

Introduction to applied bioinformatics

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2023/2024

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

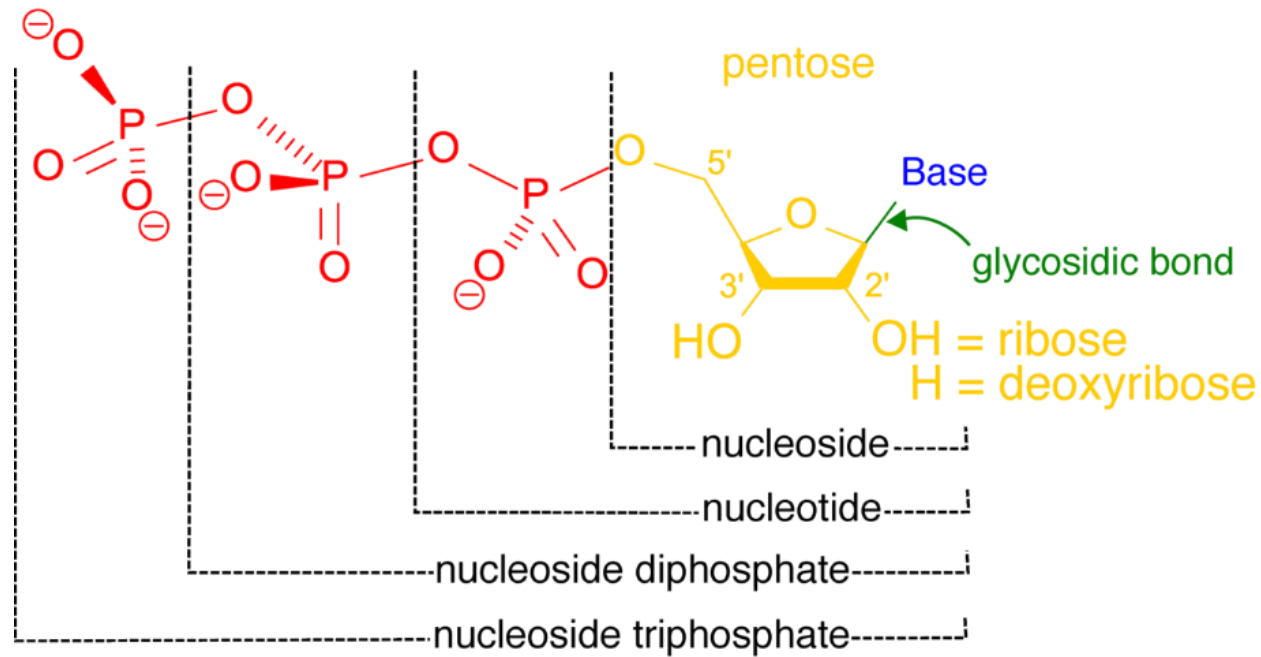
Complementarity: A=T, C≡G

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

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

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

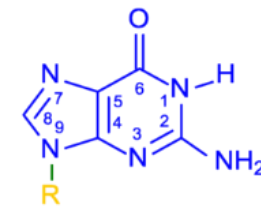
DNA/RNA



Purines

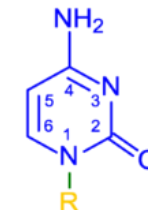


Adenine

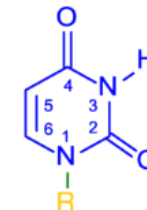


Guanine

Pyrimidines



Cytosine

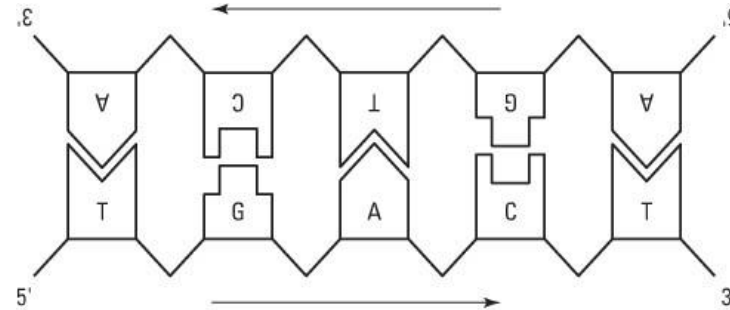
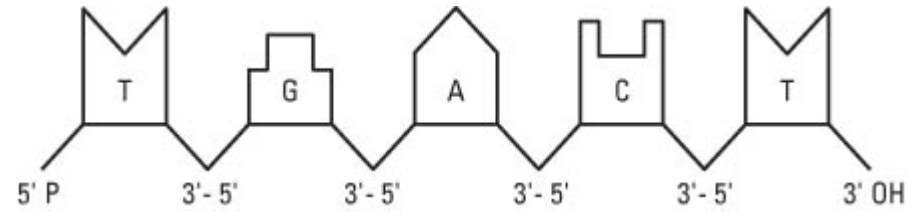
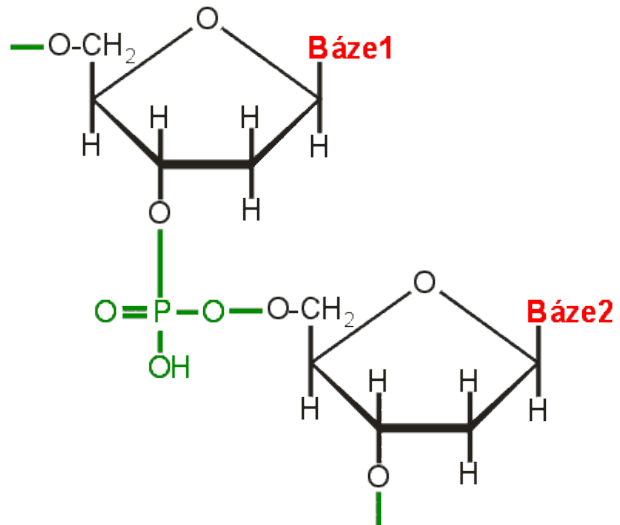
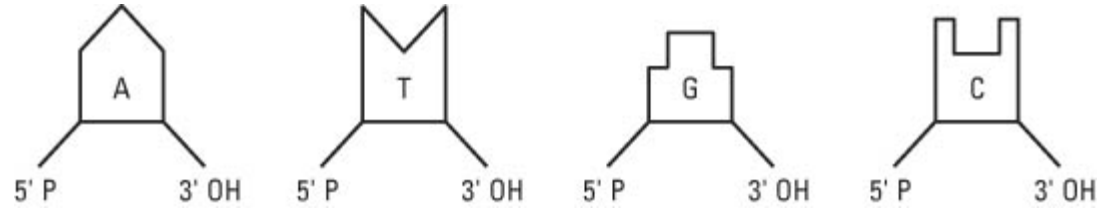
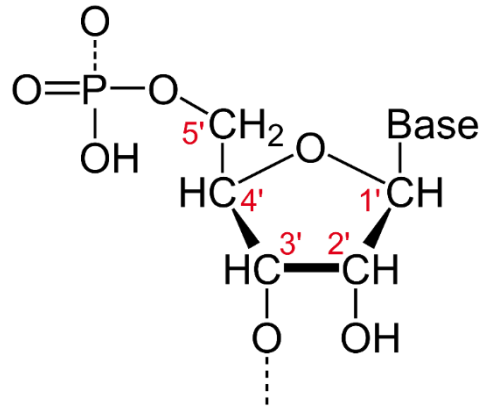


Uracil



Thymine

DNA/RNA



Prokaryotes

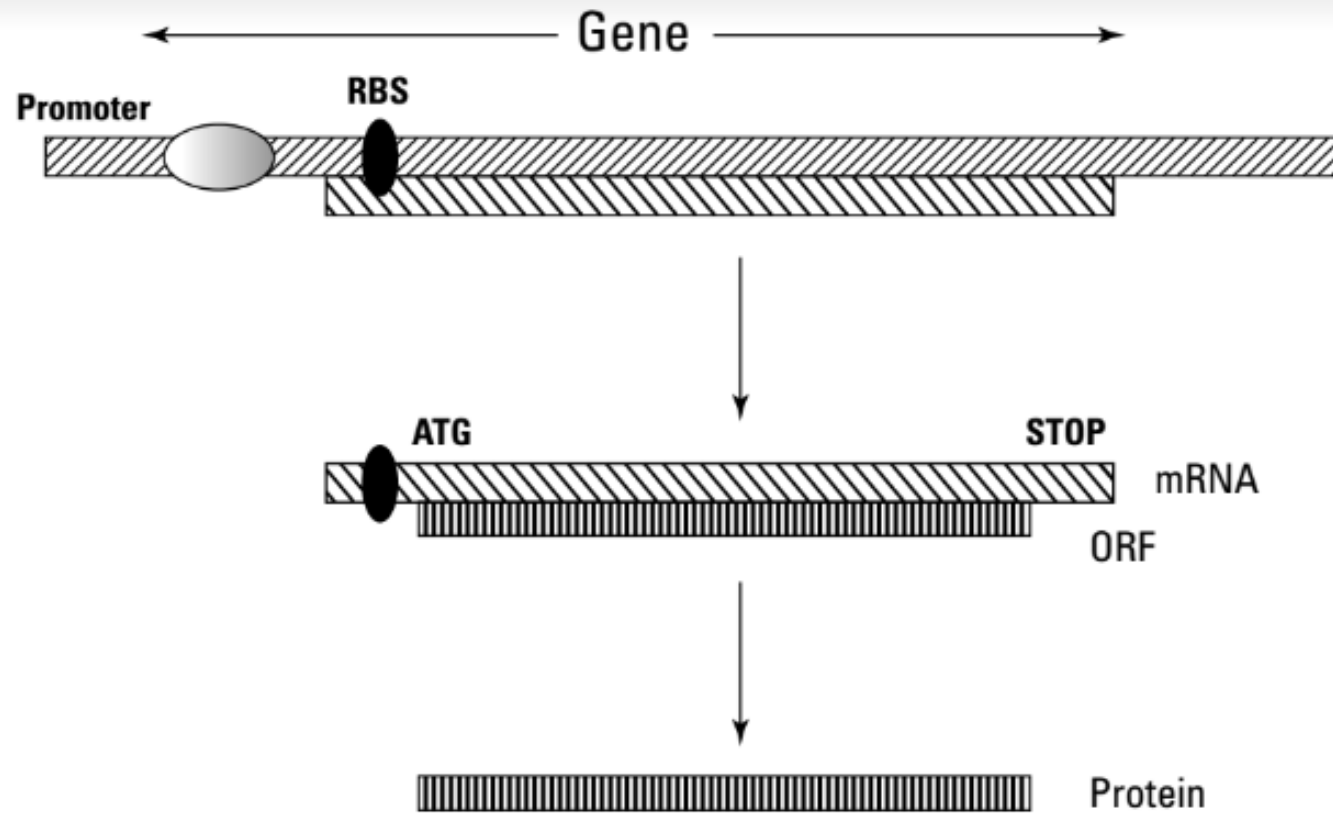
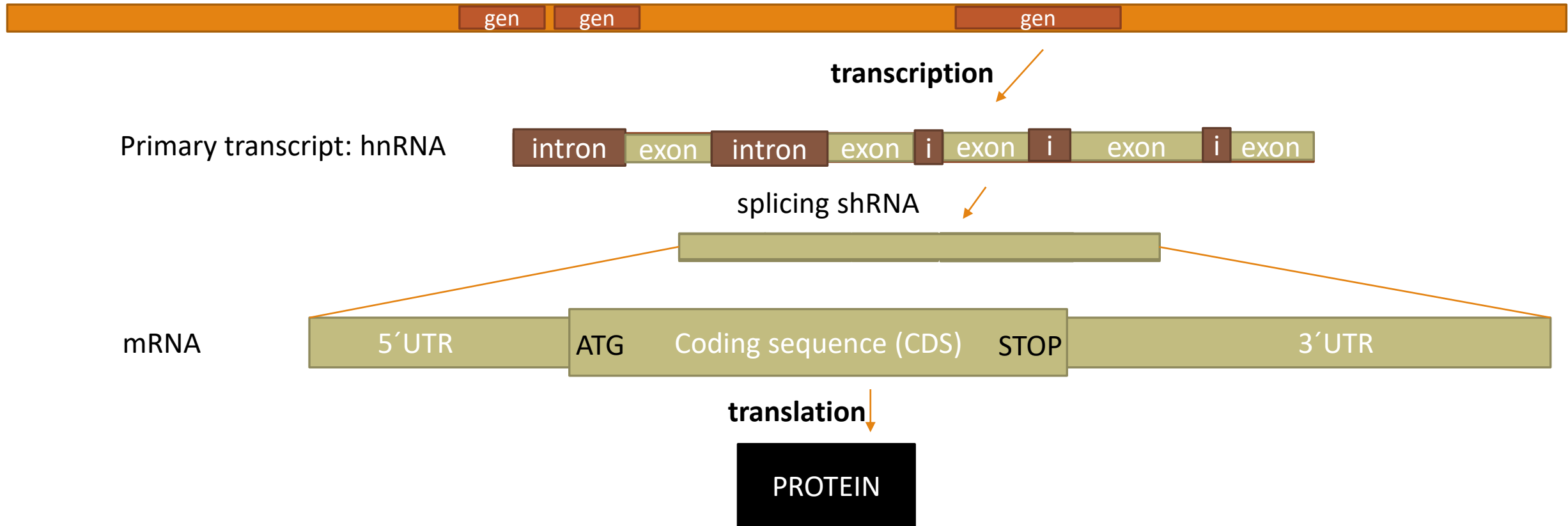


Figure 3-1:
Relationship
between
gene,
mRNA, and
protein
sequence
for
prokaryotes.

Eukaryotes

Genomic DNA / chromosomes



DNA sequence/GenBank

GenBank the leading nucleotide sequence repository maintained as a consortium:

 <http://www.ncbi.nlm.nih.gov/nucleotide/>

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

The image shows a screenshot of the NCBI website. A red arrow points to the 'Recent' dropdown menu, which is open and shows a list of database categories. The 'Nucleotide' option is circled in red. In the top right corner, the 'My NCBI' link is also circled in red. The main content area shows the NCBI logo, a search bar, and a list of popular resources including PubMed, Bookshelf, and BLAST.

NCBI Resources

Recent

- All Databases
- Nucleotide**
- Protein
- PubMed

All

- All Databases
- Assembly
- BioProject
- BioSample
- BioSystems
- Books
- ClinVar
- Clone
- Conserved Domains
- dbGaP
- dbVar
- Epigenomics
- EST
- Gene
- Genome
- GEO DataSets
- GEO Profiles
- GSS
- HomoloGene
- MedGen
- MeSH
- NCBI Web Site
- NLM Catalog
- Nucleotide**

NCBI Home

Resource List (A-Z)

- All Resources
- Chemicals & Bioassays
- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature
- Proteins
- Sequence Analysis
- Taxonomy

NCBI

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

NCBI | [Mission](#) | [Organization](#) | [Research](#) | [NCBI News](#)

Popular Resources

- PubMed
- Bookshelf
- PubMed Central
- PubMed Health
- BLAST
- Nucleotide
- Genome
- SNP
- Gene
- Protein
- PubChem

NCBI Announcements

NCBI Video: Submitting manuscripts on NIHMS

DNA databases NCBI

NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide Search Help

Advanced

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

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Nucleotide Nucleotide nqo1 Search

Create alert Advanced Help

Species Summary 20 per page Sort by Default order Send to: Filter your results:

- 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 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 **transcript = without intrones (mRNA)**

[RefSeq transcripts \(4\)](#) [RefSeq proteins \(4\)](#) [RefSeqGene \(1\)](#) [PubMed \(580\)](#)

[Orthologs](#) [Genome Browser](#) [BLAST](#) [Download](#)

RefSeq Sequences +

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

Items: 1 to 20 of 9424

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

DNA databases NCBI

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Nucleotide Nucleotide Search Help

Advanced

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

Summary Sort by Default order Send to Filter your results:

Items: 4

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)

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
Accession: NM_001386137.2 GI: 1675134183

DNA databases NCBI

NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide nqo1 Search

Create alert Advanced Help

- 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...

Summary 20 per page Sort by Default order

Send to: Filters: Manage Filters

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)

- [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](#)
- [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](#)

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:

Find items

Search details

nqo1[All Fields]

refinement:

Nucleotide Nucleotide Nqo1 and mus Search Save search Limits Advanced Help

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

Send to: Filter your results:

Results:30

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

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

Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA 1,552 bp linear mRNA

Mus musculus NAD(P)H:quinone oxidoreductase 1 (Nqo1) gene, promoter region and exon 1 1,069 bp linear DNA

Mus musculus chromosome 8, whole genome shotgun sequence 130,604,219 bp linear DNA

Homo sapiens NAD(P)H:quinone oxidoreductase (NQO1) gene, complete cds 7,447 bp linear DNA

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

- 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 Find items

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


„GenBank flatfile“

NCBI Resources ▾ How To ▾ jostovap My NCBI Sign Out

Nucleotide [Limits](#) [Advanced](#) [Help](#)

Display Settings: ▾ GenBank

Send: ▾

Change region shown ▾

Customize view ▾

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 iso1 \[J Biol Chem. 2013\]](#)

[See all...](#)

Pathways for the Nqo1 gene ▾

[Regulation of ornithine decarboxylase \(ODC\)](#)

[Metabolism of amino acids and derivatives](#)

[Metabolism](#)

[See all...](#)

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

NCBI Reference Sequence: NM_008706.5

[FASTA](#) [Graphics](#)

Go to: ▾

LOCUS NM_008706 (accession number) near ROD 27-OCT-2013
DEFINITION Mus musculus N (Nqo1), mRNA.
ACCESSION NM_008706
VERSION NM_008706.5 GI:161621259 (GenBank Identifier)
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 [ol NQO1 protein located

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JOURNAL hydrocarbon hydroxylase in the mouse
PUBMED J. Biol. Chem. 252 (1), 157-165 (1977)
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

```

- BioSystems
- CCDS
- Components (Core)
- Components (EST)
- Full text in PMC
- Gene
- GeneView in dbSNP
- HomoloGene
- Map Viewer
- Master
- Probe
- Protein
- PubMed
- PubMed (RefSeq)
- PubMed (Weighted)
- Taxonomy
- UniGene
- UniSTS
- GEO Profiles

- Recent activity Turn Off Clear
- Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA Nucleotide
 - Nqo1 [Mus musculus] Protein
 - regulation of nqo1 AND (Clinical Trial[ptyp]) (6) PubMed
 - NQO1, MPO, CYP2E1, GSTT1 and GSTM1 polymorphisms and biological effects c PubMed
 - nqo1 review AND (Clinical Trial[ptyp]) (1) PubMed
- [See more...](#)

FEATURES

SOURCE

chromosome 16

gene1..1552

exon1..140

CDS 134..958

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Location/Qualifiers
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Ox-1; Ox1; Qr1"
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phyloquinone reductase; menadione reductase;
NAD(P)H:quinone oxidoreductase 1; diaphorase 4
(NADH/NADPH); NAD(P)H menadione oxidoreductase 1, dioxin
induced NAD(P)H:quinone oxidoreductase 1"

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008706 : 1 segment

Details (i) Display: [FASTA](#) [GenBank](#) [Help](#) (x)


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        /note="putative"
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ORIGIN

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1501 tctttctatt tctttttttt ttaaatcgaa ataaatgaat acatcacaca tc

```



Nucleotide

Nucleotide ▾

Search

[Limits](#) [Advanced](#)[Help](#)[Display Settings:](#) ▾ GenBank[Send:](#) ▾

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

FASTA Sequence: NM_008706.5

[FASTA](#) [Blast](#) [Align](#)[Go to:](#) ▾

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 Kummrapurugu,A.B., Fischer,B.M., Zheng,S., Milne,G.L., Ghio,A.J.,

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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:

>NQO1_mus

```
AGGCTCAGCTCTTACTAGCCTAGCCTGTA  
GCCAGCCCTAAGGATCTCTCCGAAGAGCT  
AATGTCGG
```

```
AGGCTCAGCTCTTACTAGCCTAGCCTGTA  
GCCAGCCCTAAGGATCTCTCCGAAGAGCT  
AATGTCGG
```

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.

Nucleotide

Nucleotide ▾

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

FASTA Sequence: NM_008706.5

[FASTA](#) [Blast](#)[Go to:](#) ▾

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

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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

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ACATCACACATC

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- Mitochondrial targeting of mouse NQO1 and CYP1B1
The protein level of PGC-1α, a key metabolic regulator, is controlled by NA
NADPH:quinone oxidoreductase 1 regulates host susceptibility to ozone via iso

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)

FEATURES

FEATURES	Location/Qualifiers
source	1..2601
ORIGIN	

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

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```

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PLQWFGVAILKQWFRVFIQEFAYTYAAMYDKGPFRRKAVLSITGGSSMYSLQ
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Details Display: **FASTA** GenBank Help

NM_000903 : 1 segment

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/db_xref="MIM:125860"
/translation="MIGRDLIVLHSEKTSKSNYAMVMAAAALVYKCHEVWESDLYA

NCBI/coding sequence (CDS)

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

NCBI Reference Sequence: NM_008706.5
[GenBank](#) [Graphics](#)

>gi|161621259|ref|NM_008706.5| Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA

```
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TGGCAACCAGCTGCTCAGCCAATCAGCGTTCGGTATTACGATCCTCCCTCAACATCTGGAGCCATGGCGG
CGAGAAGAGCCCTGATTGTACTGGCCCATTCAGAGAAGACATCATTCAACTACGCCATGAAGGAGGCTGC
TGTAGAGGCTCTGAAGAAGAGAGGATGGGAGGTACTCGAATCTGACCTCTATGCTATGAACCTCAACCCC
ATCATTCCAGAAATGACATCACAGGTGAGCTGAAGGACTCGAAGAACTTTCAGTATCCTTCCGAGTCAT
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CGTCATCTCTGGCCGATTGAGAGTGGCATCCTGCGTTTCTGTGGCTTCCAGGTCTTAGAACCTCAACTG
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TGAAGTCAGATTAGGAGCCTCAGGGCAAGGTGCAGAAGCGAGCTGGAATACTCTTCTAGGTCATTATG
CAATATTCGCCATTTCTTCGGGCTAGTCCCAGTTAGATGGCATCCAGTCCCTCCATCAAGATTCGTTGTC
```

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

The protein level of PGC-1 α , 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]

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FASTA

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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
CGAGAAGAGCCCTGATTGTACTGGCCATTGAGAGAAGACATCATTCAACTACGCCATGAAGGAGGCTGC
TGTAGAGGCTCTGAAGAAGAGAGGATGGGAGGTAATCGAATCTGACCTCTATGCTATGAACCTCAACCCC
ATCATTCCAGAAATGACATCACAG
```

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Articles about the Nao1 gene

Practical part

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Link to nucleotides from UniProt

The image shows the UniProt website interface for the protein entry P15559 (NQO1_HUMAN). The top navigation bar includes the UniProt logo and search options like BLAST, Align, Peptide search, ID mapping, SPARQL, and UniProtKB. The main content area displays the protein name and key information: Protein: NAD(P)H dehydrogenase [quinone] 1, Gene: NQO1, Status: UniProtKB reviewed (Swiss-Prot), Organism: Homo sapiens (Human), Amino acids: 274, Protein existence: Evidence at protein level, and Annotation score: 5/5. Below this, there are tabs for Entry, Variant viewer (408), Feature viewer, Genomic coordinates, Publications, External links, and History. A sidebar on the left lists various categories, with 'Sequence & Isoforms' highlighted by a red arrow. The 'Function' section is expanded, showing a detailed description of the enzyme's role in redox reactions. A survey notification is visible in the bottom right corner.

UniProt BLAST Align Peptide search ID mapping SPARQL UniProtKB Advanced | List Search

Function

P15559 · NQO1_HUMAN

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

Entry Variant viewer 408 Feature viewer Genomic coordinates Publications External links History

BLAST Align Download Add Add a publication Entry feedback

Functionⁱ

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

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

Link to nucleotides from UniProt

UniProt BLAST Align Peptide search ID mapping SPARQL UniProtKB Advanced | List Search

Sequence & Isoformsⁱ

Align 3 isoforms

Sequence statusⁱ Complete

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

Sequence databases

CCDS	CCDS10883.1 [P15559-1]	RefSeq	NP_000894.1 NM_000903.2 [P15559-1]
	CCDS32471.1 [P15559-3]		NP_001020604.1 NM_001025433.1 [P15559-2]
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Length 274 Last updated 1990-04-01 v1
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110 120 130 140 150 160 170 180 190 200

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

NCBI Reference Sequence: [NM_008706.5](#)[FASTA](#) → **GRAPHIC**[Go to:](#) ▾

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

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REFERENCE 2 (bases 1 to 1552)

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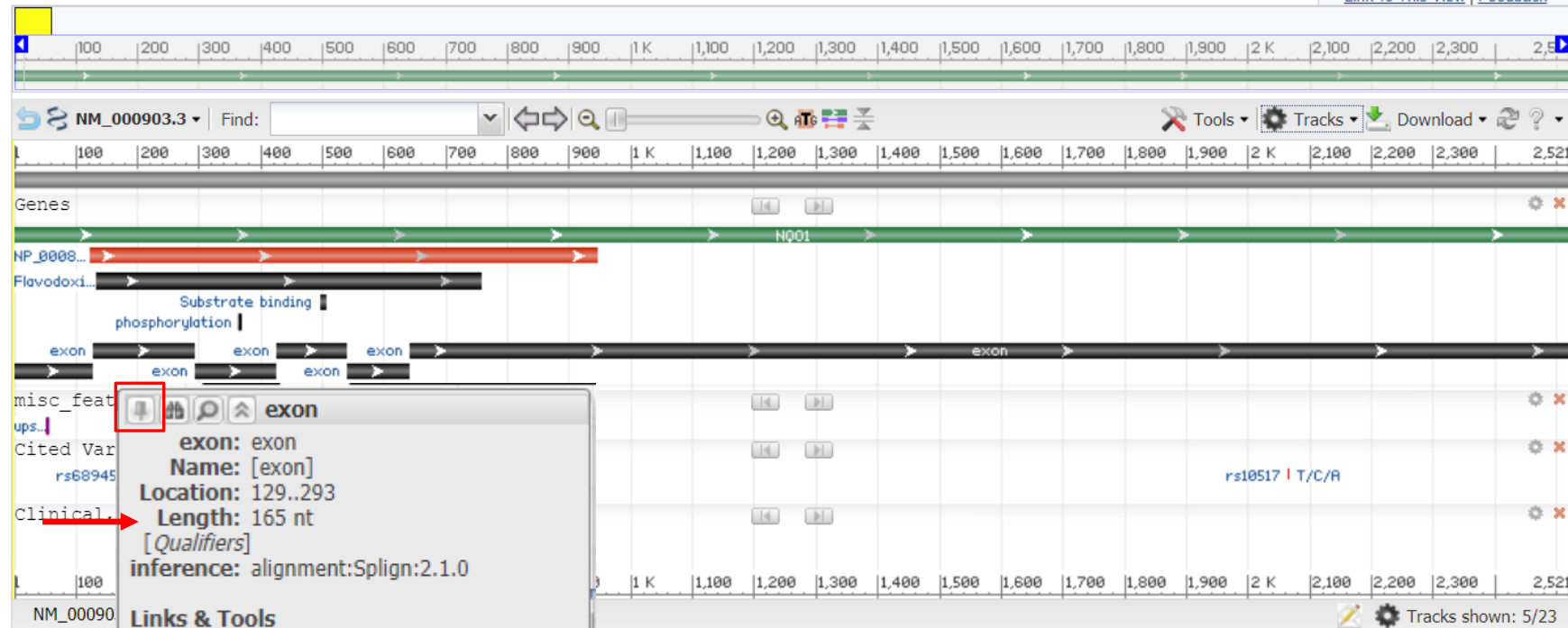
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Homo sapiens NAD(P)H quinone dehydrogenase 1 (NQO1), transcript variant 1, mRNA

NCBI Reference Sequence: NM_000903.3

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

NCBI Reference Sequence: [NM_008706.5](#)[FASTA](#) → **GRAPHIC**[Go to:](#) ▾

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)
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- 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 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 \(580\)](#)

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

NCBI Reference Sequence: NG_011504.2
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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 [/NG_011504.2/FASTA/GRAPHICS/](#)

ORIGIN

```
1 tgggctcaag caatcctccc acctcagcct cccaagttag ggggactaca gacgcataat
61 accacacggg cctaatttta tttaaaatta tgttttgtag agatggggtc ttgctgtgtt
121 gccaggctg gtctcaaatt tctggcctca agggatccgc ctgccttgcc ctcccaaagt
181 gctgggatta cagggtgtga 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 tggtagggtg agtctctgtc acccaggttg gactacagcg
481 gtgtgatctc ggctcaccgc aacctctgct tcttgggttc aagctattct cctgcctcag
541 cctcctgagt agctggcatt ataggcatgc accacaacac ccagctaaat tttttgtat
601 ttttagcaga gatgagtttt gccatattgg ccaggctggt cttgaactcc tgacttcaag
661 tgatccaccc gtctcggcct cccaaagtgc tgggattaca ggcgtgagcc acggcaccag
721 gcctagtcta gtcttttcac gtttttctgc ctgctttata ttctggccgc actggcagct
```

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

Related information
Protein
Taxonomy
Components (Core)
Full text in PMC
Gene
HomoloGene
PubMed (Weighted)
RNA

DNA database NCBI –gene sequence

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Nucleotide Nucleotide Search Help

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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

```
ATGGTGGCAGAAAGAGCACTGATCGTACTGGCTCACTCAGAGAGGACGTCCTTCAACTATGCCATGAAGG
AGGC TGC TGC AGC GGC TTT GAAGAAGAAAGGATGGGAGGTGGTGGAGTCCGGACCTCTATGCCATGAACCT
CAATCCCATCATTTCCAGAAAGGACATCACAGGTAACCTGAAGGACCTGCCAAGCTTTCAGTATCCTGCC
GAGTCTGTTCTGGCTTATAAAGAAGGCCATCTGAGCCCAGATATTGTGGCTGAACAAAAGAAGCTGGAAG
CCGCAGACCTTGTGATATTCAGTTCGCCCTGCAGTGGTTGGAGTCCCTGCCATTCTGAAAGGCTGGTT
TGAGCGAGTGTTCATAGGAGAGTTTGCTTACACTTACGCTGCCATGTATGACAAAGGACCTTCCGGAGT
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CGCTGGAGAAATATTTGGGATGAGACACCACCTGATTTTGTCCAAGCAGCCTCTTTGACCTAAACTCC
AGGCAGGATCTTAATGAAAAAGAGGTACAGGATGAGGAGAAAAACAAGAAATTTGGCCTTCTGTGGG
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```

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

TPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNNKFGLSVGHHLGKSIPTDNQIKARK"

Details Display: FASTA GenBank Help

Practical part

Find the sequence „your“ gene.

Explore graphic view
and CDS

NCBI/Gene (secondary database)

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Nucleotide Nucleotide nqo1 Search

Create alert Advanced Help

Species Summary 20 per page Sort by Default order Send to: Filter your results:

- 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

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

Database: Select

Find items

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

Filter your results:

- All (9424)
- [Bacteria \(8564\)](#)
- [INSDC \(GenBank\) \(8754\)](#)
- [mRNA \(455\)](#)
- [RefSeq \(668\)](#)

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Results by taxon

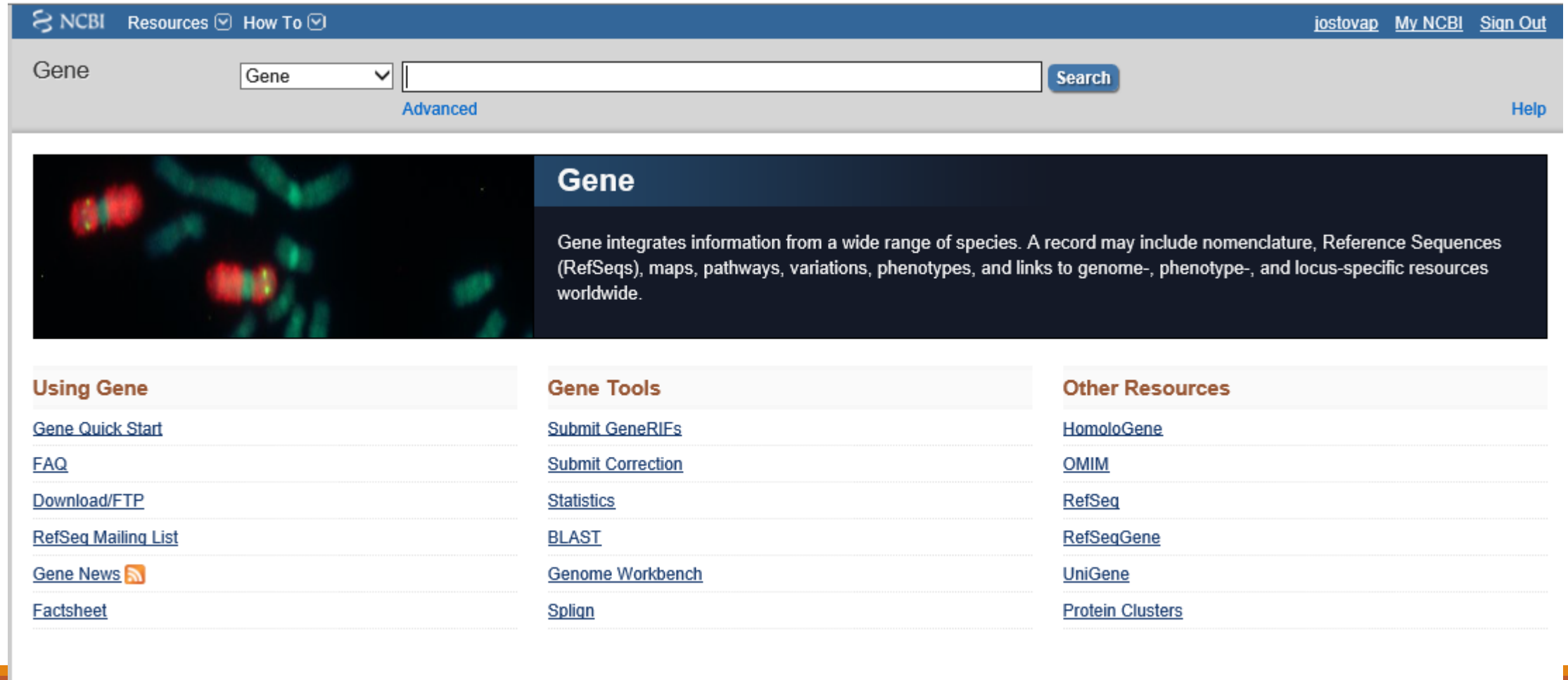
Top Organisms [Tree](#)

- [Mycobacteroides abscessus \(2510\)](#)
- [Clostridioides difficile \(2236\)](#)
- [Neisseria meningitidis \(995\)](#)
- [Legionella pneumophila \(716\)](#)
- [Neisseria gonorrhoeae \(551\)](#)
- [All other taxa \(2416\)](#)

More...

Find related data

NCBI/Gene (secondary database)



The screenshot shows the NCBI Gene database homepage. At the top, there is a navigation bar with the NCBI logo, "Resources" and "How To" dropdown menus, and user links for "jostovap", "My NCBI", and "Sign Out". Below this is a search bar with a "Gene" dropdown menu, a search input field, and a "Search" button. A "Help" link is located on the right side of the search bar. The main content area features a dark blue header with the word "Gene" in white. To the left of the header is a microscopic image of chromosomes. To the right, a paragraph describes the Gene database: "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." Below the header, there are three columns of links. The first column, "Using Gene", includes links for "Gene Quick Start", "FAQ", "Download/FTP", "RefSeq Mailing List", "Gene News" (with an RSS icon), and "Factsheet". The second column, "Gene Tools", includes links for "Submit GeneRIFs", "Submit Correction", "Statistics", "BLAST", "Genome Workbench", and "Splign". The third column, "Other Resources", includes links for "HomoloGene", "OMIM", "RefSeq", "RefSeqGene", "UniGene", and "Protein Clusters".


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Gene Gene Search Advanced Help

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](#)

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Genomic

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Alternatively spliced
Annotated genes
Protein-coding
Pseudogene

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/ Current

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more...

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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 << First < Prev Page 1 of 14 Next > Last >>
See also 29 discontinued or replaced items.

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

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Database:

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Search details

nqo1[All Fields] AND alive[prop]

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

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

Summary

Official Symbol	NQO1 <small>provided by HGNC</small>
Official Full Name	NAD(P)H quinone dehydrogenase 1 <small>provided by HGNC</small>
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

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- NCBI Reference Sequences (RefSeq)
- Related sequences
- Additional links

NCBI/Gene

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

Go to [reference sequence details](#)

Genomic Sequence:

Go to nucleotide: [Graphics](#) [FASTA](#) [GenBank](#)

NC_000016.10 Find:

Tools Tracks

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

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

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

Summary

Official Symbol	GAPDH <small>provided by HGNC</small>
Official Full Name	glyceraldehyde-3-phosphate dehydrogenase <small>provided by HGNC</small>
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 <i>E. coli</i> , <i>P. aeruginosa</i> , and <i>C. albicans</i> . 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

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- General protein information
- NCBI Reference Sequences (RefSeq)
- Related sequences
- Additional links

NCBI/Gene

Gene Advanced Help

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

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

Summary ⌵ ?

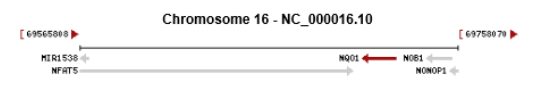
Official Symbol NQO1 provided by HGNC
Official Full Name NAD(P)H quinone dehydrogenase 1 provided by HGNC
Primary source [HGNC:HGNC:2874](#)
See related [Ensembl:ENSG00000181019](#) [MIM:125860](#) [Vega:OTTHUMG00000137575](#)
Gene type protein coding
RefSeq status REVIEWED
Organism [Homo sapiens](#)
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominidae; Homo
Also known as DTD; QR1; DHQU; DIA4; NMOR1; NMOR1
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:

Go to nucleotide: [Graphics](#) [FASTA](#) [GenBank](#)

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- General protein information
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- 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

Full Report

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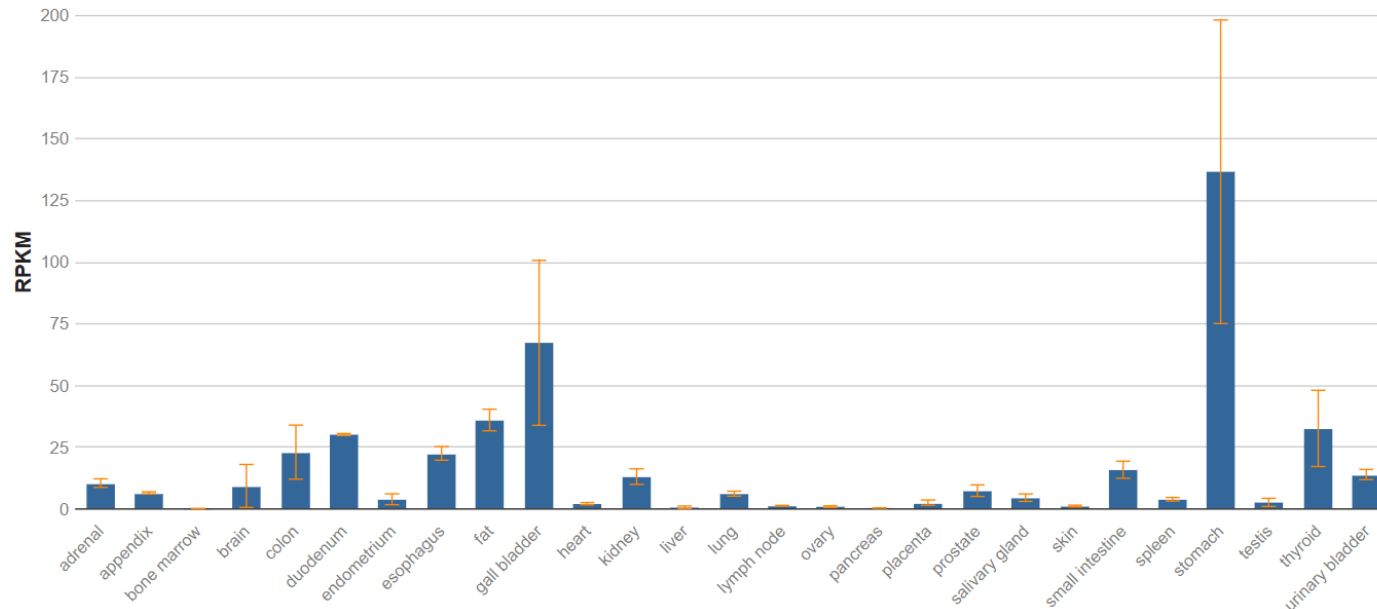
Expression



[See details](#)

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,



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[Reference sequence details](#)

[Bioss](#) [FASTA](#) [GenBank](#)

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- UCSC
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 - 3D structures

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)

Genome Browsers

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

Chromosome 16 - NC_000016.10

Genomic regions, transcripts, and products

Genomic Sequence:

NC_000016.10 Find:

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 \(69,709,401..69,726,560\)](#)

NCBI/Gene – whole gene sequence

GenBank ▾

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Homo sapiens chromosome 16, GRCh38.p14 Primary Assembly

NCBI Reference Sequence: NC_000016.10

[FASTA](#) [Graphics](#)

Go to: ▾

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.,
Fotopoulos,D., Glavina,T., Gomez,M., Gonzales,E., Goodstein,D.,

Change region shown

Whole sequence (abbreviated view)

Selected region

from: to:

Update View

Customize view

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[BioProject](#)

[Protein](#)

[PubMed](#)

[Taxonomy](#)

NCBI/GenBank – whole gene sequence

GenBank ▾

Homo sapiens chromosome 16, GRCh38.p14 Primary Assembly

NCBI Reference Sequence: NC_000016.10

[FASTA](#) [Graphics](#)

Send to: ▾

Change region shown

Whole sequence (abbreviated view)

Selected region

from: 69709401

to: 69726560

Update View

Go to: ▾

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 (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa;

Mammalia; Eutheria;

Catarrhini; Hominid

REFERENCE 1 (bases 1 to 17160)

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

Fotopoulos,D., Glavi

CDS

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/note="i

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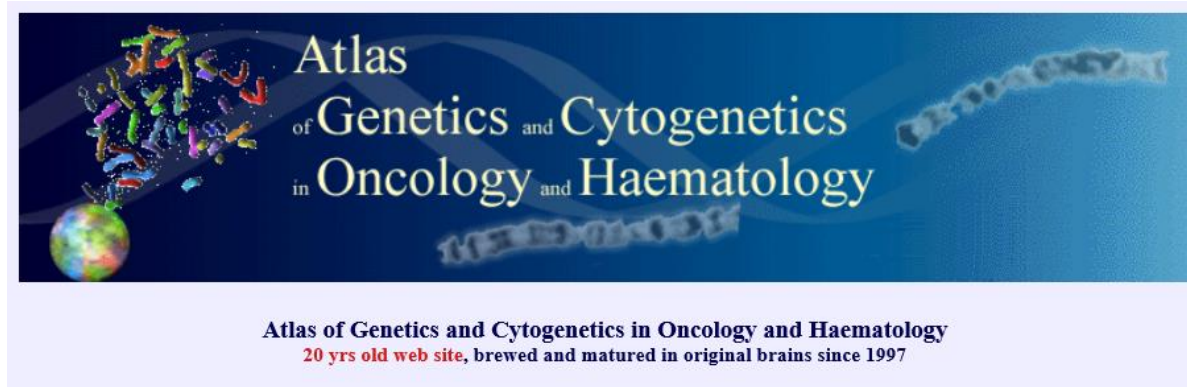
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Derived by automated computation
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/db_xref="MIM: 125860 "
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FQAGFLMKKEVQDEEKNKFLSVGHHLKSI
```

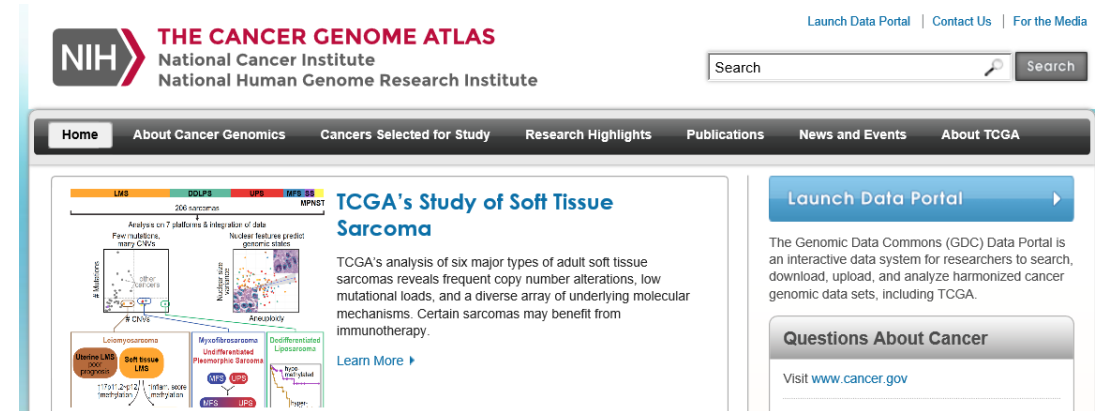
Practical part

Explore „your“ nucleotide sequence
in Gene.

Focused databases (secondary)



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



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National Cancer Institute
National Human Genome Research Institute

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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.

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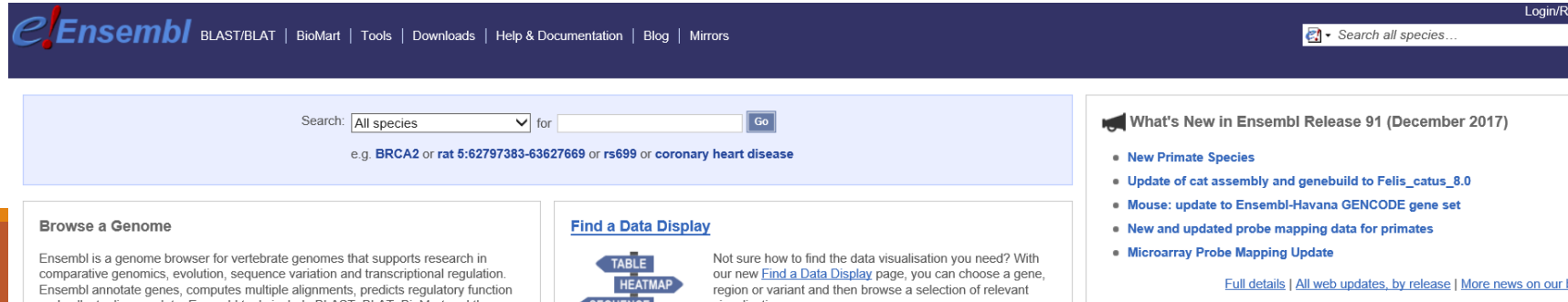
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e.g. BRCA2 or rat 5:62797383-63627669 or rs699 or coronary heart disease

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

TABLE
HEATMAP
SEQUENCE

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](#)

Practical part

Explore „your“ nucleotide sequence
in database GeneCards.

Sequence analysis

Filter DNA

DNA stats

Range Extractor DNA

Reverse complement

SMS
Format Conversion
-Combine FASTA
-EMBL to FASTA
-EMBL Feature Extractor
-EMBL Trans Extractor
-Filter DNA
-Filter Protein
-GenBank to FASTA
-GenBank Feature Extractor
-GenBank Trans Extractor
-One to Three
-Range Extractor DNA
-Range Extractor Protein
-Reverse Complement
-Split Codons
-Split FASTA
-Three to One
-Window Extractor DNA
-Window Extractor Protein
Sequence Analysis
-Codon Plot

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 cgctttgcc aactgtacacc caacctcgg  
41 ttattgtcga acctcccgct tgtgcgcgca tctgcatata  
81 gatcccggtc agtccgctac attctgcca ttagtatcc  
121 tcgaagtctt attccaogtg ctcaaagcaa gggatocga  
161 cagtataac cgctcgtgc agatccaaat tctcgattaa  
201 cactcaagta ctgattttta tcatcagga actaaaaact
```

Please check the [browser compatibility page](#) before using this program.

Filter DNA results

```
>filtered DNA sequence consisting of 1000 bases.  
ttaagatttgcctttgccactgfacaccaactcggttattgtcgaacctcccgct  
tfgcccgcatctcatatagaccggfcaagctcctcattctgccaatfgagtatcc  
tgaagctcttaccacgctcaangcaagggtatcgtacagtgataaccgctcgtgc  
agatccaaattctgattaacactcaagtaactgattttatcatcaggtactaaaaact  
cacaatttgaagcaccagcgaatcgttctctctcagctcgaacatcagagttg  
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acgttcaactgagatgactctatcggcacacgatcatgctccaaggtccaagg  
cgaattactagggtcacagactacagctacgctcggctgattctcgtctgacac  
cactgttcaaaagctccgataccgacgatcctcgtctctgtggcagcactta
```

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
```

```
tttttttttt
```

```
>Sample sequence 2 reverse complement
```

```
gagagagag
```

Practical part

Analyze „your“ nucleotide sequence.

(HW: How many cytosins and dinucleotides CG 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?
- 5) How many cytosines have the second exon? How many CG dinucleotides?

E.g use „výstřížky“



„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
CAATCCCATTCCAGAAAGGACATCACAGTAAACTGAAGGACCCCTGCGAACTTTCAGTATCCTGCC
GAGTCTGTTCTGGCTTATAAAGAAGGCCATCTGAGCCAGATATTGTGGCTGAACAAAAGAAGCTGGAAG
CCGCAGACCTTGTGATATCCAGTCCCCCTGCAGTGGTTTGGAGTCCCTGCCATTCTGAAAGGCTGGTT
TGAGCGAGTGTTCATAGGAGAGTTTGCTTACACTTACGCTGCCATGTATGACAAAGGACCCCTCCGGAGT
AAGAAGGAGTGCCTTCCATCACCCTGGTGGCAGTGGCTCCATGTACTCTCTGCAAGGGATCCACGGGG
ACATGAATGTCATTCTCTGGCCAATTCAGAGTGGCATTCTGCATTTCTGTGGCTTCCAAGTCTTAGAACC
TCAACTGACATATAGCATTTGGGCACACTCCAGCAGACGCCGAATCAAATCCTGGAAGGATGGAAGAAA
CGCCTGGAGAATATTTGGGATGAGACACCCTGTATTTTGTCCCAAGCAGCCTCTTTGACCTAAACTTCC
AGGCAGGATTCTTAATGAAAAAAGAGGTACAGGATGAGGAGAAAAACAAGAAATTTGGCCTTCTGTGGG
CCATCACTTGGGCAAGTCCATCCCACTGACAACCAGATCAAAGCTAGAAAAATGA

- 3) Chromosome 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
TGACGCGGCTTTGAAGAAGAAAGGATGGGAGGTGGTGGAGTCGGACCTCTATGCCATGAACTTCAATCCC
ATCATTCCAGAAAGGACATCACAG

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