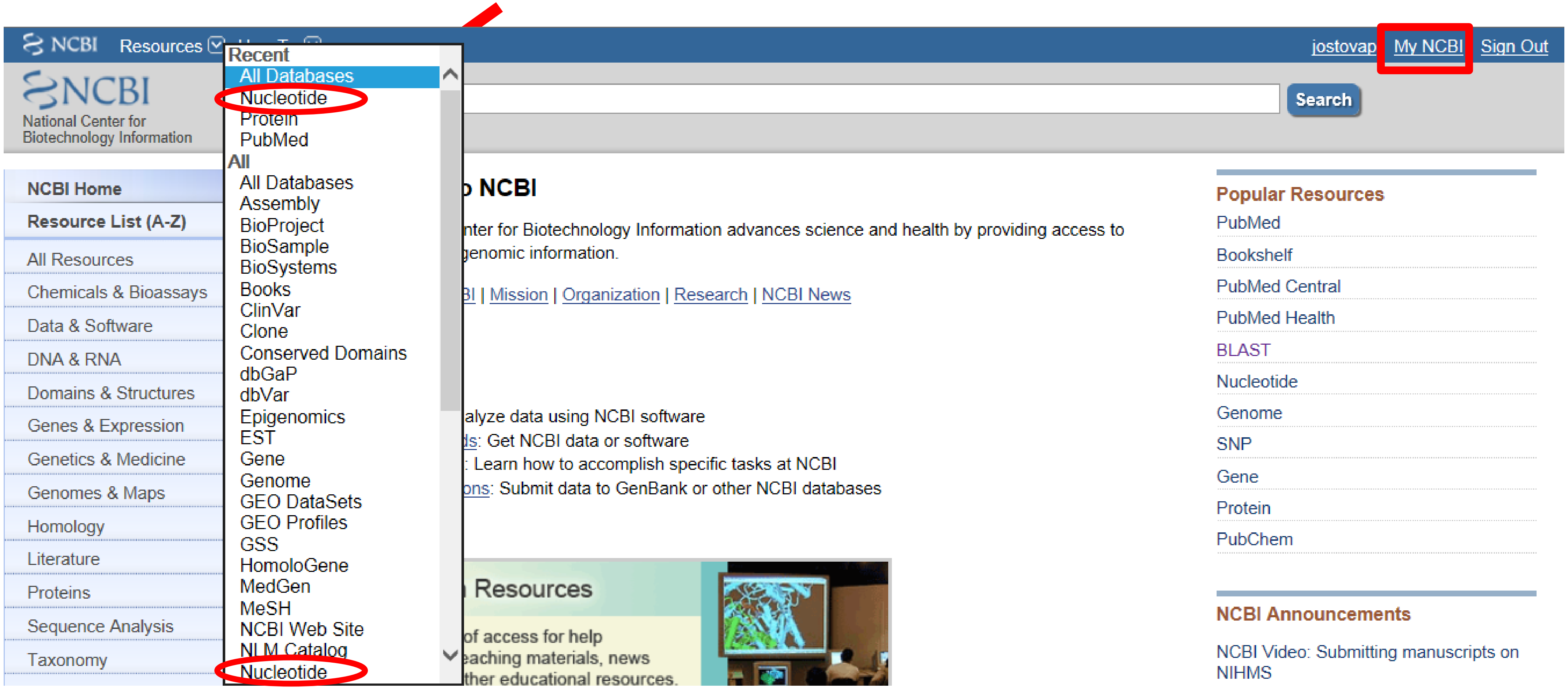
GenBank and WGS Statistics





WGS = whole genome sequencing

DNA databáze NCBI



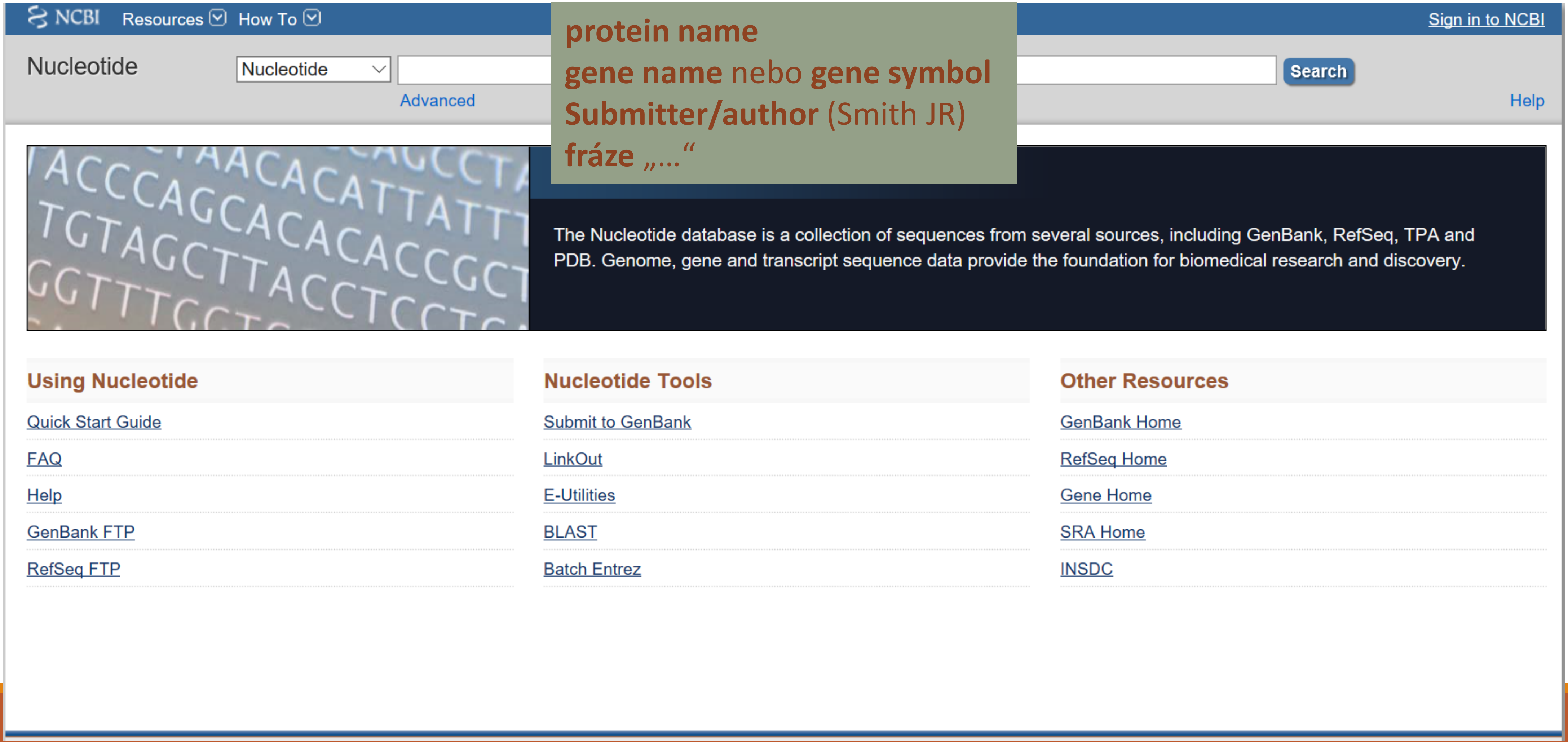
nter for Biotechnology Information advances science and health by providing access to
genomic information.

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

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

NCBI Video: Submitting manuscripts on NIHMS

DNA databáze NCBI



protein name
gene name nebo **gene symbol**
Submitter/author (Smith JR)
fráze „…“

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 databáze NCBI

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

transkript = bez intronů (mRNA)

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

RefSeq Sequences

Items: 1 to 20 of 9424

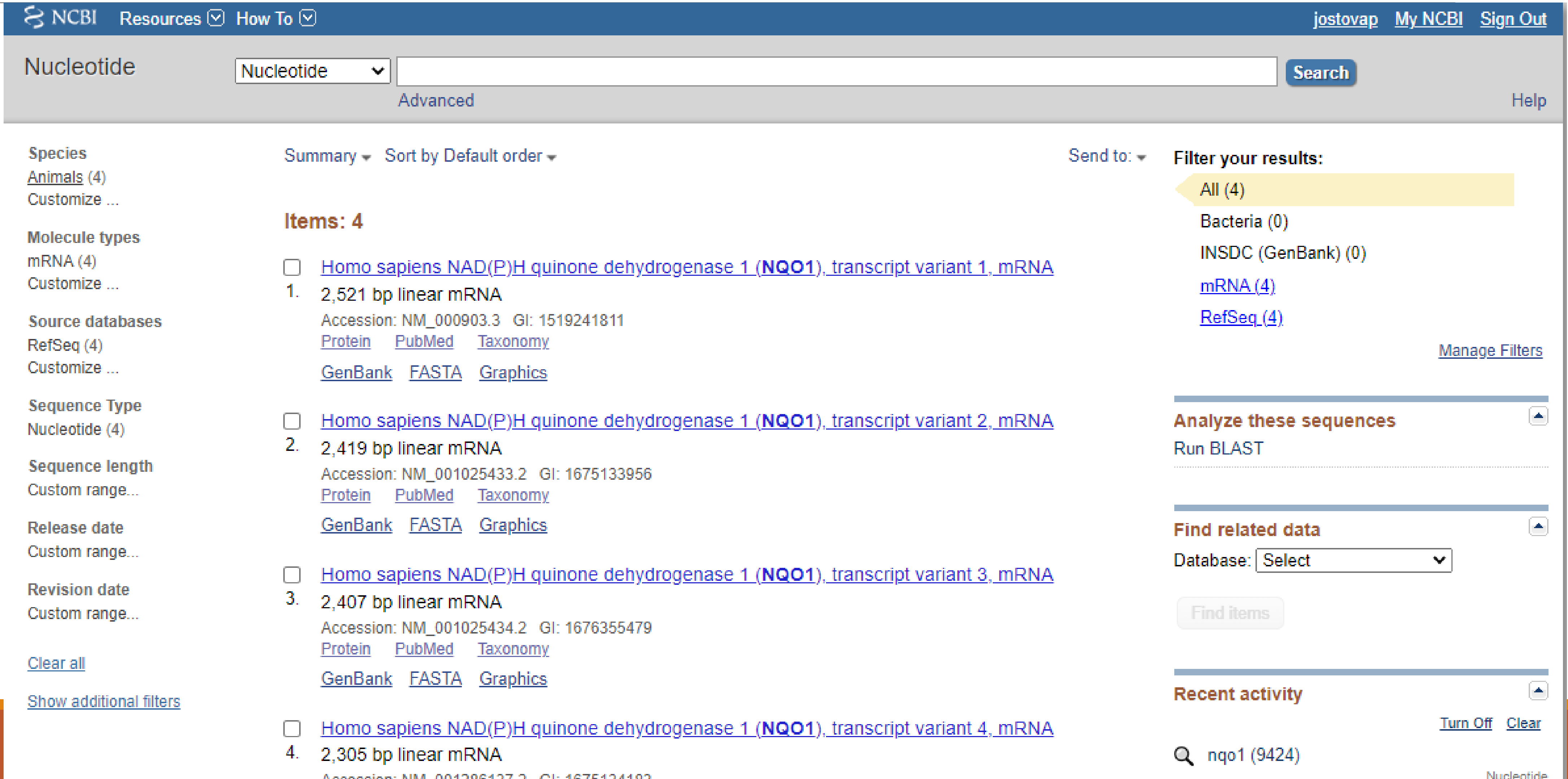
Filter your results:
All (9424)
Bacteria (8564)
INSDC (GenBank) (8754)
mRNA (455)
RefSeq (668)

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

DNA databáze NCBI



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

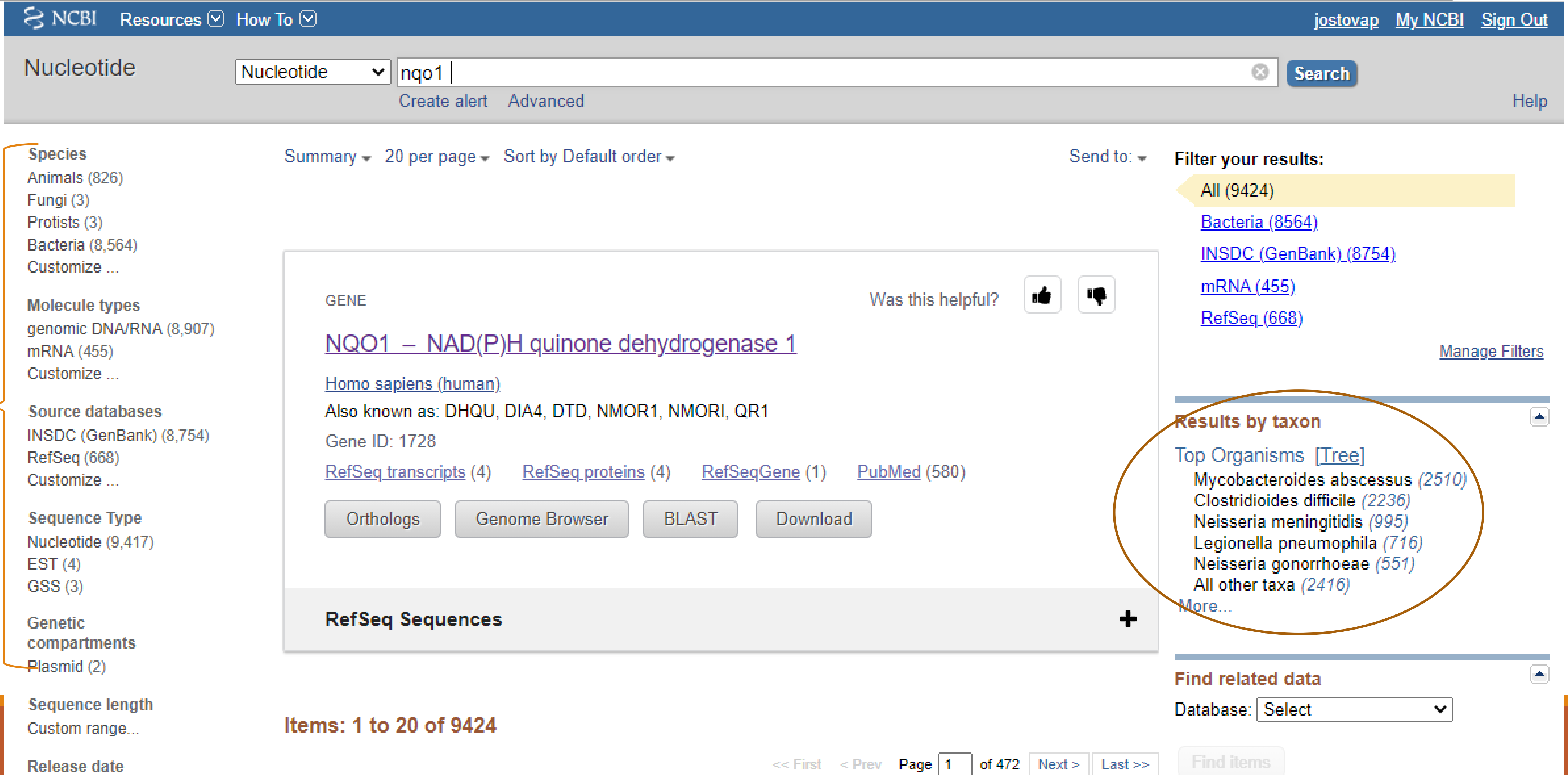
☐ 2. Homo sapiens NAD(P)H quinone dehydrogenase 1 (**NQO1**), transcript variant 2, mRNA
2,419 bp linear mRNA
Accession: NM_001025433.2 GI: 1675133956
Protein PubMed Taxonomy
GenBank FASTA Graphics

☐ 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

DNA databáze NCBI

Omezení na:



NCBI Resources How To | jostovap My NCBI Sign Out

Nucleotide | Nucleotide: nqo1 | Search

Create alert Advanced | Help

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:

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)

Orthologs | Genome Browser | BLAST | Download

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]

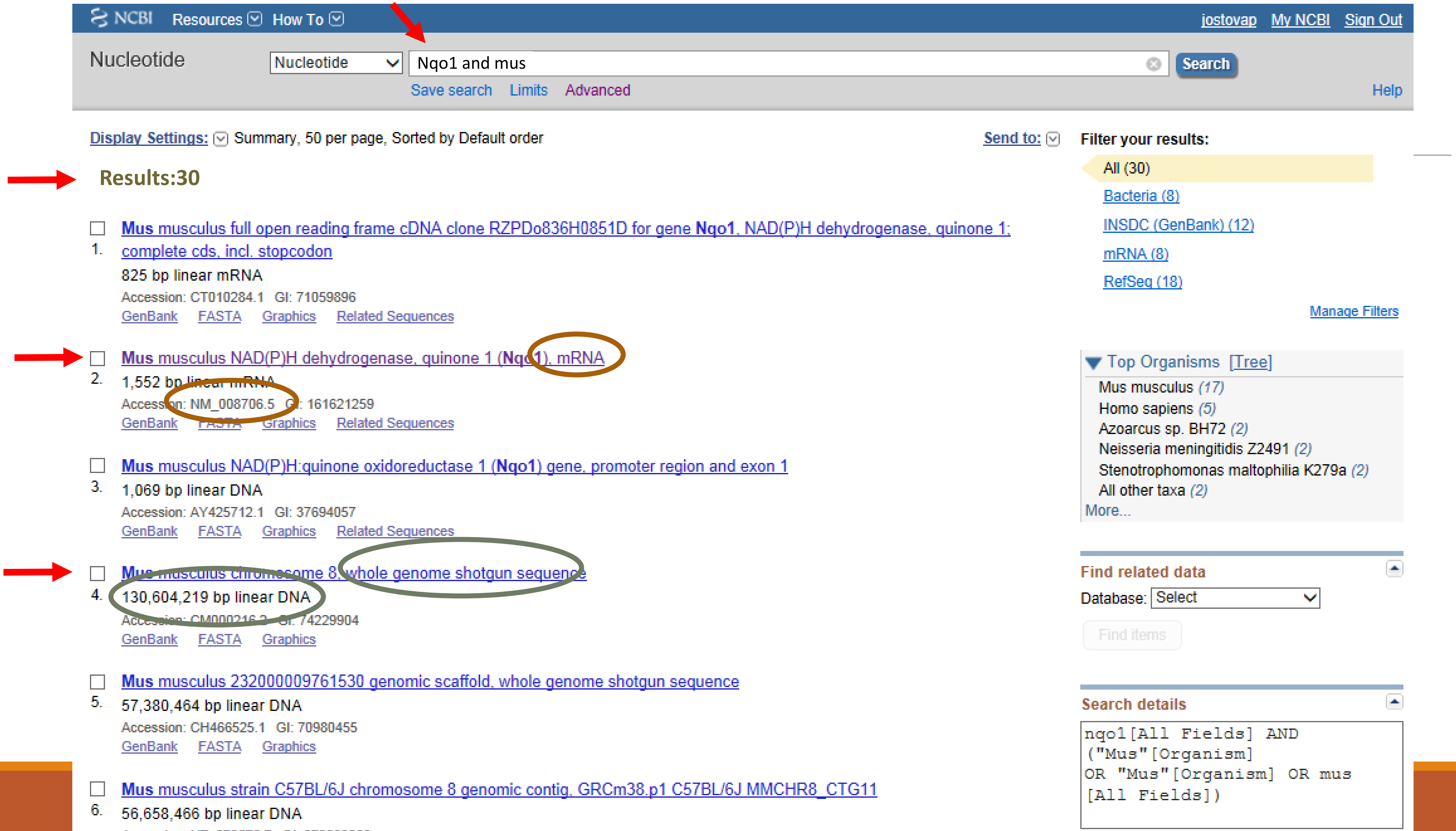
Organism	Count
Mycobacteroides abscessus	(2510)
Clostridioides difficile	(2236)
Neisseria meningitidis	(995)
Legionella pneumophila	(716)
Neisseria gonorrhoeae	(551)
All other taxa	(2416)

More...

Find related data

Database: Select

Find items



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

☐ 5. Mus musculus 232000009761530 genomic scaffold, whole genome shotgun sequence
57,380,464 bp linear DNA
Accession: CH466525.1 GI: 70980455
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)

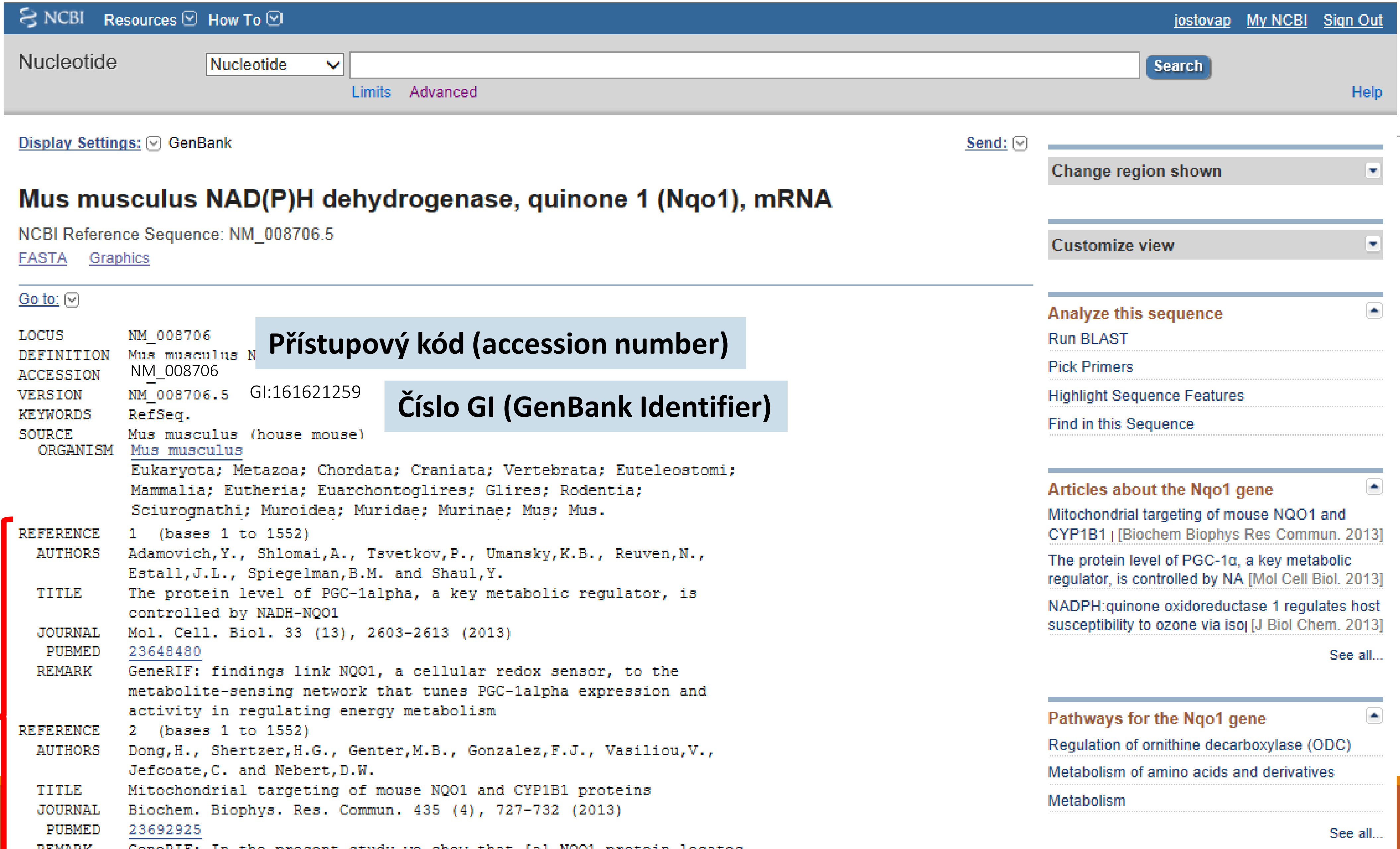
More...

Find related data
Database: Select

Search details

```
nqo1[All Fields] AND
("Mus"[Organism]
OR "Mus"[Organism] OR mus
[All Fields])
```

„GenBank flatfile“



GenBank

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

NCBI Reference Sequence: NM_008706.5

Přístupový kód (accession number)

Číslo GI (GenBank Identifier)

```
LOCUS       NM_008706
DEFINITION  Mus musculus N
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
```

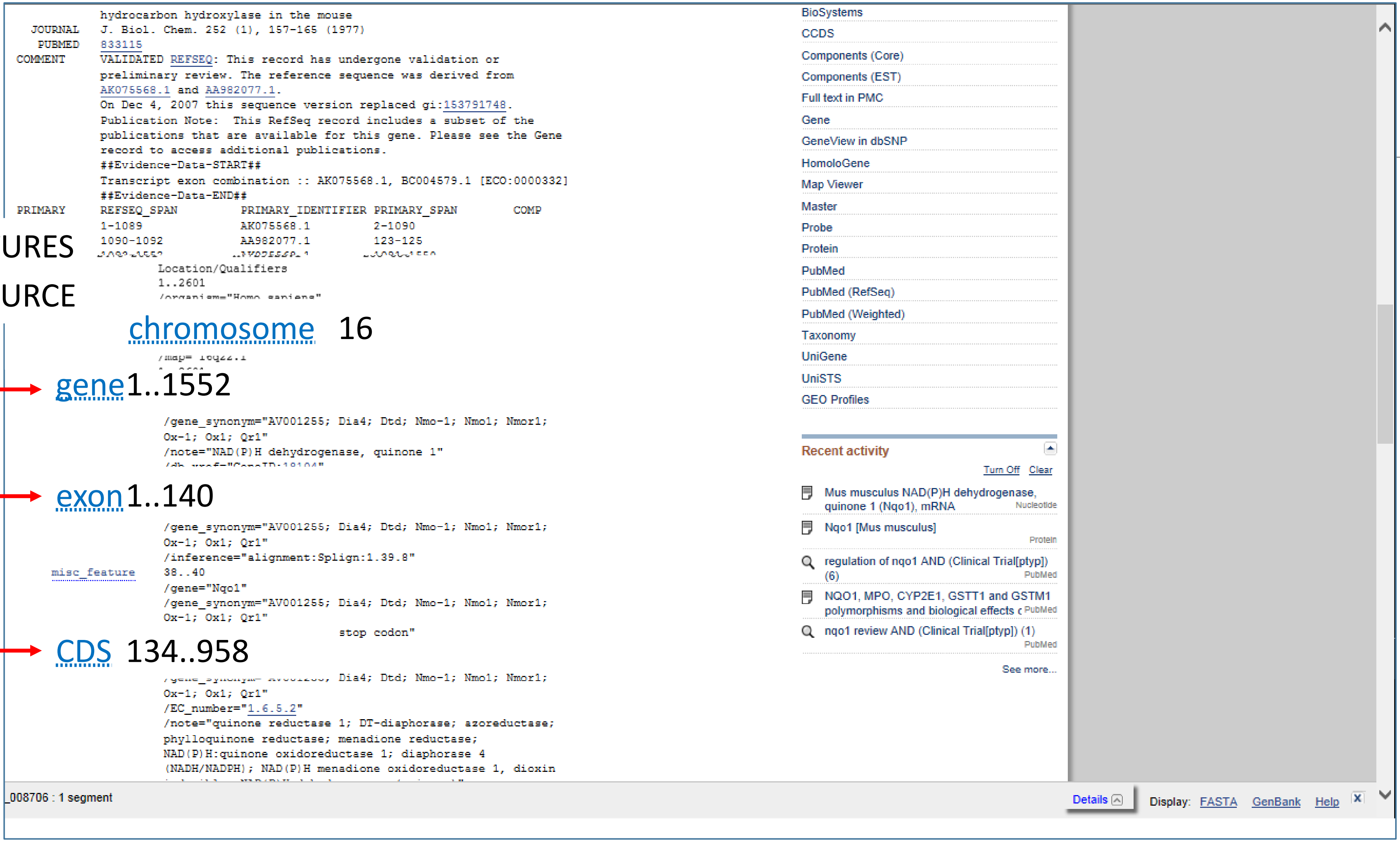
Analyze this sequence
- Run BLAST
- Pick Primers
- Highlight Sequence Features
- Find in this Sequence

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...



```
            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
            1-1089              AK075568.1         2-1090
            1090-1092           AA982077.1         123-125
                    Location/Qualifiers
                    1..2601
                    /organism="Homo sapiens"
```

FEATURES

SOURCE

chromosome 16

gene1..1552

```
                     /gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmo1; Nmor1;
                     Ox-1; Ox1; Qr1"
                     /note="NAD(P)H dehydrogenase, quinone 1"
```

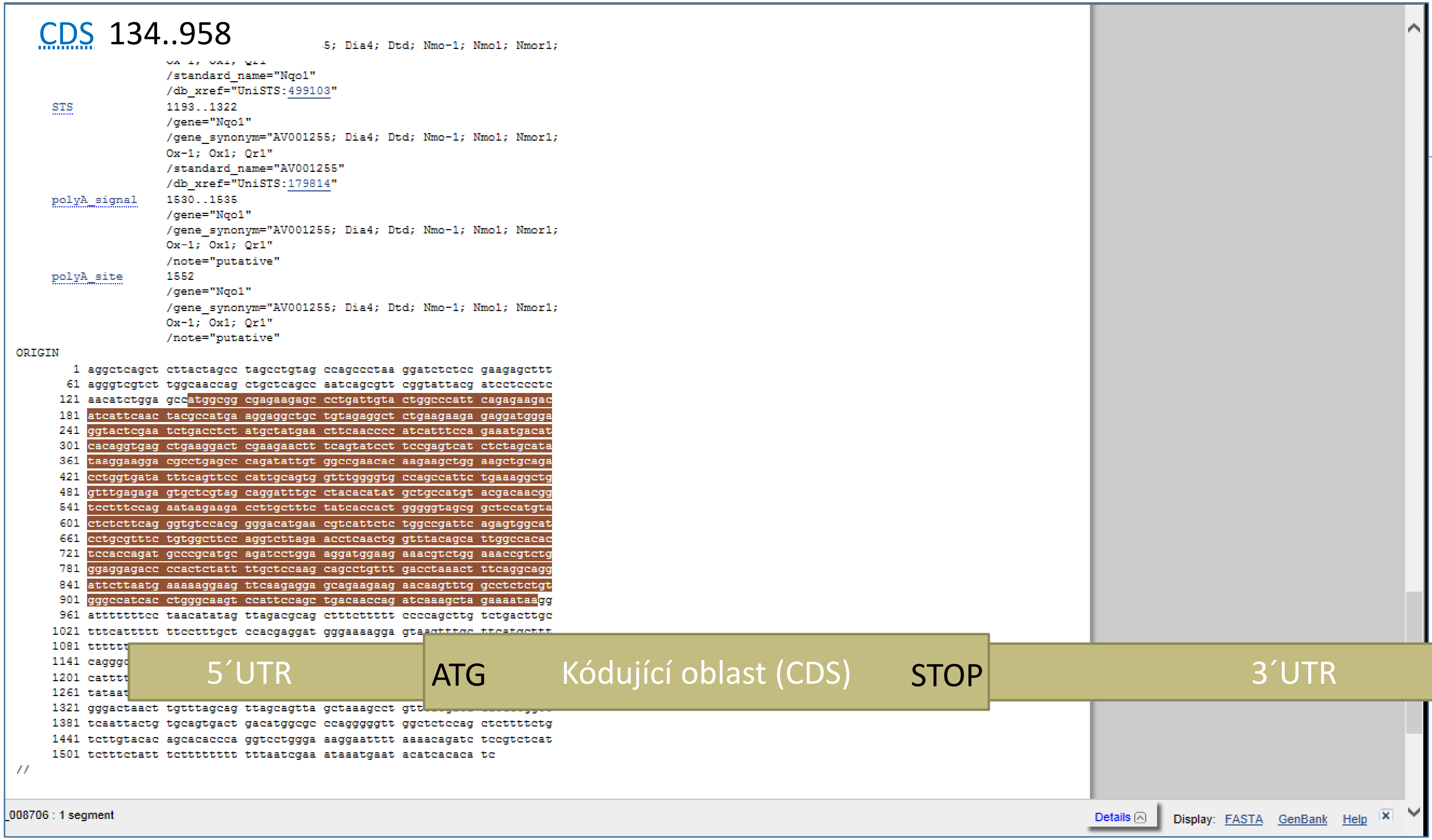
exon1..140

```
                     /gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmo1; Nmor1;
                     Ox-1; Ox1; Qr1"
                     /inference="alignment:Splign:1.39.8"
     misc_feature    38..40
                     /gene="Nqo1"
                     /gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmo1; Nmor1;
                     Ox-1; Ox1; Qr1"
                                          stop codon"
```

CDS 134..958

```
                                   Dia4; Dtd; Nmo-1; Nmo1; Nmor1;
                     Ox-1; Ox1; Qr1"
                     /EC_number="1.6.5.2"
                     /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
```

CDS 134..958



```
                                               5; Dia4; Dtd; Nmo-1; Nmol; Nmor1;
                     Ox-1; Ox1; Qr1"
                     /standard_name="Nqo1"
                     /db_xref="UniSTS:499103"
     STS             1193..1322
                     /gene="Nqo1"
                     /gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmol; Nmor1;
                     Ox-1; Ox1; Qr1"
                     /standard_name="AV001255"
                     /db_xref="UniSTS:179814"
     polyA_signal    1530..1535
                     /gene="Nqo1"
                     /gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmol; Nmor1;
                     Ox-1; Ox1; Qr1"
                     /note="putative"
     polyA_site      1552
                     /gene="Nqo1"
                     /gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmol; Nmor1;
                     Ox-1; Ox1; Qr1"
                     /note="putative"
ORIGIN
        1 aggctcagct cttactagcc tagcctgtag ccagccctaa ggatctctcc gaagagcttt
       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 atttttttcc taacatatag ttagacgcag ctttcttttt ccccagcttg tctgacttgc
     1021 tttcattttt ttcctttgct ccacgaggat gggaaaagga gtaagtttgc ttcatgcttt
     1081 tttttt
     1141 caggg
     1201 cattt
     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
//
```

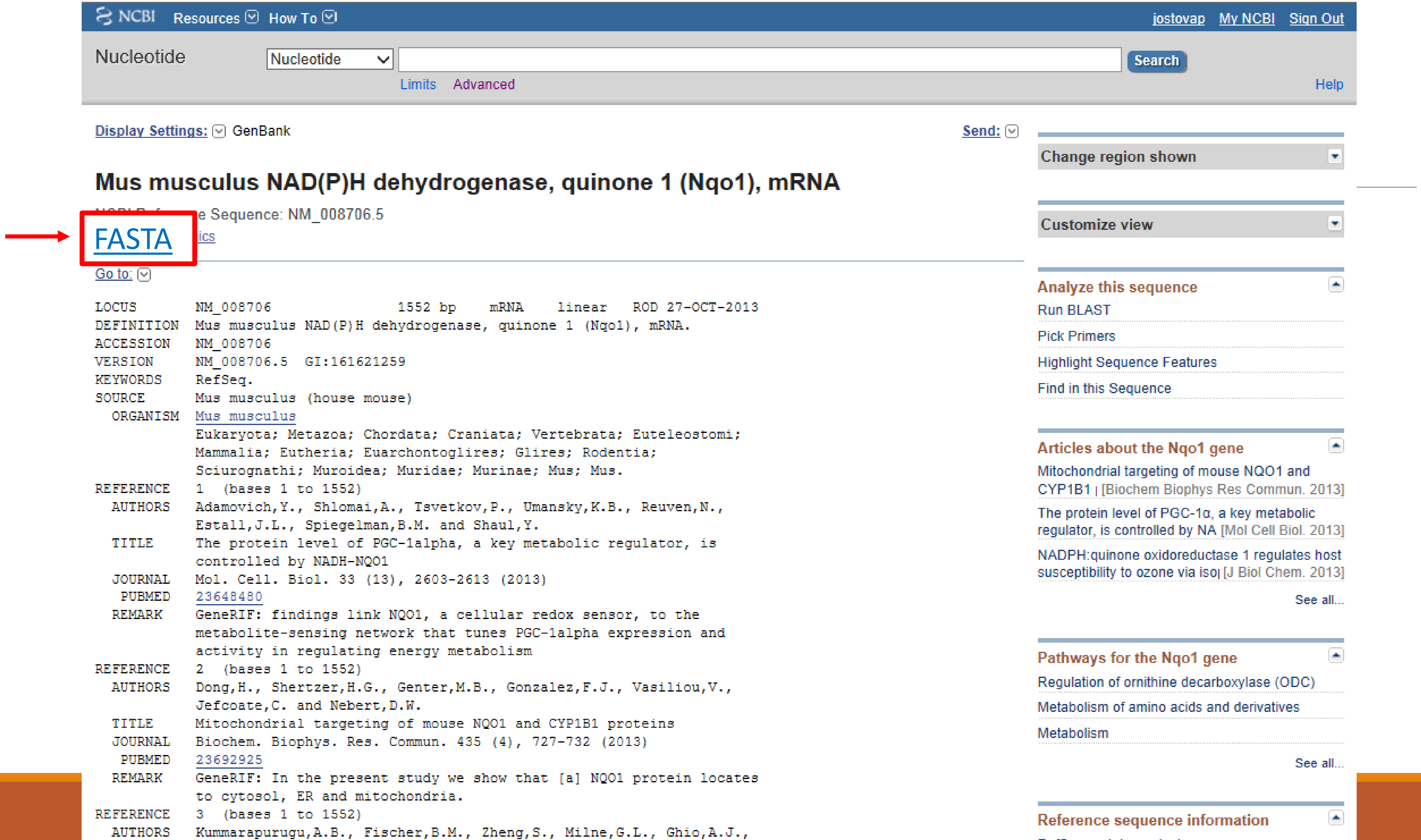
5´UTR

ATG

Kódující oblast (CDS)

STOP

3´UTR



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

NCBI R... e Sequence: NM_008706.5

FASTA ...ics

```
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

FASTA (a RAW) formát

název odvozen:

FASTA = populární program pro porovnávání sekvencí a prohledávání databází

W.R. Pearson a D.J. Lipman 1988

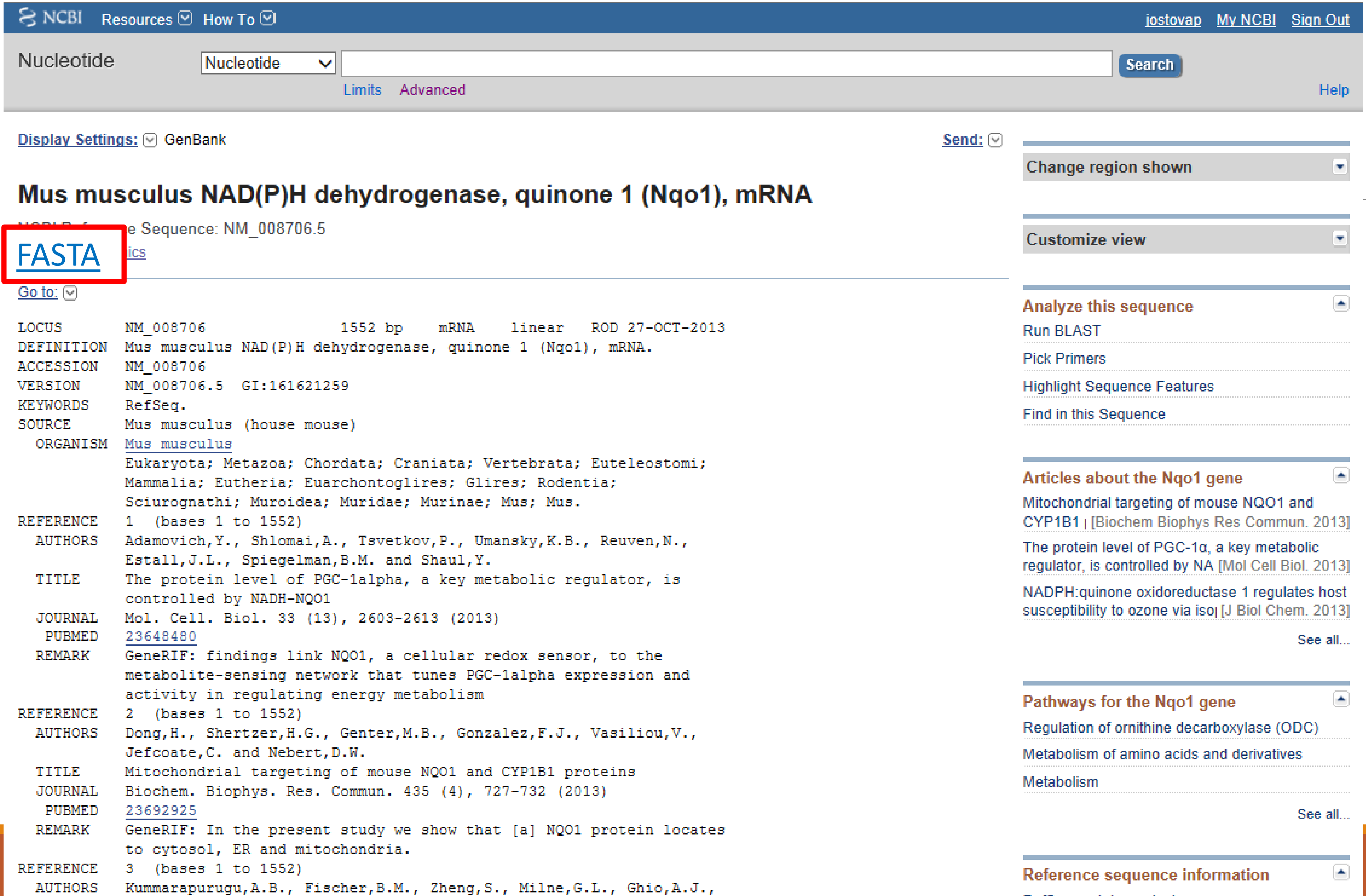
následující formát sekvence:

```
>NQO1_mus
AGGCTCAGCTCTTACTAGCCTAGCCTGTA
GCCAGCCCTAAGGATCTCTCCGAAGAGCT
AATGTCGG
```

```
AGGCTCAGCTCTTACTAGCCTAGCCTGTA
GCCAGCCCTAAGGATCTCTCCGAAGAGCT
AATGTCGG
```

1. „definiční“ řádek (hlavička) začíná **>** a obsahuje unikátní identifikátor, následovaný krátkým popisem (nemusí být).

2. řádek – vlastní sekvence (DNA/protein- v jedno-písmenném kódování (až po další symbol >, určující začátek další sekvence.



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

e Sequence: NM_008706.5

FASTA

ics

```
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...

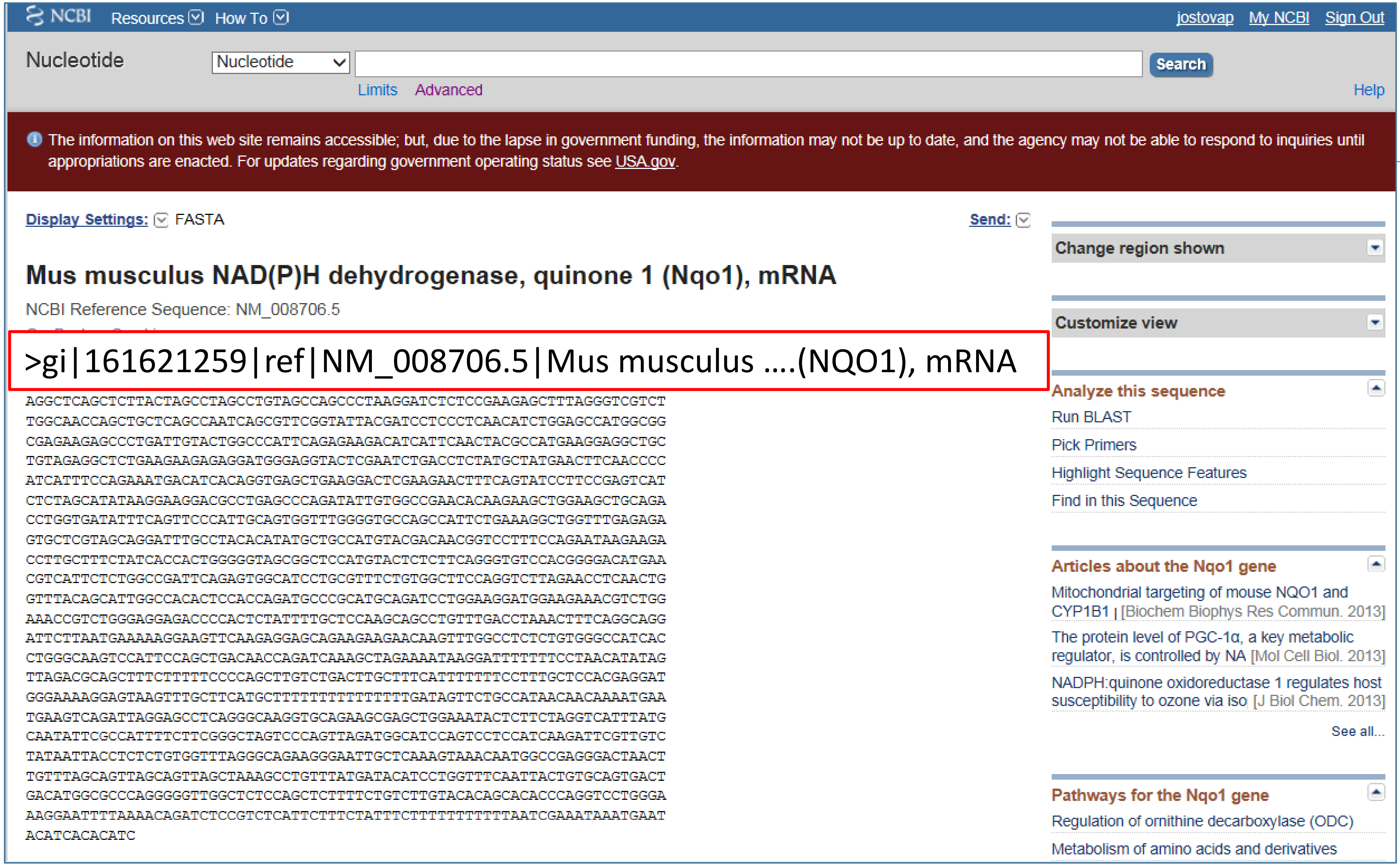
Pathways for the Nqo1 gene

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

See all...

Reference sequence information

fasta



The information on this web site remains accessible; but, due to the lapse in government funding, the information may not be up to date, and the agency may not be able to respond to inquiries until appropriations are enacted. For updates regarding government operating status see USA.gov.

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

NCBI Reference Sequence: NM_008706.5

```
>gi|161621259|ref|NM_008706.5|Mus musculus ....(NQO1), mRNA
AGGCTCAGCTCTTACTAGCCTAGCCTGTAGCCAGCCCTAAGGATCTCTCCGAAGAGCTTTAGGGTCGTCT
TGGCAACCAGCTGCTCAGCCAATCAGCGTTCGGTATTACGATCCTCCCTCAACATCTGGAGCCATGGCGG
CGAGAAGAGCCCTGATTGTACTGGCCCATTCAGAGAAGACATCATTCAACTACGCCATGAAGGAGGCTGC
TGTAGAGGCTCTGAAGAAGAGAGGATGGGAGGTACTCGAATCTGACCTCTATGCTATGAACTTCAACCCC
ATCATTTCCAGAAATGACATCACAGGTGAGCTGAAGGACTCGAAGAACTTTCAGTATCCTTCCGAGTCAT
CTCTAGCATATAAGGAAGGACGCCTGAGCCCAGATATTGTGGCCGAACACAAGAAGCTGGAAGCTGCAGA
CCTGGTGATATTTCAGTTCCCATTGCAGTGGTTTGGGGTGCCAGCCATTCTGAAAGGCTGGTTTGAGAGA
GTGCTCGTAGCAGGATTTGCCTACACATATGCTGCCATGTACGACAACGGTCCTTTCCAGAATAAGAAGA
CCTTGCTTTCTATCACCACTGGGGGTAGCGGCTCCATGTACTCTCTTCAGGGTGTCCACGGGGACATGAA
CGTCATTCTCTGGCCGATTCAGAGTGGCATCCTGCGTTTCTGTGGCTTCCAGGTCTTAGAACCTCAACTG
GTTTACAGCATTGGCCACACTCCACCAGATGCCCGCATGCAGATCCTGGAAGGATGGAAGAAACGTCTGG
AAACCGTCTGGGAGGAGACCCCACTCTATTTTGCTCCAAGCAGCCTGTTTGACCTAAACTTTCAGGCAGG
ATTCTTAATGAAAAAGGAAGTTCAAGAGGAGCAGAAGAAGAACAAGTTTGGCCTCTCTGTGGGCCATCAC
CTGGGCAAGTCCATTCCAGCTGACAACCAGATCAAAGCTAGAAAATAAGGATTTTTTTCCTAACATATAG
TTAGACGCAGCTTTCTTTTTCCCCAGCTTGTCTGACTTGCTTTCATTTTTTTCCTTTGCTCCACGAGGAT
GGGAAAAGGAGTAAGTTTGCTTCATGCTTTTTTTTTTTTTTTGATAGTTCTGCCATAACAACAAAATGAA
TGAAGTCAGATTAGGAGCCTCAGGGCAAGGTGCAGAAGCGAGCTGGAAATACTCTTCTAGGTCATTTATG
CAATATTCGCCATTTTCTTCGGGCTAGTCCCAGTTAGATGGCATCCAGTCCTCCATCAAGATTCGTTGTC
TATAATTACCTCTCTGTGGTTTAGGGCAGAAGGGAATTGCTCAAAGTAAACAATGGCCGAGGGACTAACT
TGTTTAGCAGTTAGCAGTTAGCTAAAGCCTGTTTATGATACATCCTGGTTTCAATTACTGTGCAGTGACT
GACATGGCGCCCAGGGGGTTGGCTCTCCAGCTCTTTTCTGTCTTGTACACAGCACACCCAGGTCCTGGGA
AAGGAATTTTAAAACAGATCTCCGTCTCATTCTTTCTATTTCTTTTTTTTTTTAATCGAAATAAATGAAT
ACATCACACATC
```

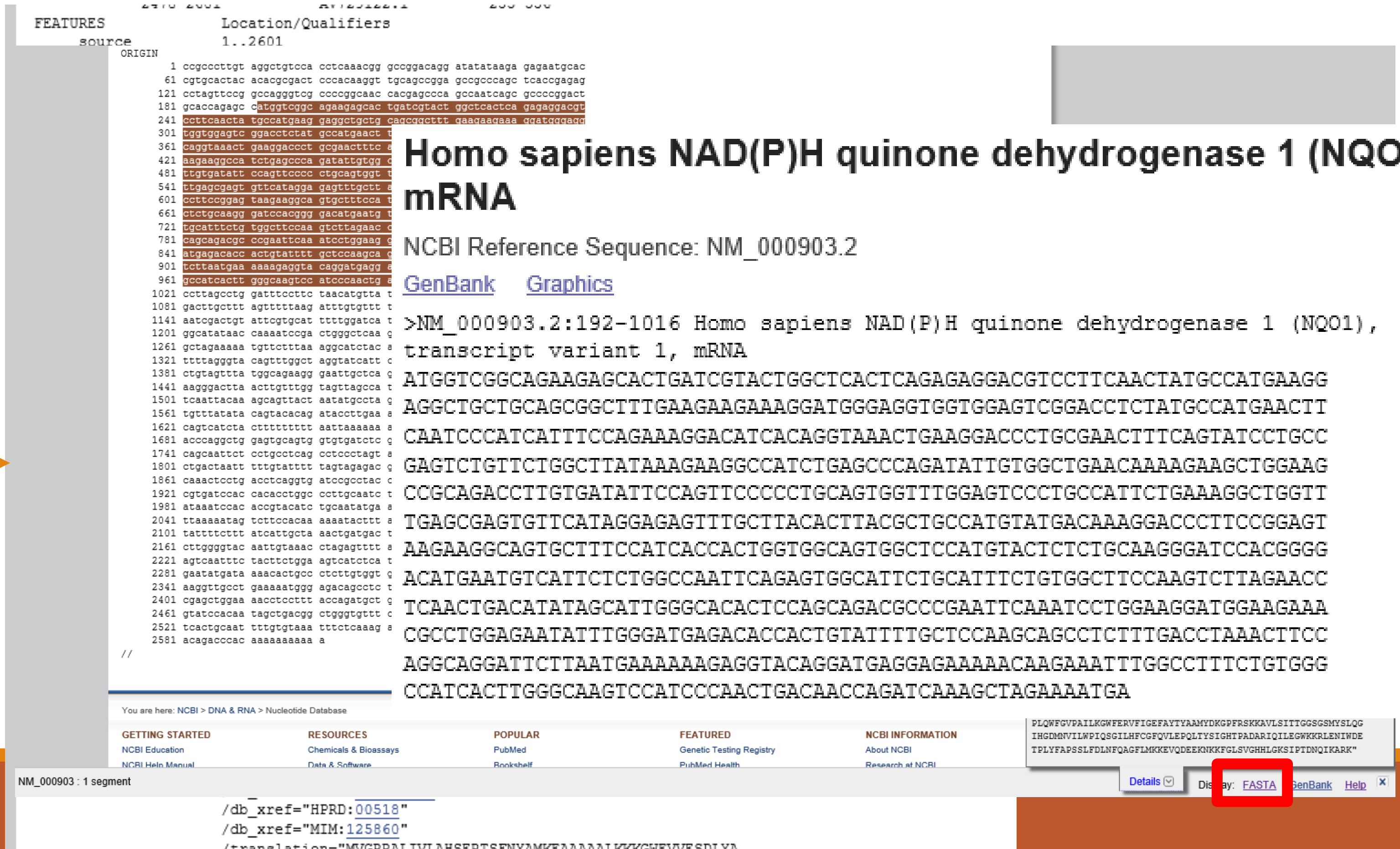
Mitochondrial targeting of mouse NQO1 and CYP1B1 | [Biochem Biophys Res Commun. 2013]

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]

NCBI/Jen kódující sekvence (CDS)

„nakliknout“ oblast CDS → zabarví se příslušná část sekvence hnědě (FASTA odkaz vpravo dole ukáže jen tuto část)



```
FEATURES             Location/Qualifiers
     source          1..2601
ORIGIN
        1 ccgcccttgt aggctgtcca cctcaaacgg gccggacagg atatataaga gagaatgcac
       61 cgtgcactac acacgcgact cccacaaggt tgcagccgga gccgcccagc tcaccgagag
      121 cctagttccg gccagggtcg ccccggcaac cacgagccca gccaatcagc gccccggact
      181 gcaccagagc catggtcggc agaagagcac tgatcgtact ggctcactca gagaggacgt
```

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

NCBI Reference Sequence: NM_000903.2

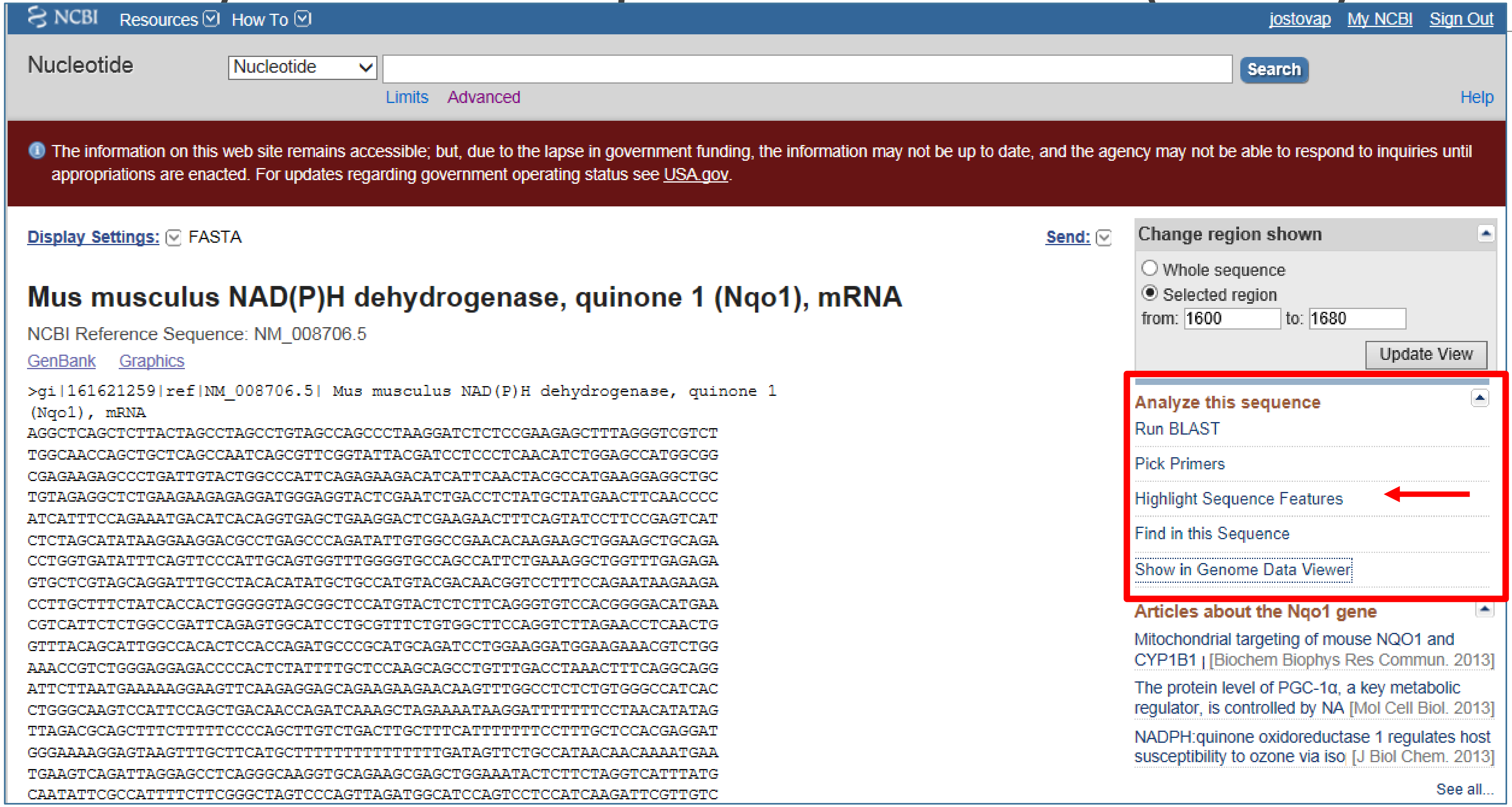
GenBank Graphics

```
>NM_000903.2:192-1016 Homo sapiens NAD(P)H quinone dehydrogenase 1 (NQO1),
transcript variant 1, mRNA
ATGGTCGGCAGAAGAGCACTGATCGTACTGGCTCACTCAGAGAGGACGTCCTTCAACTATGCCATGAAGG
AGGCTGCTGCAGCGGCTTTGAAGAAGAAAGGATGGGAGGTGGTGGAGTCGGACCTCTATGCCATGAACTT
CAATCCCATCATTTCCAGAAAGGACATCACAGGTAAACTGAAGGACCCTGCGAACTTTCAGTATCCTGCC
GAGTCTGTTCTGGCTTATAAAGAAGGCCATCTGAGCCCAGATATTGTGGCTGAACAAAAGAAGCTGGAAG
CCGCAGACCTTGTGATATTCCAGTTCCCCCTGCAGTGGTTTGGAGTCCCTGCCATTCTGAAAGGCTGGTT
TGAGCGAGTGTTCATAGGAGAGTTTGCTTACACTTACGCTGCCATGTATGACAAAGGACCCTTCCGGAGT
AAGAAGGCAGTGCTTTCCATCACCACTGGTGGCAGTGGCTCCATGTACTCTCTGCAAGGGATCCACGGGG
ACATGAATGTCATTCTCTGGCCAATTCAGAGTGGCATTCTGCATTTCTGTGGCTTCCAAGTCTTAGAACC
TCAACTGACATATAGCATTGGGCACACTCCAGCAGACGCCCGAATTCAAATCCTGGAAGGATGGAAGAAA
CGCCTGGAGAATATTTGGGATGAGACACCACTGTATTTTGCTCCAAGCAGCCTCTTTGACCTAAACTTCC
AGGCAGGATTCTTAATGAAAAAAGAGGTACAGGATGAGGAGAAAAACAAGAAATTTGGCCTTTCTGTGGG
CCATCACTTGGGCAAGTCCATCCCAACTGACAACCAGATCAAAGCTAGAAAATGA
```

```
PLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRSKKAVLSITTGGSGSMYSLQG
IHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTPADARIQILEGWKKRLENIWDE
TPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK"
```

```
                     /db_xref="HPRD:00518"
                     /db_xref="MIM:125860"
```

NCBI/Jen kódující sekvence (CDS)



The information on this web site remains accessible; but, due to the lapse in government funding, the information may not be up to date, and the agency may not be able to respond to inquiries until appropriations are enacted. For updates regarding government operating status see USA.gov.

Display Settings: FASTA

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

NCBI Reference Sequence: NM_008706.5

```
>gi|161621259|ref|NM_008706.5| Mus musculus NAD(P)H dehydrogenase, quinone 1
(Nqo1), mRNA
AGGCTCAGCTCTTACTAGCCTAGCCTGTAGCCAGCCCTAAGGATCTCTCCGAAGAGCTTTAGGGTCGTCT
TGGCAACCAGCTGCTCAGCCAATCAGCGTTCGGTATTACGATCCTCCCTCAACATCTGGAGCCATGGCGG
CGAGAAGAGCCCTGATTGTACTGGCCCATTCAGAGAAGACATCATTCAACTACGCCATGAAGGAGGCTGC
TGTAGAGGCTCTGAAGAAGAGAGGATGGGAGGTACTCGAATCTGACCTCTATGCTATGAACTTCAACCCC
ATCATTTCCAGAAATGACATCACAGGTGAGCTGAAGGACTCGAAGAACTTTCAGTATCCTTCCGAGTCAT
CTCTAGCATATAAGGAAGGACGCCTGAGCCCAGATATTGTGGCCGAACACAAGAAGCTGGAAGCTGCAGA
CCTGGTGATATTTCAGTTCCCATTGCAGTGGTTTGGGGTGCCAGCCATTCTGAAAGGCTGGTTTGAGAGA
GTGCTCGTAGCAGGATTTGCCTACACATATGCTGCCATGTACGACAACGGTCCTTTCCAGAATAAGAAGA
CCTTGCTTTCTATCACCACTGGGGGTAGCGGCTCCATGTACTCTCTTCAGGGTGTCCACGGGGACATGAA
CGTCATTCTCTGGCCGATTCAGAGTGGCATCCTGCGTTTCTGTGGCTTCCAGGTCTTAGAACCTCAACTG
GTTTACAGCATTGGCCACACTCCACCAGATGCCCGCATGCAGATCCTGGAAGGATGGAAGAAACGTCTGG
AAACCGTCTGGGAGGAGACCCCACTCTATTTTGCTCCAAGCAGCCTGTTTGACCTAAACTTTCAGGCAGG
ATTCTTAATGAAAAAGGAAGTTCAAGAGGAGCAGAAGAAGAACAAGTTTGGCCTCTCTGTGGGCCATCAC
CTGGGCAAGTCCATTCCAGCTGACAACCAGATCAAAGCTAGAAAATAAGGATTTTTTTCCTAACATATAG
TTAGACGCAGCTTTCTTTTTCCCCAGCTTGTCTGACTTGCTTTCATTTTTTTCCTTTGCTCCACGAGGAT
GGGAAAAGGAGTAAGTTTGCTTCATGCTTTTTTTTTTTTTTTGATAGTTCTGCCATAACAACAAAATGAA
TGAAGTCAGATTAGGAGCCTCAGGGCAAGGTGCAGAAGCGAGCTGGAAATACTCTTCTAGGTCATTTATG
CAATATTCGCCATTTTCTTCGGGCTAGTCCCAGTTAGATGGCATCCAGTCCTCCATCAAGATTCGTTGTC
```

Change region shown

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

Analyze this sequence

- Run BLAST
- Pick Primers
- Highlight Sequence Features
- Find in this Sequence
- Show in Genome Data Viewer

Articles about the Nqo1 gene

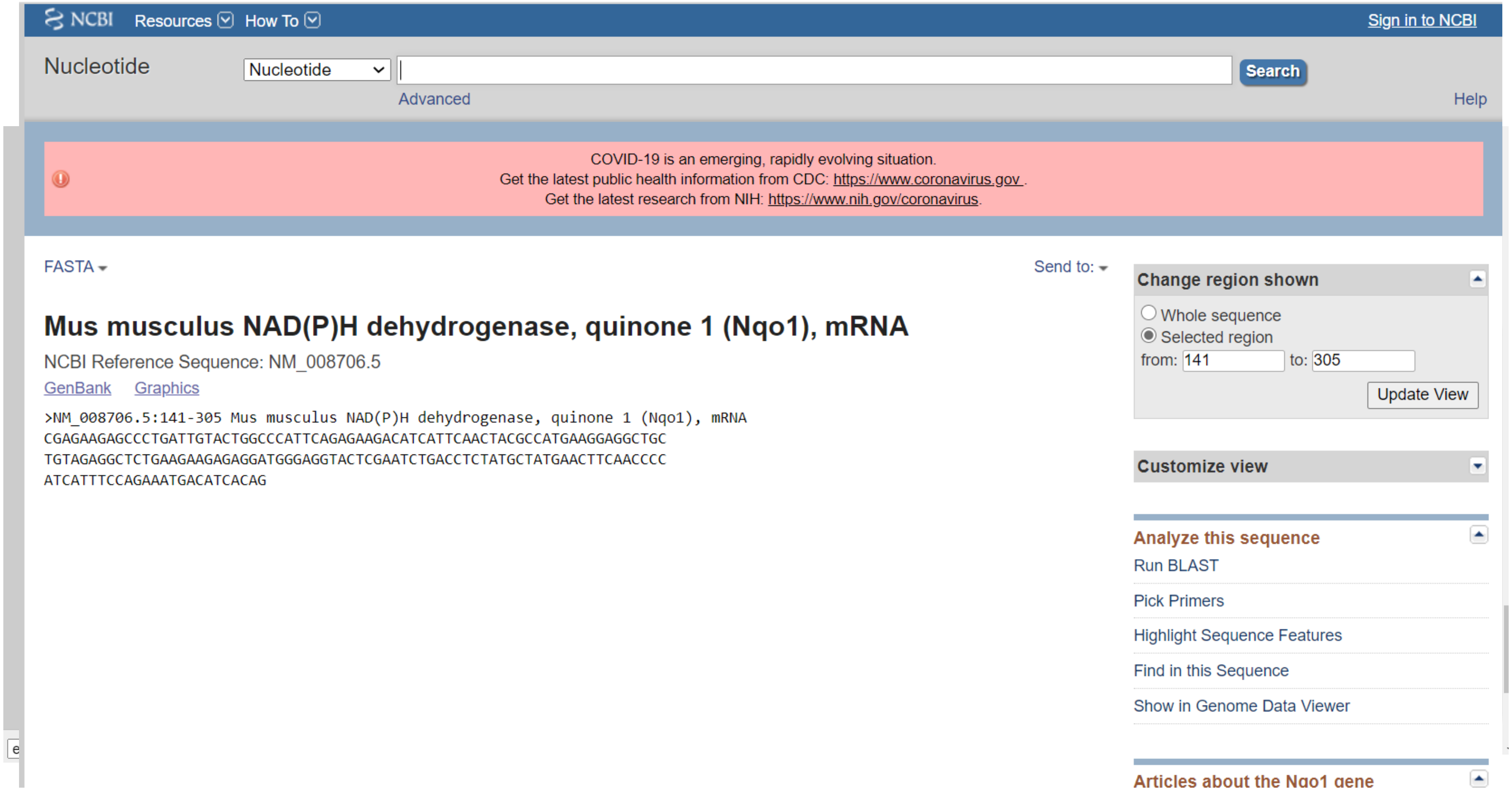
Mitochondrial targeting of mouse NQO1 and CYP1B1 | [Biochem Biophys Res Commun. 2013]

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...

V řádku dole:



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.

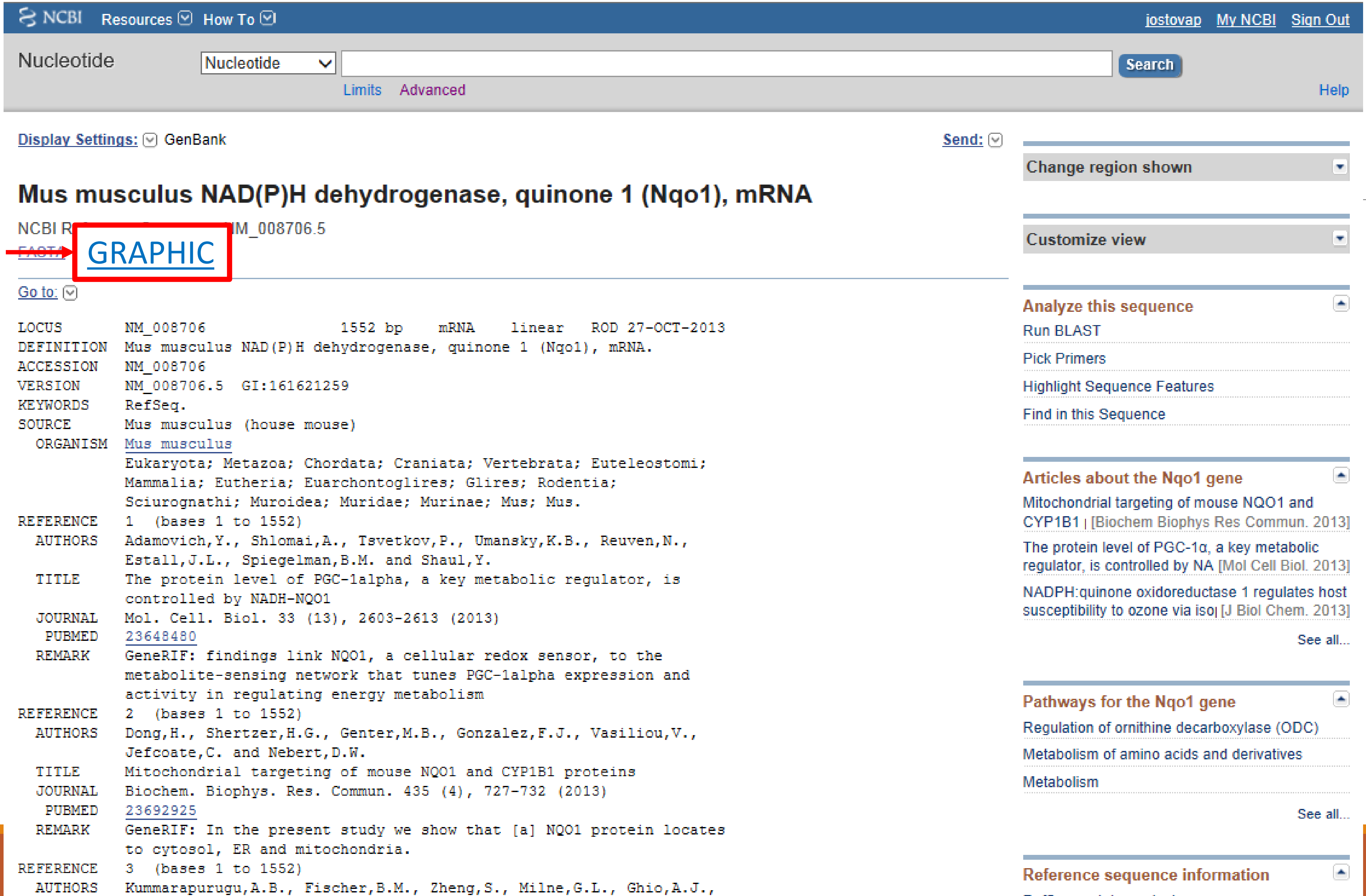
Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA

NCBI Reference Sequence: NM_008706.5

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

Change region shown

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



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

NCBI R M_008706.5

FASTA **GRAPHIC**

```
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...

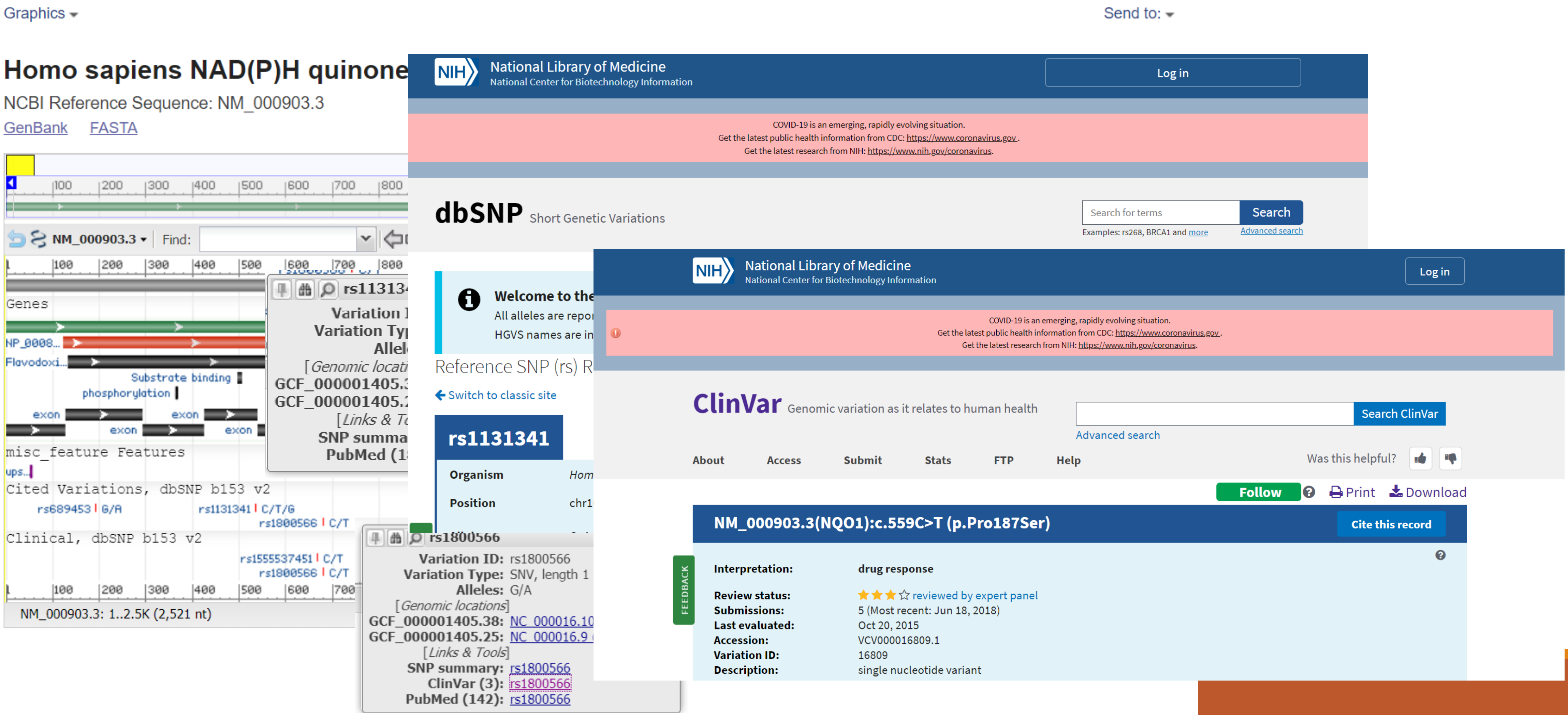
Pathways for the Nqo1 gene

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

See all...

Reference sequence information

NCBI/Graphic



Homo sapiens NAD(P)H quinone

NCBI Reference Sequence: NM_000903.3

GenBank FASTA

rs11313

Variation I
Variation Typ
Allel
[Genomic locati
GCF_000001405.3
GCF_000001405.2
[Links & To
SNP summa
PubMed (1

rs1800566

Variation ID: rs1800566
Variation Type: SNV, length 1
Alleles: G/A
[Genomic locations]
GCF_000001405.38: NC_000016.10
GCF_000001405.25: NC_000016.9
[Links & Tools]
SNP summary: rs1800566
ClinVar (3): rs1800566
PubMed (142): rs1800566

NIH National Library of Medicine
National Center for Biotechnology Information

Log in

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.

dbSNP Short Genetic Variations

Welcome to the
All alleles are repo
HGVS names are in

Reference SNP (rs) R

Switch to classic site

rs1131341

Organism	*Hom*
Position	chr1

NIH National Library of Medicine
National Center for Biotechnology Information

Log in

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.

ClinVar Genomic variation as it relates to human health

NM_000903.3(NQO1):c.559C>T (p.Pro187Ser)

Cite this record

Interpretation:	drug response
Review status:	★★★☆ reviewed by expert panel
Submissions:	5 (Most recent: Jun 18, 2018)
Last evaluated:	Oct 20, 2015
Accession:	VCV000016809.1
Variation ID:	16809
Description:	single nucleotide variant

Ukázka možností NCBI/flatfile

organismus

mRNA, CDS, region

Find in sequence

Vyhledejte si „vlastní“ sekvenci

vyzkoušejte možnosti

-podívejte se GRAPHIC zobrazení a obsažené SNP

DNA databáze NCBI


NCBI Resources How To jostovap My NCBI Sign Out

Nucleotide

Nucleotide nqo1 Search

Create alert Advanced Help

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:

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)

Orthologs Genome Browser BLAST Download

gen = včetně intronů (~ genomová DNA)

RefSeq Sequences

Items: 1 to 20 of 9424

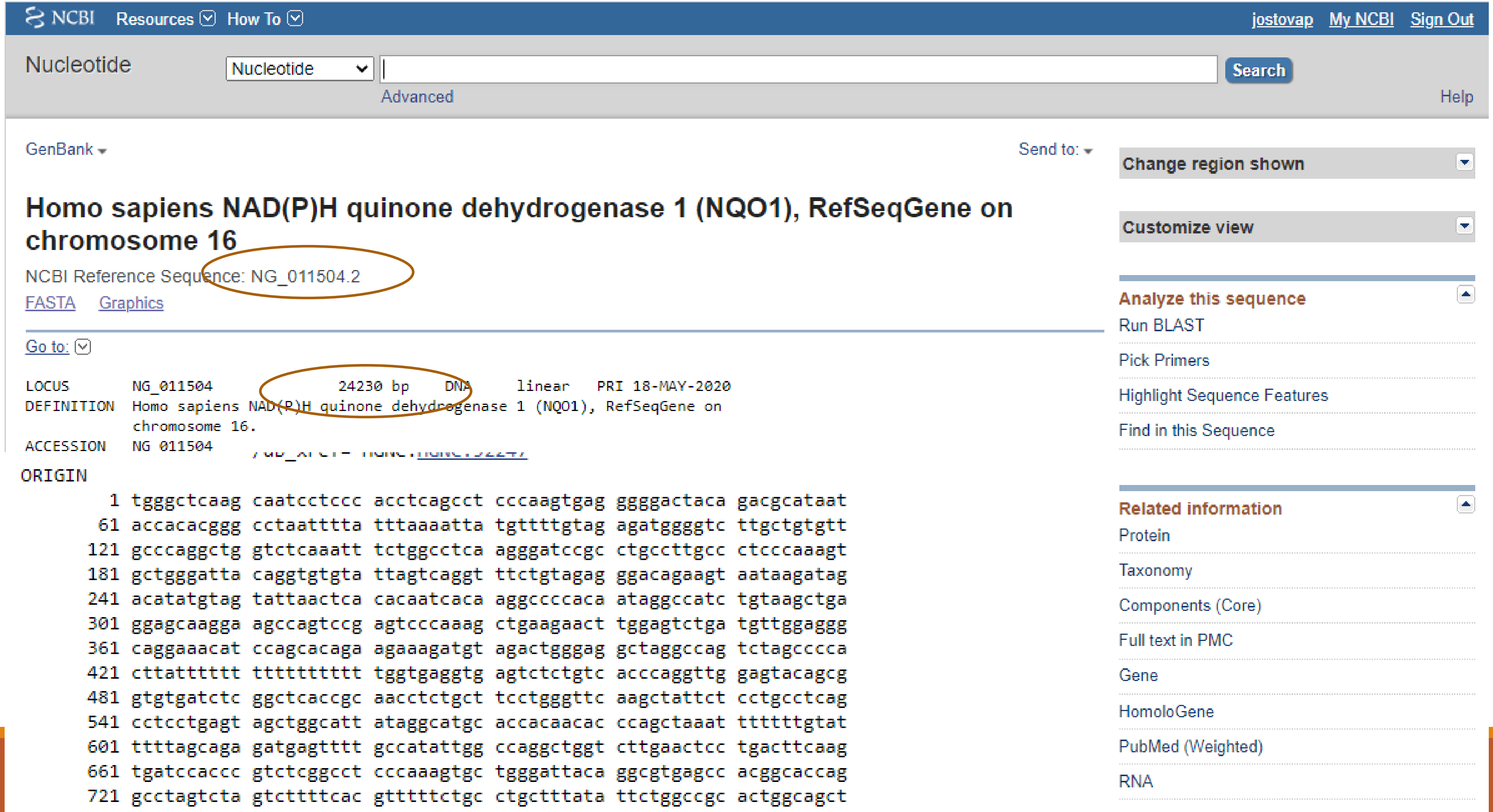
<< First < Prev Page 1 of 472 Next > Last >>

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 databáze NCBI – sekvence genu

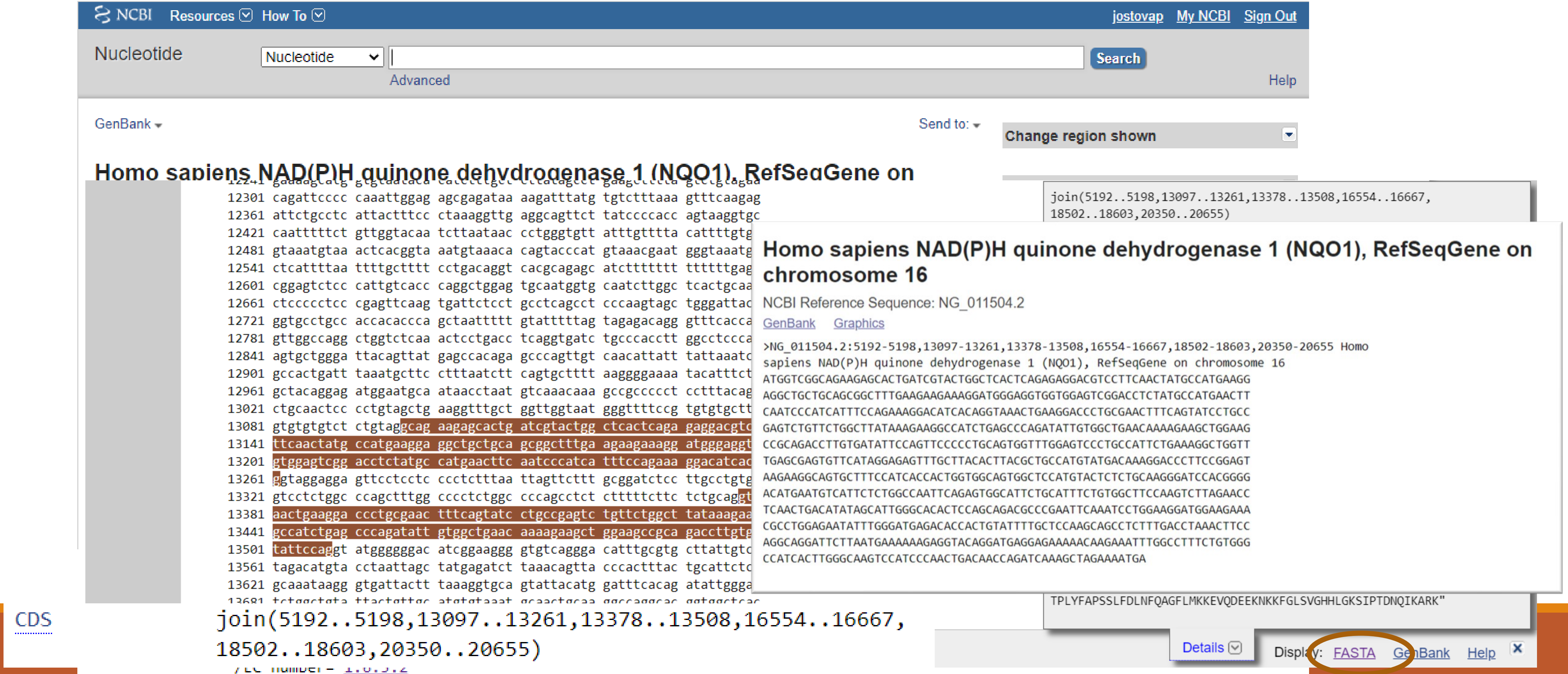


Homo sapiens NAD(P)H quinone dehydrogenase 1 (NQO1), RefSeqGene on chromosome 16

NCBI Reference Sequence: NG_011504.2

```
LOCUS       NG_011504               24230 bp    DNA     linear   PRI 18-MAY-2020
DEFINITION  Homo sapiens NAD(P)H quinone dehydrogenase 1 (NQO1), RefSeqGene on
            chromosome 16.
ACCESSION   NG 011504
ORIGIN
        1 tgggctcaag caatcctccc acctcagcct cccaagtgag ggggactaca gacgcataat
       61 accacacggg cctaatttta tttaaaatta tgttttgtag agatggggtc ttgctgtgtt
      121 gcccaggctg gtctcaaatt tctggcctca agggatccgc ctgccttgcc ctcccaaagt
      181 gctgggatta caggtgtgta ttagtcaggt ttctgtagag ggacagaagt aataagatag
      241 acatatgtag tattaactca cacaatcaca aggccccaca ataggccatc tgtaagctga
      301 ggagcaagga agccagtccg agtcccaaag ctgaagaact tggagtctga tgttggaggg
      361 caggaaacat ccagcacaga agaaagatgt agactgggag gctaggccag tctagcccca
      421 cttatttttt tttttttttt tggtgaggtg agtctctgtc acccaggttg gagtacagcg
      481 gtgtgatctc ggctcaccgc aacctctgct tcctgggttc aagctattct cctgcctcag
      541 cctcctgagt agctggcatt ataggcatgc accacaacac ccagctaaat ttttttgtat
      601 ttttagcaga gatgagtttt gccatattgg ccaggctggt cttgaactcc tgacttcaag
      661 tgatccaccc gtctcggcct cccaaagtgc tgggattaca ggcgtgagcc acggcaccag
      721 gcctagtcta gtcttttcac gtttttctgc ctgctttata ttctggccgc actggcagct
```

DNA databáze NCBI – sekvence genu



Homo sapiens NAD(P)H quinone dehydrogenase 1 (NQO1), RefSeqGene on

```
12301 cagattcccc caaattggag agcgagataa aagatttatg tgtctttaaa gtttcaagag
12361 attctgcctc attactttcc ctaaaggttg aggcagttct tatccccacc agtaaggtgc
12421 caatttttct gttggtacaa tcttaataac cctgggtgtt atttgtttta cattttgtg
12481 gtaaatgtaa actcacggta aatgtaaaca cagtacccat gtaaacgaat gggtaaatg
12541 ctcattttaa ttttgctttt cctgacaggt cacgcagagc atcttttttt tttttgag
12601 cggagtctcc cattgtcacc caggctggag tgcaatggtg caatcttggc tcactgcaa
12661 ctccccctcc cgagttcaag tgattctcct gcctcagcct cccaagtagc tgggattac
12721 ggtgcctgcc accacaccca gctaattttt gtatttttag tagagacagg gtttcacca
12781 gttggccagg ctggtctcaa actcctgacc tcaggtgatc tgcccacctt ggcctccca
12841 agtgctggga ttacagttat gagccacaga gcccagttgt caacattatt tattaaatc
12901 gccactgatt taaatgcttc ctttaatctt cagtgctttt aaggggaaaa tacatttct
13021 ctgcaactcc cctgtagctg aaggtttgct ggttggtaat gggttttccg tgtgtgctt
12961 gctacaggag atggaatgca ataacctaat gtcaaacaaa gccgccccct cctttacag
13081 gtgtgtgtct ctgtaggcag aagagcactg atcgtactgg ctcactcaga gaggacgtc
13141 ttcaactatg ccatgaagga ggctgctgca gcggctttga agaagaaagg atgggaggt
13201 gtggagtcgg acctctatgc catgaacttc aatcccatca tttccagaaa ggacatcac
13261 ggtaggagga gttcctcctc ccctctttaa ttagttcttt gcggatctcc ttgcctgtg
13321 gtcctctggc ccagctttgg cccctctggc cccagcctct ctttttcttc tctgcaggt
13381 aactgaagga ccctgcgaac tttcagtatc ctgccgagtc tgttctggct tataaagaa
13441 gccatctgag cccagatatt gtggctgaac aaaagaagct ggaagccgca gaccttgtg
13501 tattccaggt atgggggac atcggaaggg gtgtcaggga catttgcgtg cttattgtc
13561 tagacatgta cctaattagc tatgagatct taaacagtta cccactttac tgcattctc
13621 gcaaataagg gtgattactt taaaggtgca gtattacatg gatttcacag atattggga
```

CDS join(5192..5198,13097..13261,13378..13508,16554..16667,
18502..18603,20350..20655)

join(5192..5198,13097..13261,13378..13508,16554..16667,
18502..18603,20350..20655)

Homo sapiens NAD(P)H quinone dehydrogenase 1 (NQO1), RefSeqGene on chromosome 16

NCBI Reference Sequence: NG_011504.2

GenBank Graphics

```
>NG_011504.2:5192-5198,13097-13261,13378-13508,16554-16667,18502-18603,20350-20655 Homo
sapiens NAD(P)H quinone dehydrogenase 1 (NQO1), RefSeqGene on chromosome 16
ATGGTCGGCAGAAGAGCACTGATCGTACTGGCTCACTCAGAGAGGACGTCCTTCAACTATGCCATGAAGG
AGGCTGCTGCAGCGGCTTTGAAGAAGAAAGGATGGGAGGTGGTGGAGTCGGACCTCTATGCCATGAACTT
CAATCCCATCATTTCCAGAAAGGACATCACAGGTAAACTGAAGGACCCTGCGAACTTTCAGTATCCTGCC
GAGTCTGTTCTGGCTTATAAAGAAGGCCATCTGAGCCCAGATATTGTGGCTGAACAAAAGAAGCTGGAAG
CCGCAGACCTTGTGATATTCCAGTTCCCCCTGCAGTGGTTTGGAGTCCCTGCCATTCTGAAAGGCTGGTT
TGAGCGAGTGTTCATAGGAGAGTTTGCTTACACTTACGCTGCCATGTATGACAAAGGACCCTTCCGGAGT
AAGAAGGCAGTGCTTTCCATCACCACTGGTGGCAGTGGCTCCATGTACTCTCTGCAAGGGATCCACGGGG
ACATGAATGTCATTCTCTGGCCAATTCAGAGTGGCATTCTGCATTTCTGTGGCTTCCAAGTCTTAGAACC
TCAACTGACATATAGCATTGGGCACACTCCAGCAGACGCCCGAATTCAAATCCTGGAAGGATGGAAGAAA
CGCCTGGAGAATATTTGGGATGAGACACCACTGTATTTTGCTCCAAGCAGCCTCTTTGACCTAAACTTCC
AGGCAGGATTCTTAATGAAAAAAGAGGTACAGGATGAGGAGAAAAACAAGAAATTTGGCCTTTCTGTGGG
CCATCACTTGGGCAAGTCCATCCCAACTGACAACCAGATCAAAGCTAGAAAATGA
```

```
TPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK"
```

DNA databáze NCBI – sekvence genu

Nemáte-li v kartě NG_ sekvenci ….

Najdeme ji přes databázi GENE – viz dále

Ukázka možností NCBI/gen

organismus

mRNA, CDS, region

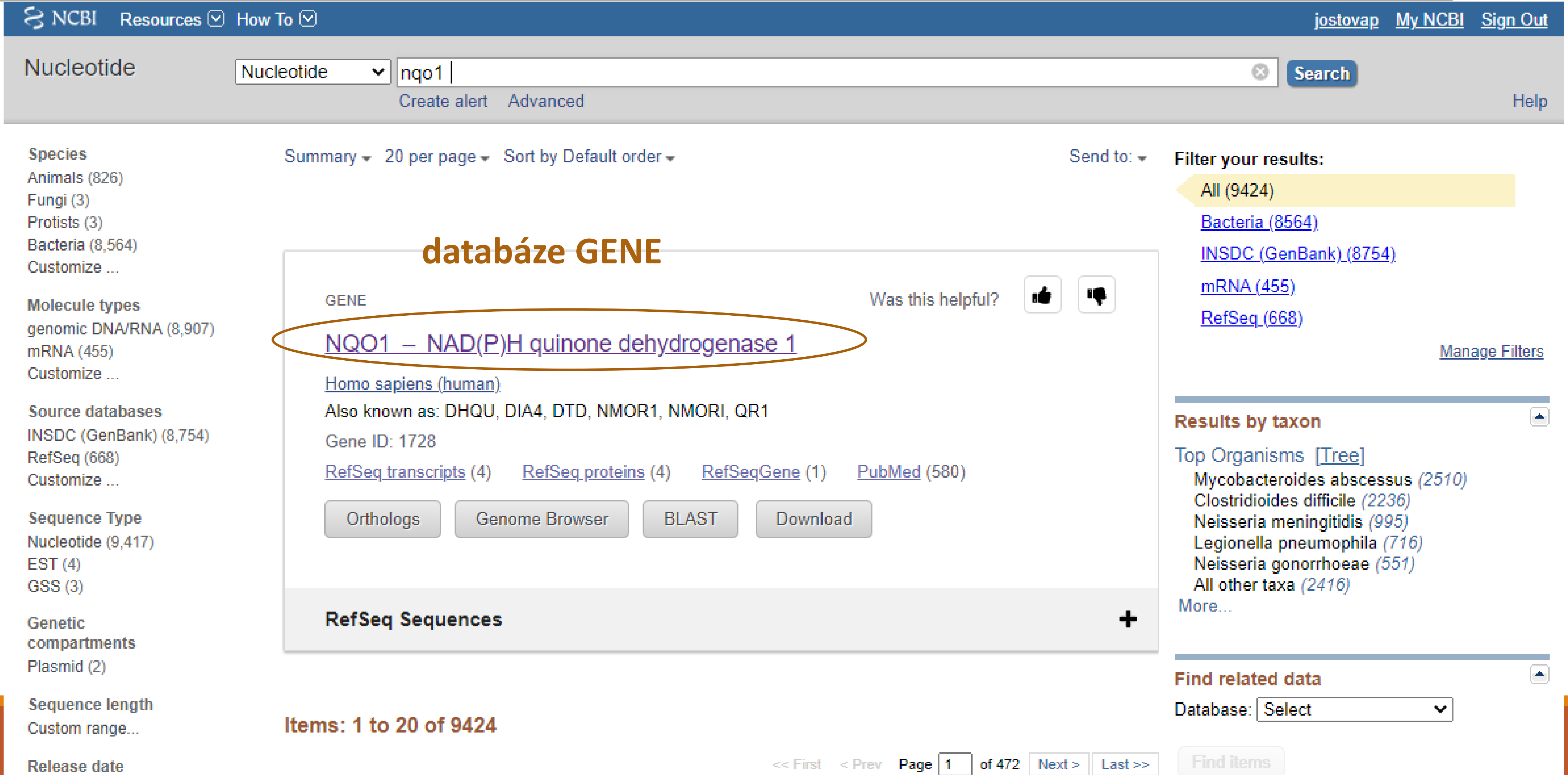
Find in sequence

Vyhledejte si „vlastní“ sekvenci

vyzkoušejte možnosti

-podívejte se GRAPHIC zobrazení

DNA databáze NCBI



NCBI Resources How To jostovap My NCBI Sign Out

Nucleotide

Nucleotide: nqo1 | Search

Create alert Advanced Help

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:

databáze 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)

Orthologs Genome Browser BLAST Download

RefSeq Sequences +

Items: 1 to 20 of 9424

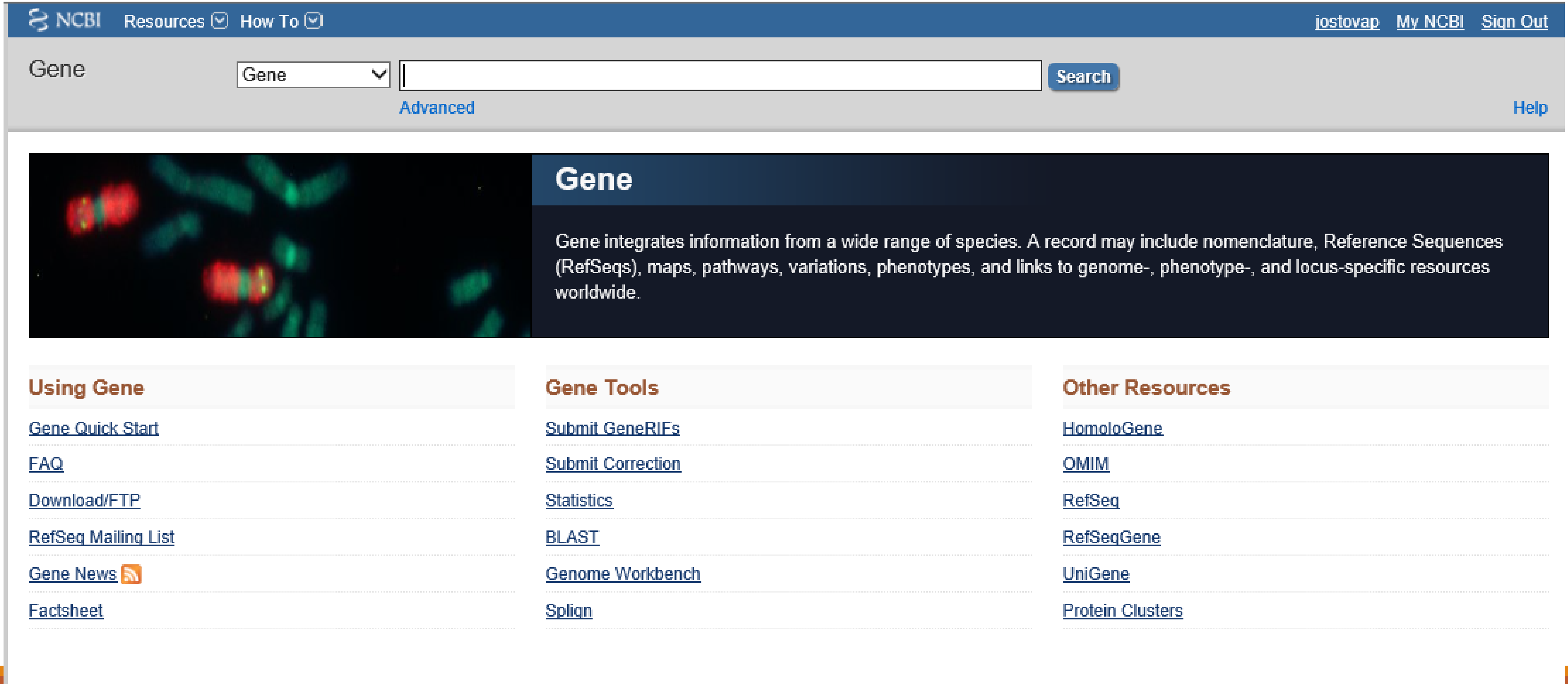
<< First < Prev Page 1 of 472 Next > Last >>

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

NCBI/Gene (sekundární databáze)



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.

Using Gene

- Gene Quick Start
- FAQ
- Download/FTP
- RefSeq Mailing List
- Gene News
- Factsheet

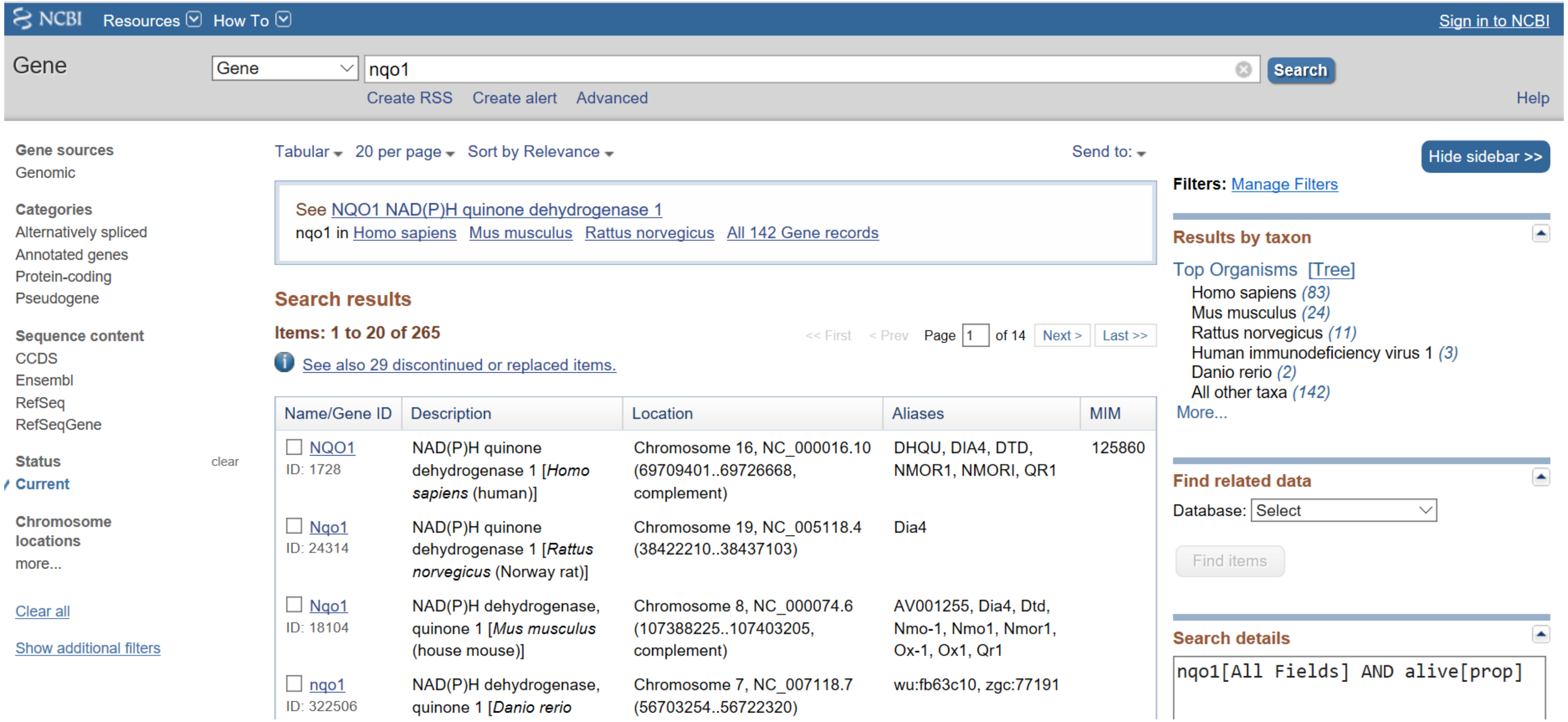
Gene Tools

- Submit GeneRIFs
- Submit Correction
- Statistics
- BLAST
- Genome Workbench
- Splign

Other Resources

- HomoloGene
- OMIM
- RefSeq
- RefSeqGene
- UniGene
- Protein Clusters

NCBI/Gene



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

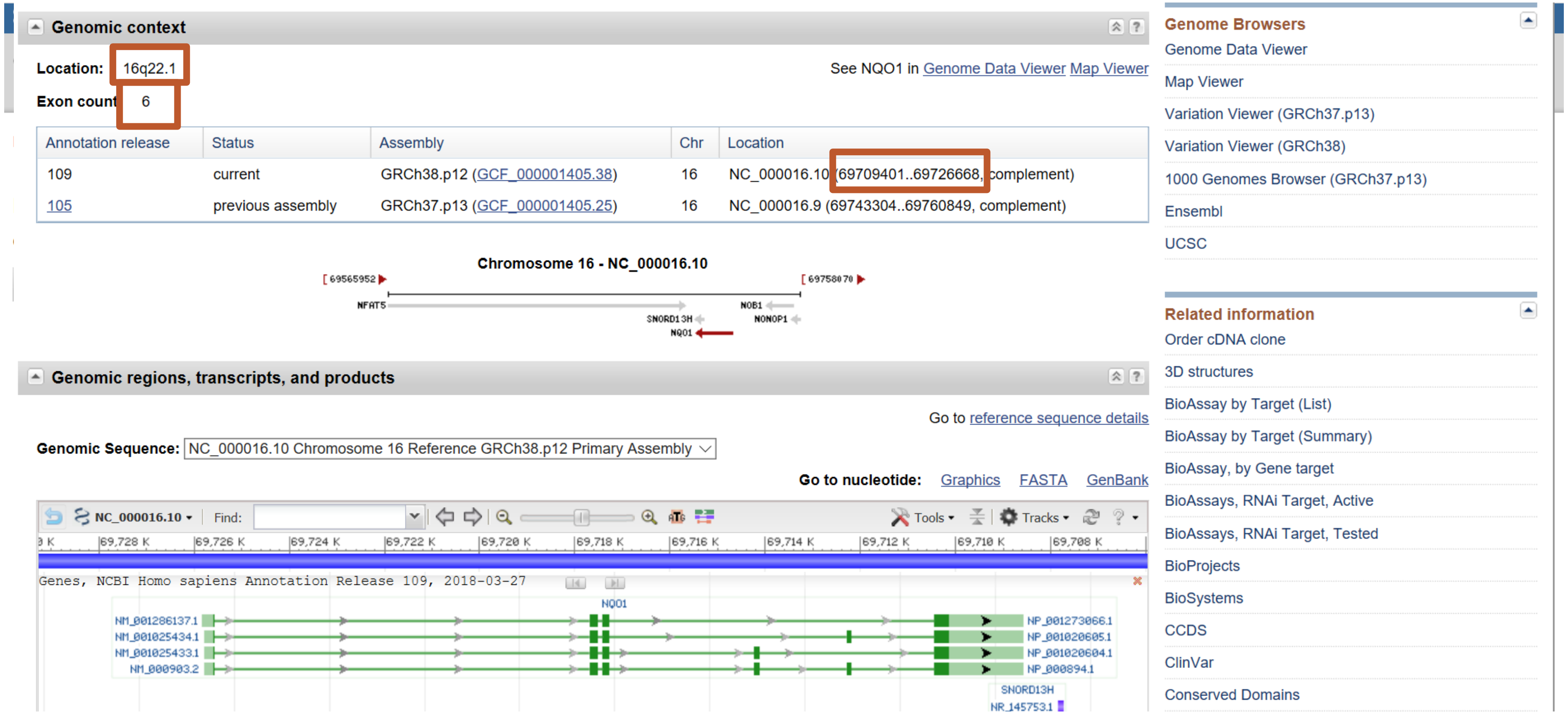
NQO1 NAD(P)H quinone dehydrogenase 1 [*Homo sapiens* (human)]

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

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

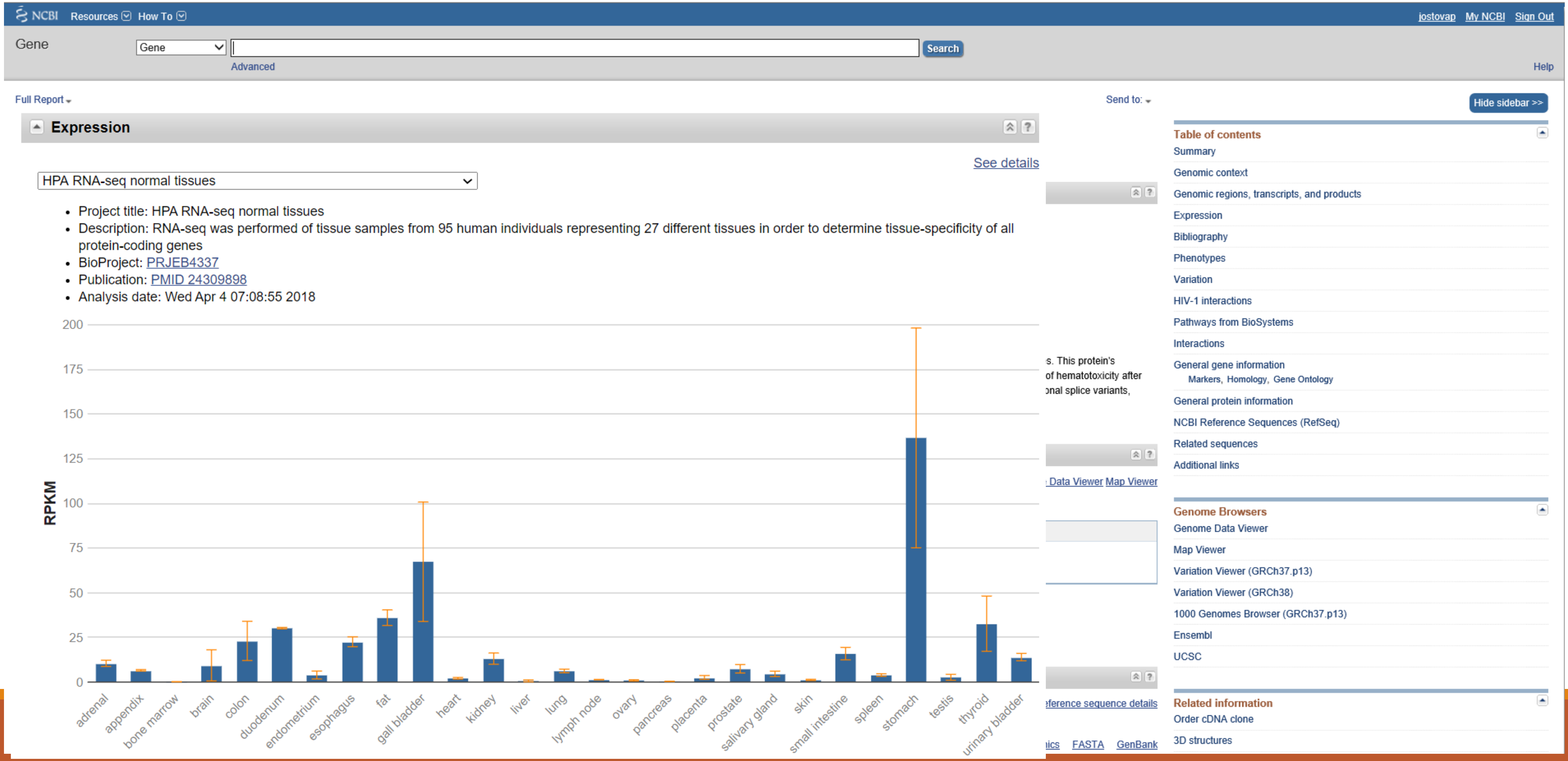
NCBI/Gene-pseudogeny?

GAPDH glyceraldehyde-3-phosphate dehydrogenase [*Homo sapiens* (human)]

Gene ID: 2597, updated on 29-Mar-2018

Official Symbol	GAPDH provided by HGNC
Official Full Name	glyceraldehyde-3-phosphate dehydrogenase provided by HGNC
Primary source	HGNC:HGNC:4141
See related	Ensembl:ENSG00000111640 MIM:138400; Vega:OTTHUMG00000137379
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	G3PD; GAPD; HEL-S-162eP
Summary	This gene encodes a member of the glyceraldehyde-3-phosphate dehydrogenase protein family. The encoded protein has been identified as a moonlighting protein based on its ability to perform mechanistically distinct functions. The product of this gene catalyzes an important energy-yielding step in carbohydrate metabolism, the reversible oxidative phosphorylation of glyceraldehyde-3-phosphate in the presence of inorganic phosphate and nicotinamide adenine dinucleotide (NAD). The encoded protein has additionally been identified to have uracil DNA glycosylase activity in the nucleus. Also, this protein contains a peptide that has antimicrobial activity against E. coli, P. aeruginosa, and C. albicans. Studies of a similar protein in mouse have assigned a variety of additional functions including nitrosylation of nuclear proteins, the regulation of mRNA stability, and acting as a transferrin receptor on the cell surface of macrophage. Many pseudogenes similar to this locus are present in the human genome. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Nov

NCBI/Gene

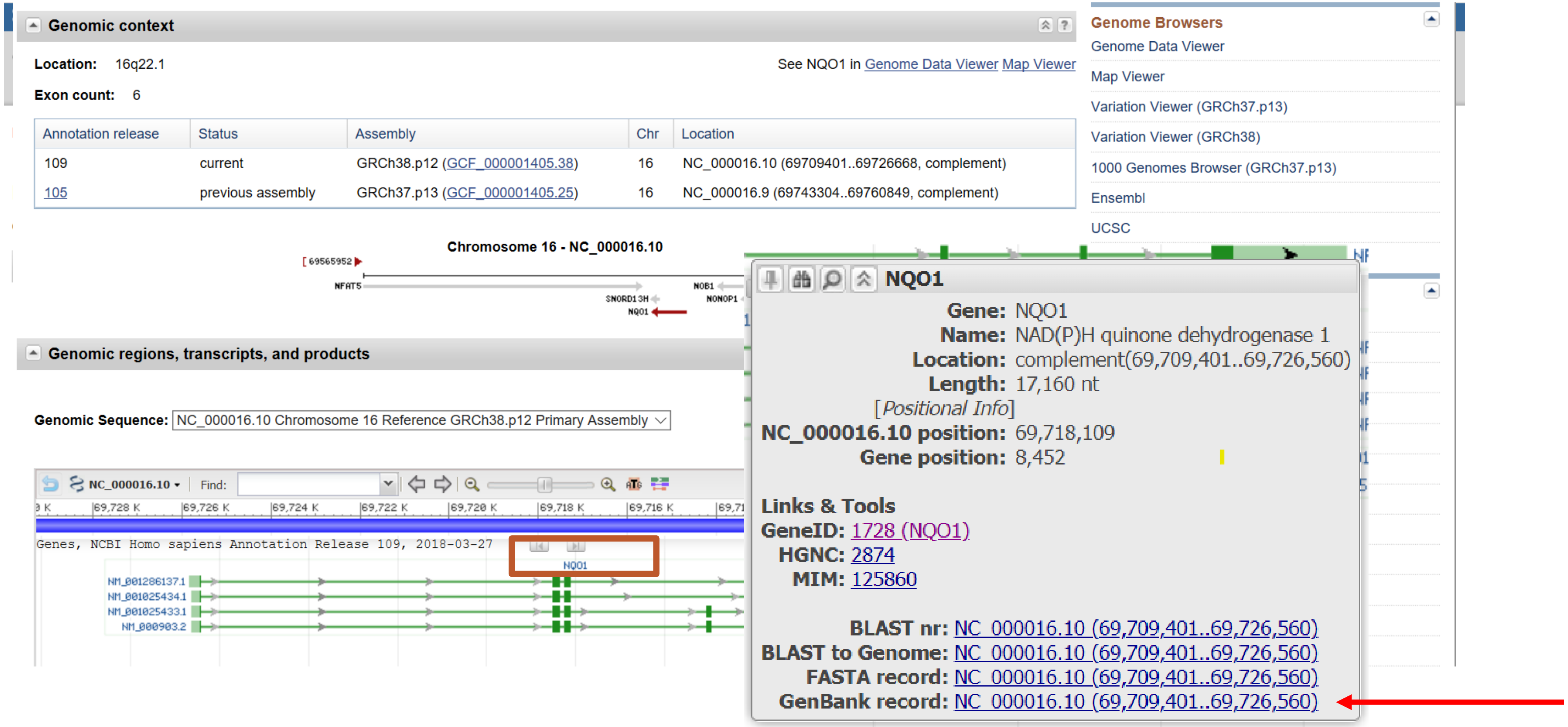


HPA RNA-seq normal tissues

- 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

s. This protein's
of hematotoxicity after
onal splice variants,

NCBI/Gene – sekvence celého genu



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

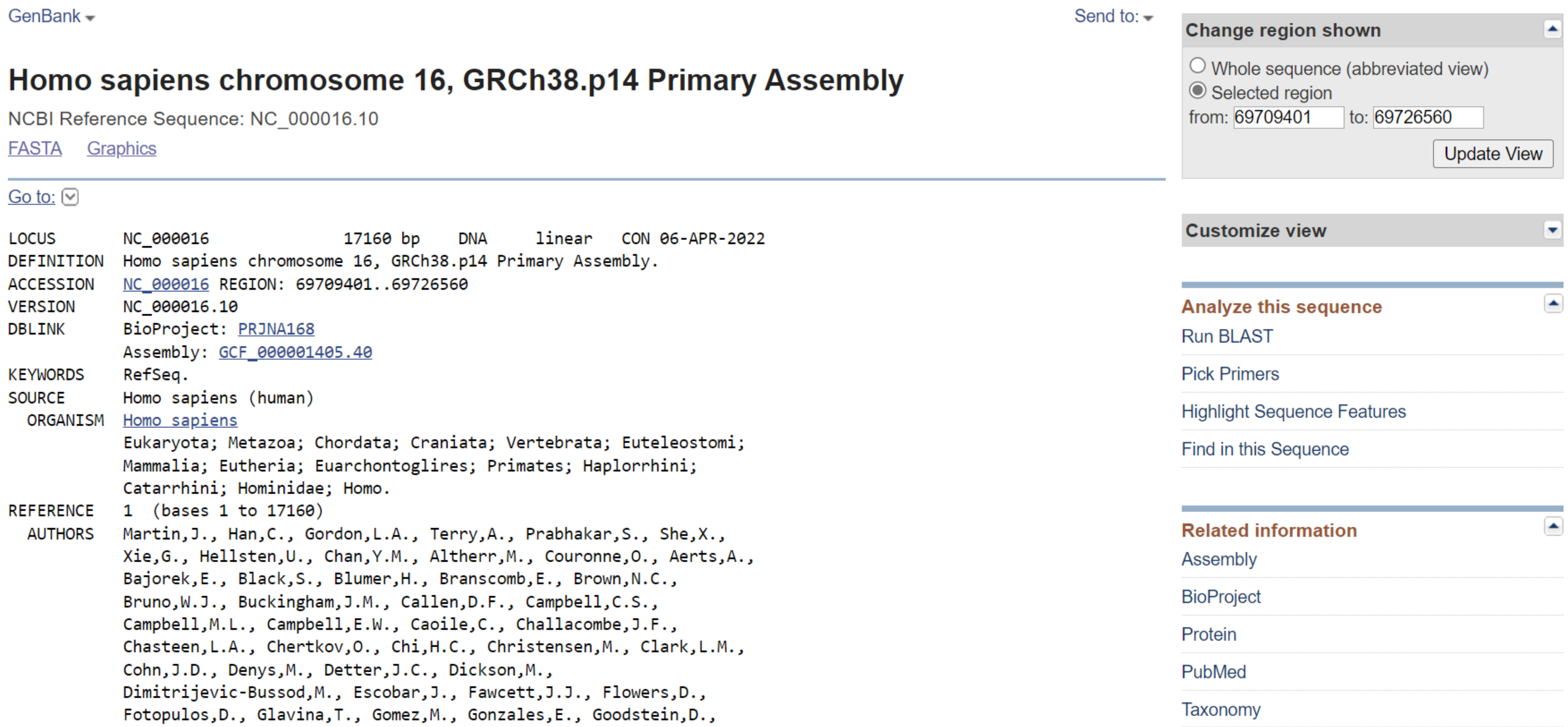
Gene: NQO1
Name: NAD(P)H quinone dehydrogenase 1
Location: complement(69,709,401..69,726,560)
Length: 17,160 nt
[*Positional Info*]
NC_000016.10 position: 69,718,109
Gene position: 8,452

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 – sekvence celého genu



Homo sapiens chromosome 16, GRCh38.p14 Primary Assembly

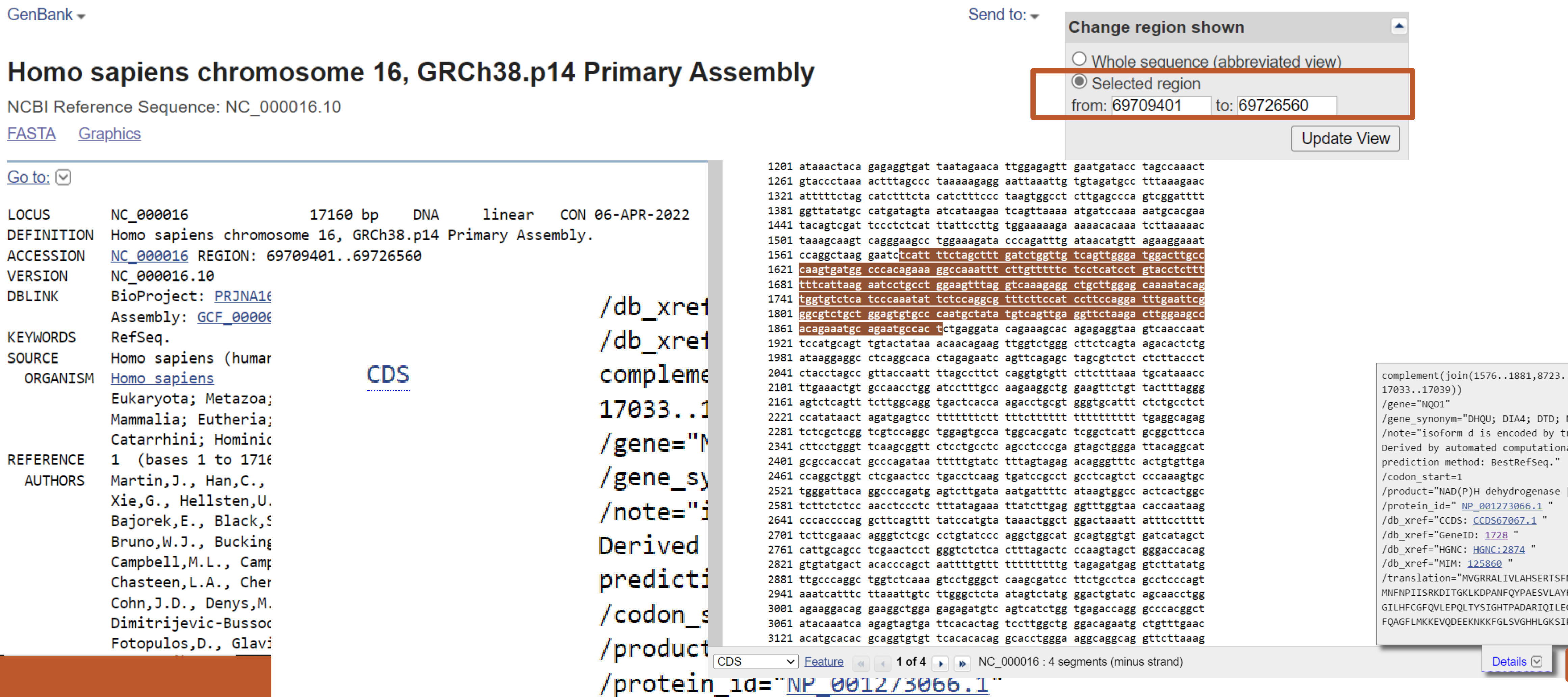
NCBI Reference Sequence: NC_000016.10

Change region shown

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

```
LOCUS       NC_000016              17160 bp    DNA     linear   CON 06-APR-2022
DEFINITION  Homo sapiens chromosome 16, GRCh38.p14 Primary Assembly.
ACCESSION   NC_000016 REGION: 69709401..69726560
VERSION     NC_000016.10
DBLINK      BioProject: PRJNA168
            Assembly: GCF_000001405.40
KEYWORDS    RefSeq.
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.,
            Bajorek,E., Black,S., Blumer,H., Branscomb,E., Brown,N.C.,
            Bruno,W.J., Buckingham,J.M., Callen,D.F., Campbell,C.S.,
            Campbell,M.L., Campbell,E.W., Caoile,C., Challacombe,J.F.,
            Chasteen,L.A., Chertkov,O., Chi,H.C., Christensen,M., Clark,L.M.,
            Cohn,J.D., Denys,M., Detter,J.C., Dickson,M.,
            Dimitrijevic-Bussod,M., Escobar,J., Fawcett,J.J., Flowers,D.,
            Fotopulos,D., Glavina,T., Gomez,M., Gonzales,E., Goodstein,D.,
```

NCBI/Gene – sekvence celého genu



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

```
LOCUS       NC_000016              17160 bp    DNA     linear   CON 06-APR-2022
DEFINITION  Homo sapiens chromosome 16, GRCh38.p14 Primary Assembly.
ACCESSION   NC_000016 REGION: 69709401..69726560
VERSION     NC_000016.10
DBLINK      BioProject: PRJNA16
            Assembly: GCF_00000
KEYWORDS    RefSeq.
SOURCE      Homo sapiens (humar
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa;
            Mammalia; Eutheria;
            Catarrhini; Hominic
REFERENCE   1  (bases 1 to 1716
  AUTHORS   Martin,J., Han,C.,
            Xie,G., Hellsten,U.
            Bajorek,E., Black,S
            Bruno,W.J., Bucking
            Campbell,M.L., Camp
            Chasteen,L.A., Cher
            Cohn,J.D., Denys,M.
            Dimitrijevic-Bussoc
            Fotopulos,D., Glavi
```

```
/db_xref
/db_xref
compleme
17033..1
/gene="N
/gene_sy
/note="i
Derived
predicti
/codon_s
/product
/protein_id="NP_001273066.1"
```

```
1201 ataaactaca gagaggtgat taatagaaca ttggagagtt gaatgatacc tagccaaact
1261 gtaccctaaa actttagccc taaaaagagg aattaaattg tgtagatgcc tttaaagaac
1321 atttttctag catctttcta catctttccc taagtggcct cttgagccca gtcggatttt
1381 ggttatatgc catgatagta atcataagaa tcagttaaaa atgatccaaa aatgcacgaa
1441 tacagtcgat tccctctcat ttattccttg tggaaaaaga aaaacacaaa tcttaaaaac
1501 taaagcaagt cagggaagcc tggaaagata cccagatttg ataacatgtt agaaggaaat
1561 ccaggctaag gaatctcatt ttctagcttt gatctggttg tcagttggga tggacttgcc
1621 caagtgatgg cccacagaaa ggccaaattt cttgtttttc tcctcatcct gtacctcttt
1681 tttcattaag aatcctgcct ggaagtttag gtcaaagagg ctgcttggag caaaatacag
1741 tggtgtctca tcccaaatat tctccaggcg tttcttccat ccttccagga tttgaattcg
1801 ggcgtctgct ggagtgtgcc caatgctata tgtcagttga ggttctaaga cttggaagcc
1861 acagaaatgc agaatgccac tctgaggata cagaaagcac agagaggtaa gtcaaccaat
1921 tccatgcagt tgtactataa acaacagaag ttggtctggg cttctcagta agacactctg
1981 ataaggaggc ctcaggcaca ctagagaatc agttcagagc tagcgtctct ctcttaccct
2041 ctacctagcc gttaccaatt ttagccttct caggtgtgtt cttctttaaa tgcataaacc
2101 ttgaaactgt gccaacctgg atcctttgcc aagaaggctg gaagttctgt tactttaggg
2161 agtctcagtt tcttggcagg tgactcacca agacctgcgt gggtgcattt ctctgcctct
2221 ccatataact agatgagtcc tttttttctt tttctttttt tttttttttt tgaggcagag
2281 tctcgctcgg tcgtccaggc tggagtgcca tggcacgatc tcggctcatt gcggcttcca
2341 cttcctgggt tcaagcggtt ctcctgcctc agcctcccga gtagctggga ttacaggcat
2401 gcgccaccat gcccagataa tttttgtatc tttagtagag acagggtttc actgtgttga
2461 ccaggctggt ctcgaactcc tgacctcaag tgatccgcct gcctcagtct cccaaagtgc
2521 tgggattaca ggcccagatg agtcttgata aatgattttc ataagtggcc actcactggc
2581 tcttctctcc aacctccctc tttatagaaa ttatcttgag ggtttggtaa caccaataag
2641 cccaccccag gcttcagttt tatccatgta taaactggct ggactaaatt atttcctttt
2701 tcttcgaaac agggtctcgc cctgtatccc aggctggcat gcagtggtgt gatcatagct
2761 cattgcagcc tcgaactcct gggtctctca ctttagactc ccaagtagct gggaccacag
2821 gtgtatgact acacccagct aatttgtttt tttttttttg tagagatgag gtcttatatg
2881 ttgcccaggc tggtctcaaa gtcctgggct caagcgatcc ttctgcctca gcctcccagt
2941 aaatcatttc ttaaattgtc ttgggctcta atagtctatg ggactgtatc agcaacctgg
3001 agaaggacag gaaggctgga gagagatgtc agtcatctgg tgagaccagg gcccacggct
3061 atacaaatca agagtagtga ttcacactag tccttggctg ggacagaatg ctgtttgaac
3121 acatgcacac gcaggtgtgt tcacacacag gcacctggga aggcaggcag gttcttaaag
```

```
complement(join(1576..1881,8723..
17033..17039))
/gene="NQO1"
/gene_synonym="DHQU; DIA4; DTD;
/note="isoform d is encoded by tr
Derived by automated computationa
prediction method: BestRefSeq."
/codon_start=1
/product="NAD(P)H dehydrogenase
/protein_id=" NP_001273066.1 "
/db_xref="CCDS: CCDS67067.1 "
/db_xref="GeneID: 1728 "
/db_xref="HGNC: HGNC:2874 "
/db_xref="MIM: 125860 "
/translation="MVGRRALIVLAHSERTSF
MNFNPIISRKDITGKLKDPANFQYPAESVLAY
GILHFCGFQVLEPQLTYSIGHTPADARIQILE
FQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSI
```

CDS 1 of 4 NC_000016 : 4 segments (minus strand)

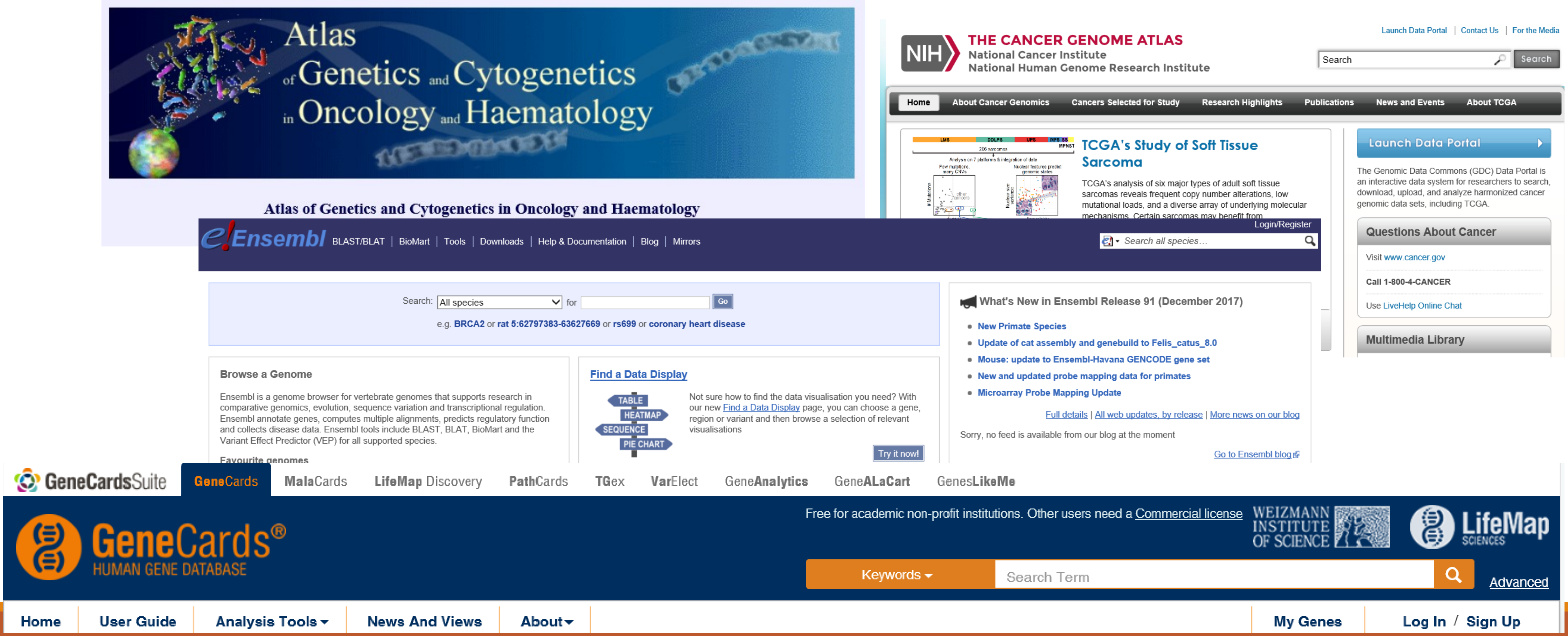
praktická ukázka GENE

Vyhledejte si „vlastní“ gen

prohlédněte si databázi GENE

Vyzkoušejte různé „linky“

Specializované databáze (sekundární)



Atlas of Genetics and Cytogenetics in Oncology and Haematology

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

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.

Visit www.cancer.gov

Call 1-800-4-CANCER

Use LiveHelp Online Chat

Search: All species for

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 Variant Effect Predictor (VEP) for all supported species.

Favourite genomes

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

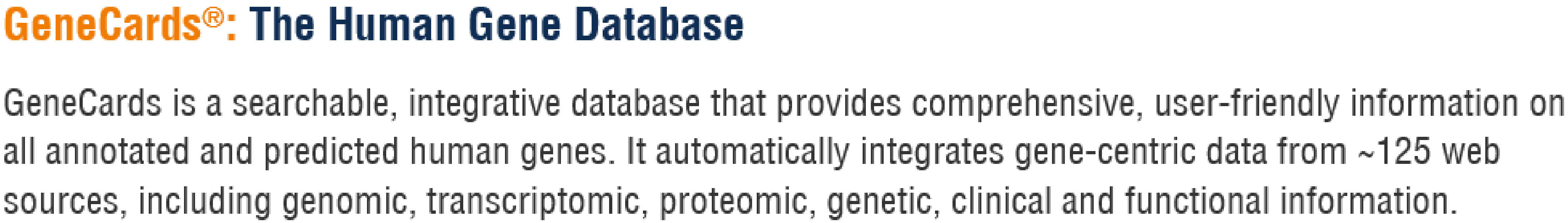
Full details | All web updates, by release | More news on our blog

Sorry, no feed is available from our blog at the moment

Go to Ensembl blog

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

Specializované databáze (sekundární)



GeneCards®: The Human Gene Database

GeneCards is a searchable, integrative database that provides comprehensive, user-friendly information on all annotated and predicted human genes. It automatically integrates gene-centric data from ~125 web sources, including genomic, transcriptomic, proteomic, genetic, clinical and functional information.

Cvičení 1-**Vyhledávání v molekulárně genetických databázích**
(prof.Beránek)

Vyhledejte si „vlastní“ gen
v jiných databázích

Vyzkoušejte různé „linky“

„Bioinformatika nukleových kyselin I“

Vyhledávání NK sekvencí, **specializované databáze**

Analýza vlastností sekvencí-složení, „reverse complement“, identifikace restrikčních míst (Palindromy)

Práce s kódující DNA=práce s proteiny / překlad DNA sekvence-otvírání čtecího rámce

Návrh primerů pro PCR, rt-PCR

Předpověď sekundárních struktur

Porovnávání sekvencí

Vyhledání SNPs

„čtení“ sekvenačních dat a spojování fragmentů

Vyhledávání hladin expresí jednotlivých genů

mikroRNA

Celé genomy

….

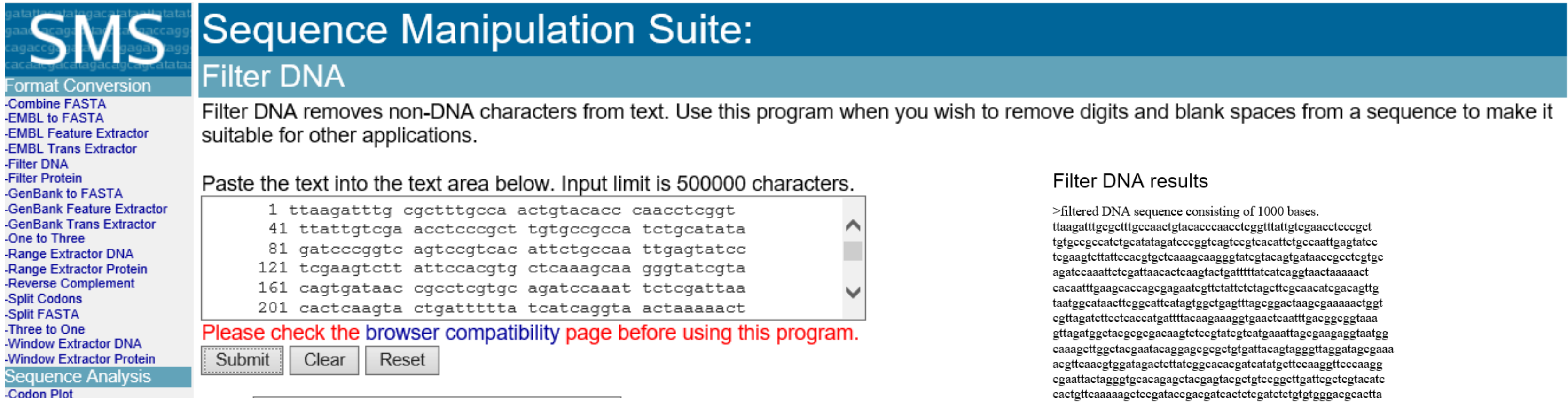
Charakteristiky sekvencí

Filter DNA

DNA stats

Range Extraktor 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.

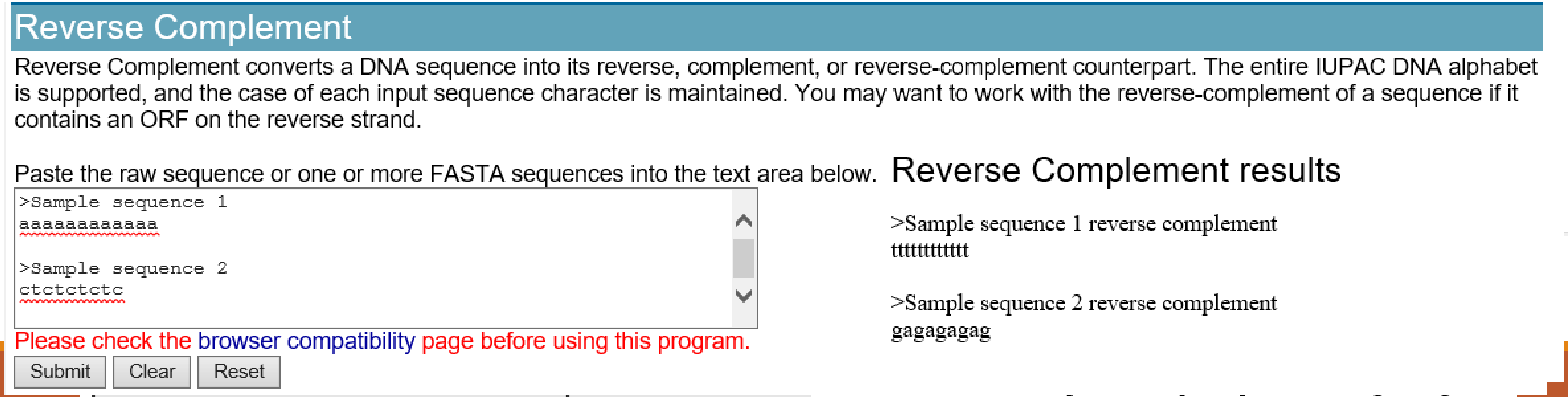
Paste the text into the text area below. Input limit is 500000 characters.

```
  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
```

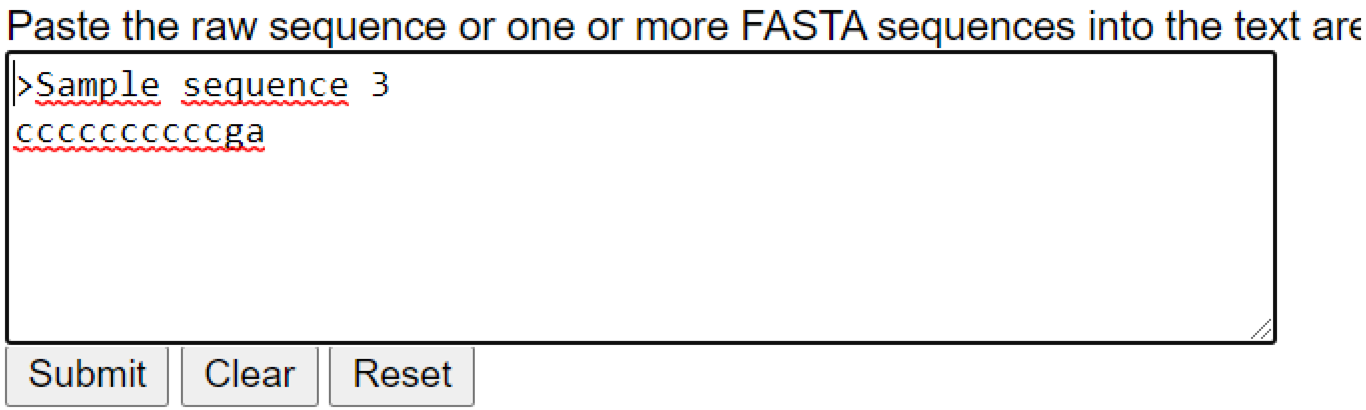
Please check the browser compatibility page before using this program.

Reverse Complement results

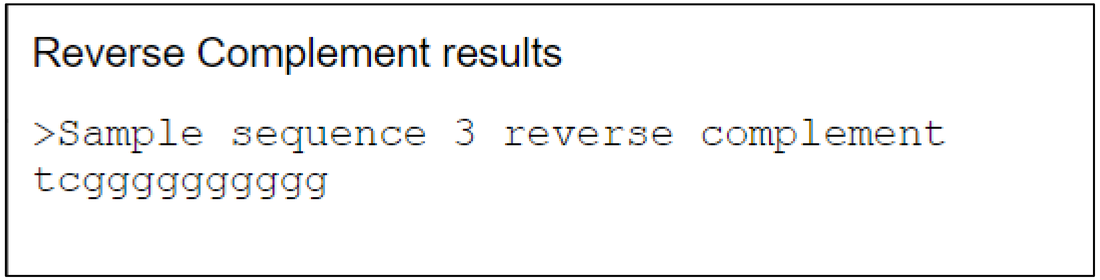
```
>Sample sequence 1 reverse complement
tttttttttttt

>Sample sequence 2 reverse complement
gagagagag
```

atttttttttttc

Reverse complement


Paste the raw sequence or one or more FASTA sequences into the text are

```
>Sample sequence 3
cccccccccga
```


Reverse Complement results

```
>Sample sequence 3 reverse complement
tcggggggggg
```

Vyzkoušejte si analyzovat „vlastní“ gen

Vyzkoušejte SMS suite.

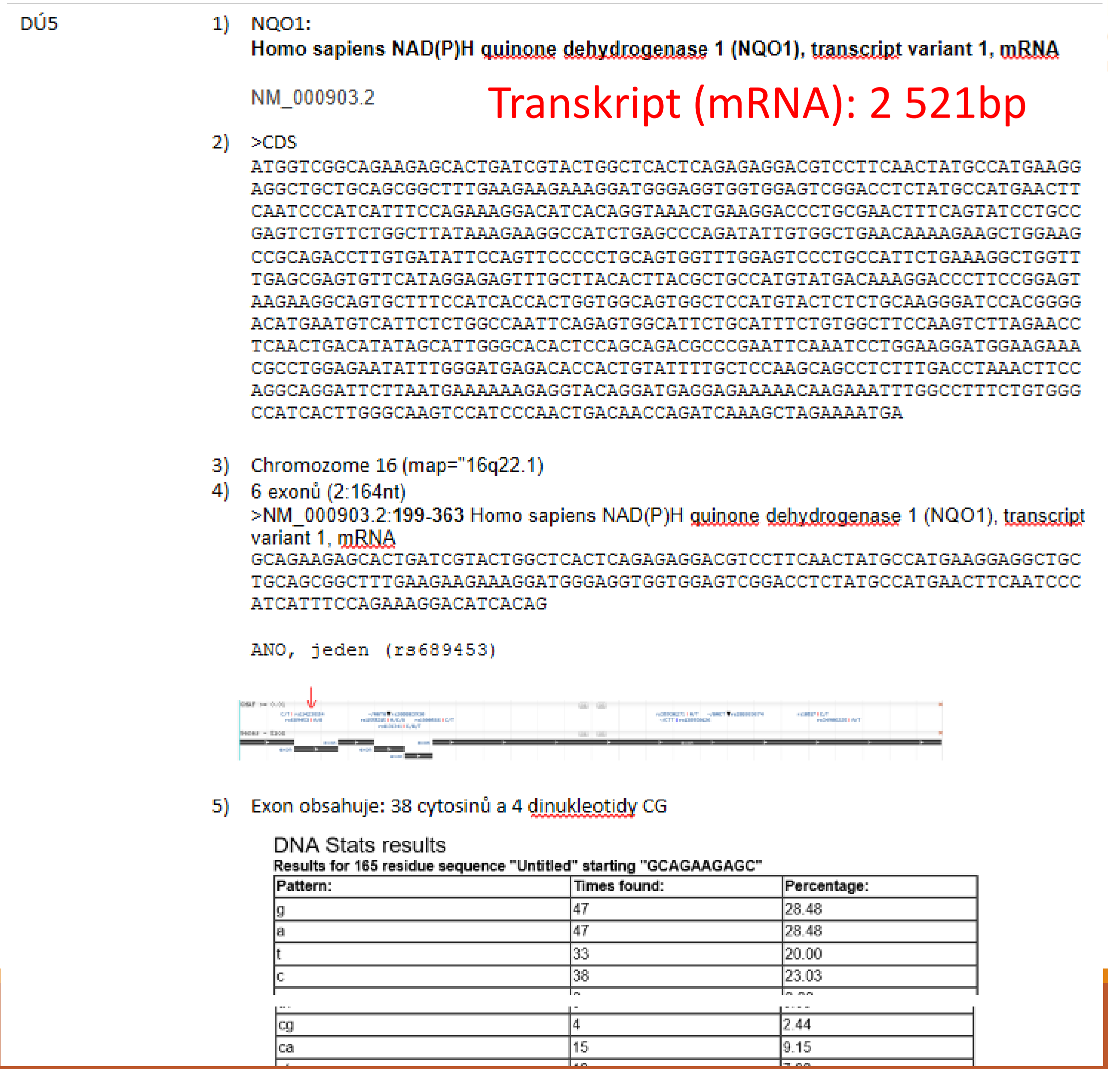
DÚ5: nukleotidová sekvence

Pracujte s „vaším“ genem/proteinem/enzymem (př. NQO1)

1) Vyhledejte si vaši nukleotidovou sekvenci transkriptu (mRNA=RefSeq_transcript) a genu (RefSeq_gene).
   - Zapište si přístupové kódy. (NM_... a NG_...)
   - Jak dlouhé jsou tyto sekvence ? (stačí 1. transkript, máte-li více)
2) Vyberte pouze kódující sekvenci (CDS), uložte formát fasta.
3) Na kterém chromozomu leží? Kolik má exonů? Jak je dlouhý 2. exon? Stáhněte sekvenci 2. exonu.
4) Obsahuje 2.exon nějaké významné varianty (SNP)?
5) Kolik obsahuje 2. exon Cytosinů? Kolik dinukleotidů CG?

➢vše zpracujte do bloku OneNote

DÚ5: Příklad řešení



DÚ5

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

NM_000903.2

Transkript (mRNA): 2 521bp

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)`

5) 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

Homo sapiens NAD(P)H quinone dehydrogenase 1 (NQO1), RefSeqGene on chromosome 16

NCBI Reference Sequence: NG_011504.2

Gen: 24 230 bp

2) Porovnání NQO1 mRNA a CDS