

Introduction to applied bioinformatics

PETRA MATOUŠKOVÁ

2025/2026

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

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

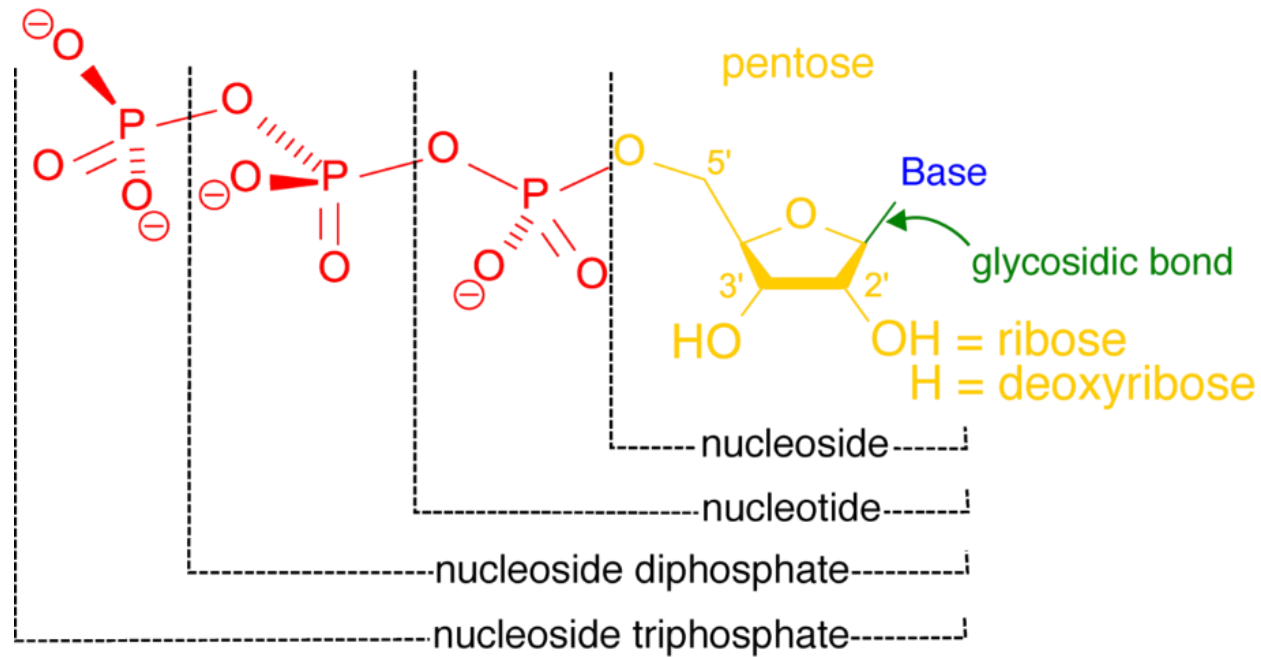
Complementarity: A=T, C≡G

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

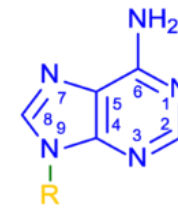
400-nt (nucleotides) = 400 bp (base pairs)...kbp, Mbp

		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

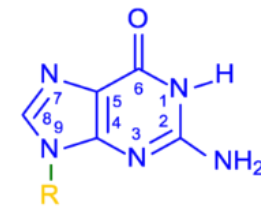
DNA/RNA



Purines

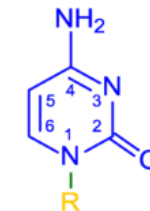


Adenine

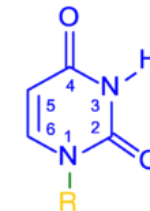


Guanine

Pyrimidines



Cytosine

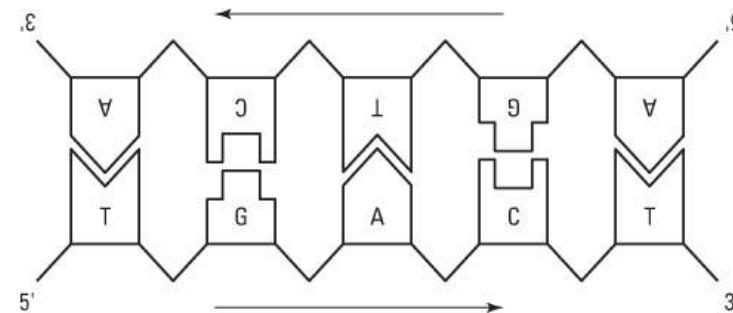
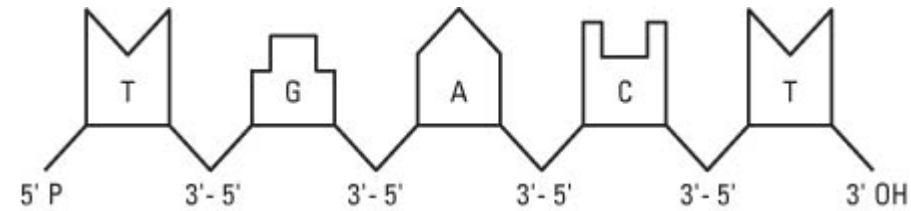
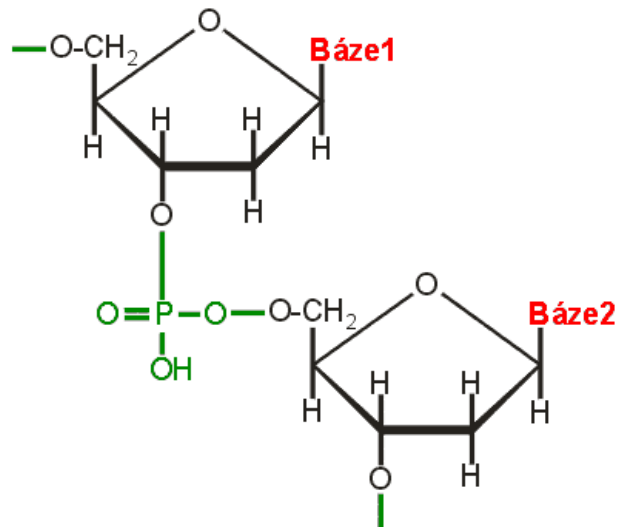
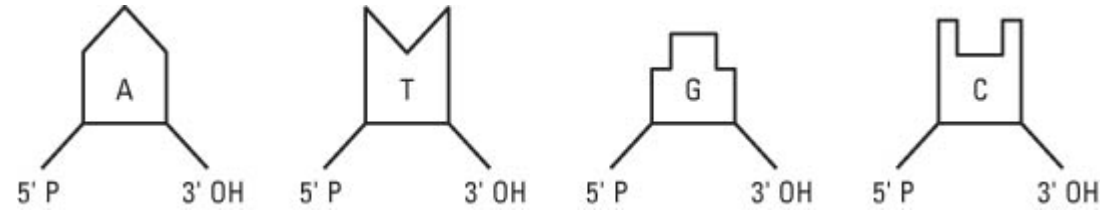
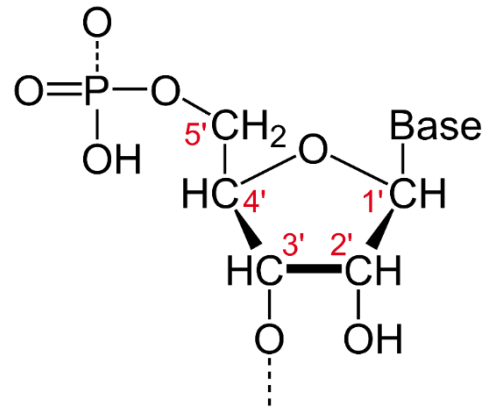


Uracil

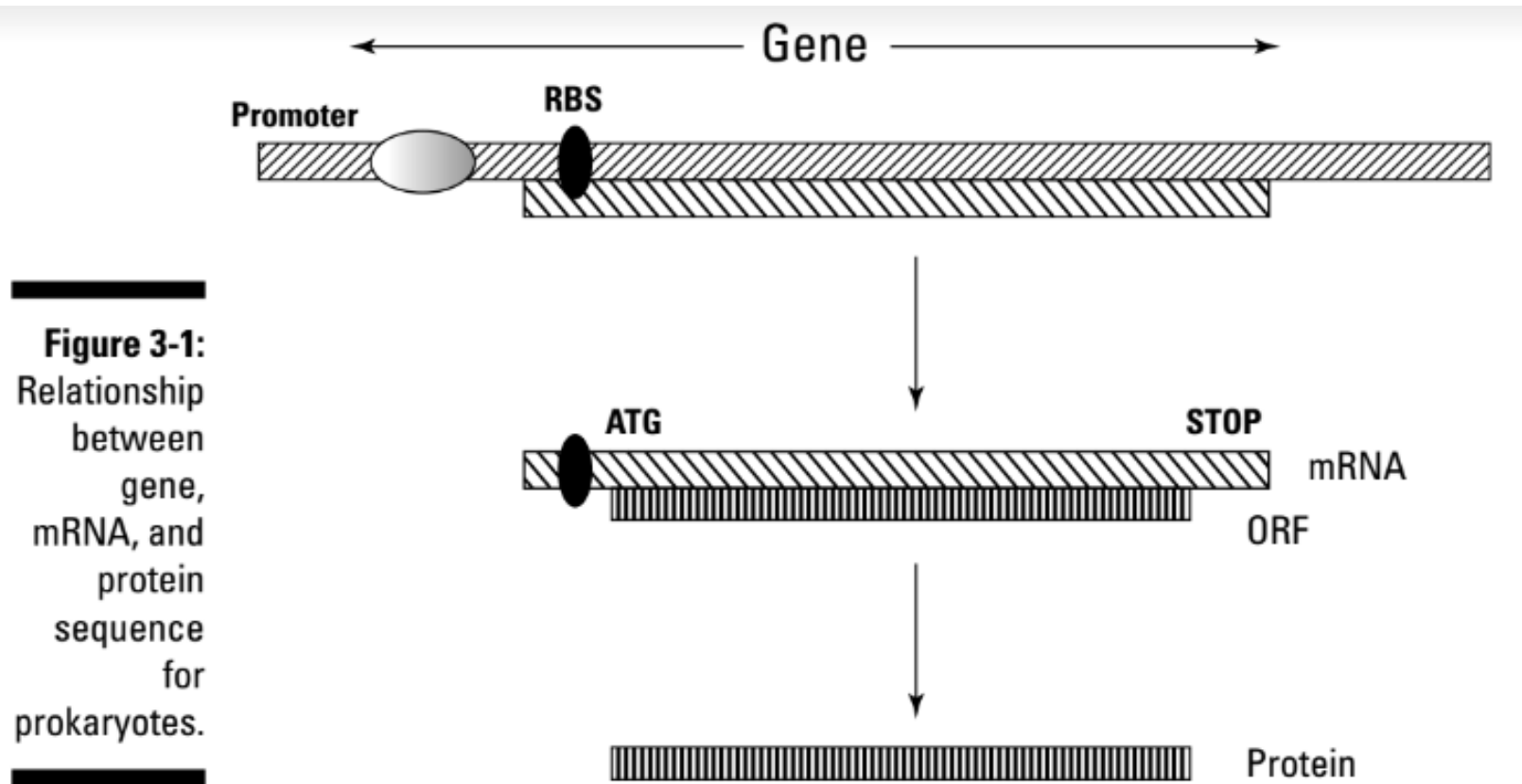


Thymine

DNA/RNA



Prokaryotes



Eukaryotes

Genomic DNA / chromosomes



transcription

Primary transcript: hnRNA



splicing shRNA

mRNA



translation

PROTEIN



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/>

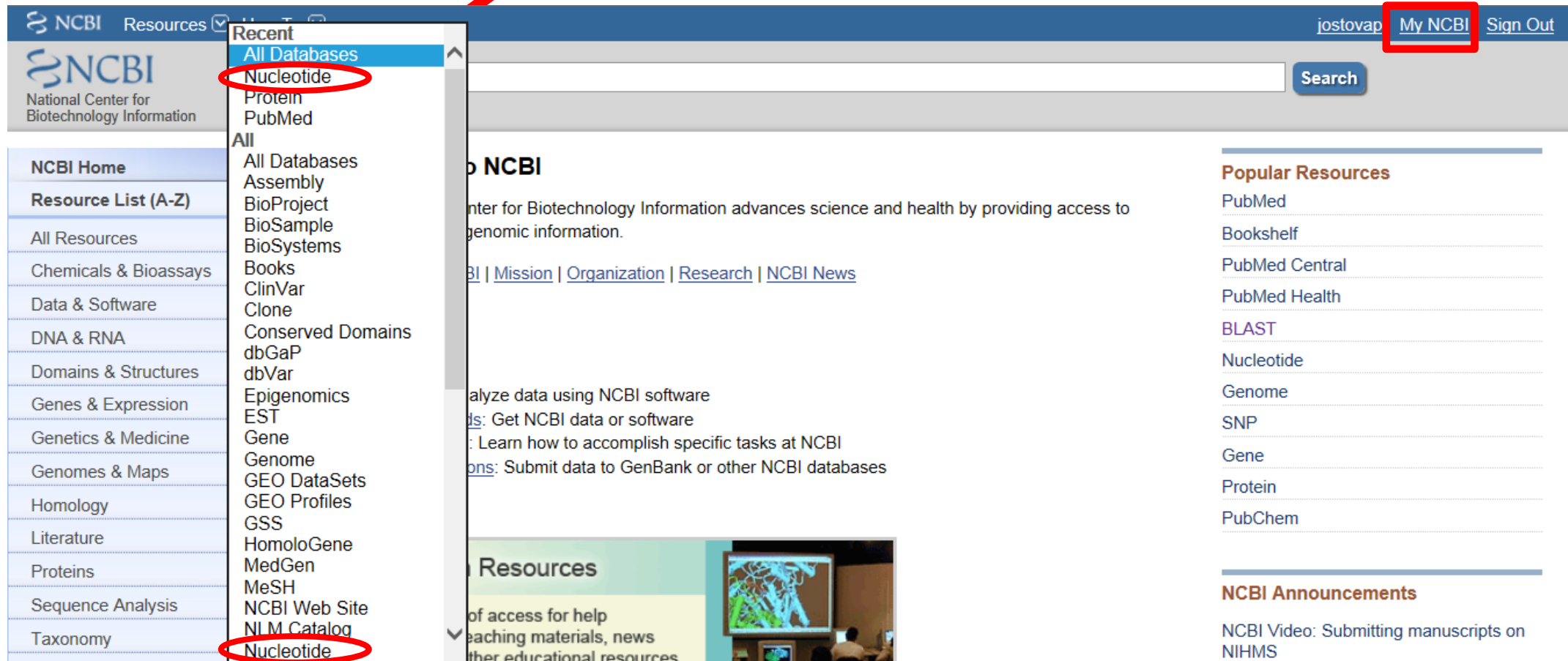


DNA Data Bank of Japan (DDBJ)

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



DNA databases NCBI



The screenshot shows the NCBI homepage with a dropdown menu open under the 'Resources' tab. The 'Recent' section of the dropdown menu is highlighted, and 'Nucleotide' is selected and circled in red. The 'My NCBI' link in the top right corner is also circled in red. The 'Popular Resources' section on the right lists various tools and databases, including PubMed, Bookshelf, PubMed Central, PubMed Health, BLAST, Nucleotide, Genome, SNP, Gene, Protein, and PubChem. The 'NCBI Announcements' section at the bottom right mentions a video about submitting manuscripts on NIHMS.

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

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](#)

Nucleotide

Nucleotide

▼

Advanced

[Sign in to NCBI](#)

Search

[Help](#)



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](#)

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

DNA databases NCBI

 NCBI [Resources](#) [How To](#)

jostovap [My NCBI](#) [Sign Out](#)

Nucleotide

Nucleotide

×

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: ▾

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

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

+

Items: 1 to 20 of 9424

<< First

< Prev

Page 1

of 472

Next >

Last >>

Find items

DNA databases NCBI

transcript = without introns (mRNA)

Showing 4 of 4 (by status, accession number)

corresponding protein

Transcript	nt	Protein	aa	Isoform	Status
NM_000903.3	2,521	NP_000894.1	274	a	MANE Select
NM_001025433.2	2,419	NP_001020604.1	240	b	curated
NM_001025434.2	2,407	NP_001020605.1	236	c	curated
NM_001286137.2	2,305	NP_001273066.1	202	d	curated

View full table

DNA databases NCBI

 NCBI [Resources](#)  [How To](#) 

jostovap [My NCBI](#) [Sign Out](#)

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 

Items: 4

☐ [Homo sapiens NAD\(P\)H quinone dehydrogenase 1 \(NQO1\), transcript variant 1, mRNA](#)

1. 2,521 bp linear mRNA

Accession: NM_000903.3 GI: 1519241811

[Protein](#) [PubMed](#) [Taxonomy](#)

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

☐ [Homo sapiens NAD\(P\)H quinone dehydrogenase 1 \(NQO1\), transcript variant 2, mRNA](#)

2. 2,419 bp linear mRNA

Accession: NM_001025433.2 GI: 1675133956

[Protein](#) [PubMed](#) [Taxonomy](#)

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

☐ [Homo sapiens NAD\(P\)H quinone dehydrogenase 1 \(NQO1\), transcript variant 3, mRNA](#)

3. 2,407 bp linear mRNA

Accession: NM_001025434.2 GI: 1676355479

[Protein](#) [PubMed](#) [Taxonomy](#)

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

☐ [Homo sapiens NAD\(P\)H quinone dehydrogenase 1 \(NQO1\), transcript variant 4, mRNA](#)

4. 2,305 bp linear mRNA

Accession: NM_001286137.2 GI: 1675124182

Send to: 

Filter your results:

All (4)

Bacteria (0)

INSDC (GenBank) (0)

[mRNA \(4\)](#)

[RefSeq \(4\)](#)

[Manage Filters](#)

Analyze these sequences 

Run BLAST

Find related data 

Database:

Select 

Find items

Recent activity 

Turn Off

Clear

🔍 nqo1 (9424)

Nucleotide

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

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: [Select](#)
[Find items](#)

Search details
nqo1[All Fields]

refinement:

[Display Settings:](#) v Summary, 50 per page, Sorted by Default order

[Send to:](#) v

Filter your results:

All (30)

[Bacteria \(8\)](#)

[INSDC \(GenBank\) \(12\)](#)

[mRNA \(8\)](#)

[RefSeq \(18\)](#)

[Manage Filters](#)

▼ 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 v

[Find items](#)

Search details

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

Results:30

☐ [Mus musculus full open reading frame cDNA clone RZPDo836H0851D for gene Nqo1, NAD\(P\)H dehydrogenase, quinone 1:](#)

1. [complete cds, incl. stopcodon](#)

825 bp linear mRNA

Accession: CT010284.1 GI: 71059896

[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

☐ [Mus musculus NAD\(P\)H dehydrogenase, quinone 1 \(Nqo1\), mRNA](#)

2. [1,552 bp linear mRNA](#)

Accession: NM_008706.5 GI: 161621259

[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

☐ [Mus musculus NAD\(P\)H:quinone oxidoreductase 1 \(Nqo1\) gene, promoter region and exon 1](#)

3. [1,069 bp linear DNA](#)

Accession: AY425712.1 GI: 37694057

[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

☐ [Mus musculus chromosome 8, whole genome shotgun sequence](#)

4. [130,604,219 bp linear DNA](#)

Accession: CM000216.2 GI: 74229904

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

☐ [Homo sapiens NAD\(P\)H:quinone oxireductase \(NQO1\) gene, complete cds](#)

8. [7,447 bp linear DNA](#)

Accession: AH005427.2 GI: 1049010536

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

☐ [Mus musculus strain C57BL/6J chromosome 8 genomic contig. GRCm38.p1 C57BL/6J MMCHR8_CTG11](#)

6. [56,658,466 bp linear DNA](#)

Accession: NT_078575.7 GI: 272222222

„GenBank flatfile“

 [Resources](#)  [How To](#) 

[jostovap](#) [My NCBI](#) [Sign Out](#)

Nucleotide

Nucleotide 

Search

[Limits](#) [Advanced](#)

[Help](#)

[Display Settings:](#)  GenBank

[Send:](#) 

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		
KEYWORDS	RefSeq.	(GenBank Identifier)		
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			

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...](#)

hydrocarbon hydroxylase in the mouse
 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, BC004679.1 [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

exon1..140

misc_feature

CDS 134..958

/gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmol; Nmor1;
 Ox-1; Ox1; Qr1"
 /note="NAD(P)H dehydrogenase, quinone 1"
 /db_xref="GeneID:18104"

/gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmol; Nmor1;
 Ox-1; Ox1; Qr1"
 /inference="alignment:Splign:1.39.8"
 38..40

/gene="Nqo1"
 /gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmol; Nmor1;
 Ox-1; Ox1; Qr1"
 stop codon"

/gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmol; Nmor1;
 Ox-1; Ox1; Qr1"
 /EC_number="1.6.5.2"
 /note="quinone reductase 1; DT-diaphorase; azoreductase;
 phyloquinone reductase; menadione reductase;
 NAD(P)H:quinone oxidoreductase 1; diaphorase 4
 (NADH/NADPH); NAD(P)H menadione oxidoreductase 1, dioxin

_008706 : 1 segment

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...

Details

Display: FASTA GenBank Help

STS 740..941
/gene="Nqo1"
/gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmo1; Nmor1;
Ox-1; Ox1; Qr1"
/standard_name="Nqo1"
/db_xref="UniSTS:499103"
STS 1193..1322
/gene="Nqo1"
/gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmo1; 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; Nmo1; Nmor1;
Ox-1; Ox1; Qr1"
/note="putative"
polyA_site 1552
/gene="Nqo1"
/gene_synonym="AV001255; Dia4; Dtd; Nmo-1; Nmo1; Nmor1;
Ox-1; Ox1; Qr1"
/note="putative"

ORIGIN

```
1 aggcctcagct cttactagcc tagcctgtag ccagccctaa ggcctctctc gaagagcttt
61 agggctcgtct tggcaaccag ctgctcagcc aatcagcgtt cgggtattacg atcctccctc
121 aacatctgga gccatggcgg cgagaagagc cctgattgta ctggcccatc cagagaagac
181 atcattcaac tacgccatga aggaggctgc tgtagaggct ctgaagaaga gaggatggga
241 ggtactcgaa tctgacctct atgctatgaa ctccaacccc atcatttcca gaaatgacat
301 cacaggtgag ctgaaggact cgaagaactt tcagtatcct tccgagtcac ctctagcata
361 taaggaagga cgccctgagcc cagatattgt ggcgaacac aagaagctgg aagctgcaga
421 cctggtgata ttccagttcc cattgcagtg gtttggggtg ccagccatcc tgaaggctg
481 gtttgagaga gtgctcgtag caggatttgc ctacacatat gctgccatgt acgacaacgg
541 tcctttccag aataagaaga ccttgcttcc taccaccact gggggtagcg gctccatgta
601 ctctcttcag ggtgtccacg gggacatgaa cgtcattctc tggccgatcc agagtggcat
661 cctgcgtttc tgtggcttcc aggtcttaga acctcaactg gtttacagca ttggccacac
721 tccaccagat gcccgcatgc agatcctgga aggatggaag aaacgtcttg aaaccgtctg
781 ggaggagacc ccactctatt ttgctccaag cagcctgttt gacctaaact ttcaggcagg
841 attcttaagt aaaaagggaag ttcaagagga gcagaagaag aacaagtttg gcctctctgt
901 gggccatcac ctgggcaagt ccattccagc tgacaaccag atcaaagcta gaaaataagg
961 atttttttcc taacatatag ttgacgcag ctttcttttt cccagcttgg tctgacttgc
1021 tttcattttt ttcttttgc ccacgaggat gggaaaagga gtaagttttc ttcattgctt
1081 tttttt
1141 cagggc
1201 catttt
1261 tataat
1321 gggactaaat tgttttagcag tttagcagta gctaaagcct gtttggcctccttggc
1381 tcaattactg tgcagtgaat gacatggcgc ccagggggtt ggctctccag ctcttttctg
1441 tcttgtacac agcacaccca ggtcctggga aaggaatttt aaaacagatc tccgtctcat
1501 tctttctatt tctttttttt tttaatcgaa ataatgaat acatcacaca tc
```

//

_008706 : 1 segment

[Details](#)

Display: [FASTA](#) [GenBank](#) [Help](#)

Nucleotide

Nucleotide ▾

[Limits](#) [Advanced](#)

Search

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

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

FASTA Sequence: NM_008706.5

[FASTA](#) [GenBank](#)[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 Kummarapurugu,A.B., Fischer,B.M., Zheng,S., Milne,G.L., Ghio,A.J.,

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 iso](#) [J Biol Chem. 2013][See all...](#)[Pathways for the Nqo1 gene](#) ▴[Regulation of ornithine decarboxylase \(ODC\)](#)[Metabolism of amino acids and derivatives](#)[Metabolism](#)[See all...](#)[Reference sequence information](#) ▴



FASTA (and RAW) format

FASTA is the name of a popular sequence alignment-and-database-scanning program created by W.R. Pearson and D.J. Lipman in 1988

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

>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 ▾

[Limits](#) [Advanced](#)

Search

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

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

FASTA Sequence: NM_008706.5

[FASTA](#) [GenBank](#)[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 Kummarapurugu,A.B., Fischer,B.M., Zheng,S., Milne,G.L., Ghio,A.J.,

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 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](#) ▴

Nucleotide Nucleotide Search Limits Advanced Help

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

Send:

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

AGGCTCAGCTCTTACTAGCCTAGCCTGTAGCCAGCCCTAAGGATCTCTCGAAGAGCTTTAGGGTCGTCT
TGGCAACCAGCTGCTCAGCCAATCAGCGTTCGGTATTACGATCCTCCCTCAACATCTGGAGCCATGGCGG
CGAGAAGAGCCCTGATTGTACTGGCCATTTCAGAGAAGACATCATCAACTACGCCATGAAGGAGGCTGC
TGTAGAGGCTCTGAAGAAGAGAGGATGGGAGGTACTCGAATCTGACCTCTATGCTATGAACTTCAACCCC
ATCATTTCAGAAATGACATCACAGGTGAGCTGAAGGACTCGAAGAAGCTTCAGTATCCTTCCGAGTCAT
CTCTAGCATATAAGGAAGGACGCTGAGCCAGATATTGTGGCCGAACACAAGAAGCTGGAAGCTGCAGA
CCTGGTGATATTTCAGTTCCATTGTCAGTGGTTTGGGGTGCCAGCCATTCTGAAAGGCTGGTTTGAGAGA
GTGCTCGTAGCAGGATTGCTACACATATGCTGCCATGTACGACAACGGTCCTTCCAGAATAAGAAGA
CCTTGCTTTCTATCACCAGTGGGGGTAGCGGCTCCATGTACTCTCTTCAGGGTGTCCACGGGGACATGAA
CGTCATTCTCTGGCCGATTTCAGAGTGGCATCCTGCGTTTCTGTGGCTTCCAGGTCTTAGAACCTCAACTG
GTTTACAGCATTGGCCACATCCACCAGATGCCCGCATGCAGATCCTGGAAGGATGGAAGAAACGTCTGG
AAACCGTCTGGGAGGAGACCCCACTCTATTTTGCTCCAAGCAGCCTGTTTGACCTAAACTTTTCAGGCAGG
ATTCTTAATGAAAAAGGAAGTTCAAGAGGAGCAGAAGAAGAACAAAGTTTGGCCTCTCTGTGGCCATCAC
CTGGGCAAGTCCATTCCAGCTGACAACCAGATCAAAGCTAGAAAATAAGGATTTTTTCTTAACATATAG
TTAGACGCAGCTTTCTTTTCCAGCTTGTCTGACTTGCTTTCATTTTTTCTTTGCTCCACGAGGAT
GGGAAAAGGAGTAAGTTTGCTTCATGCTTTTTTTTTTTTTTTTGTATAGTCTGCCATAACAACAAAATGAA
TGAAGTCAGATTAGGAGCCTCAGGGCAAGGTGCAGAAGCGAGCTGGAAATACTCTTCTAGGTCAATTTATG
CAATATTGCCATTTTCTTGGGCTAGTCCAGTTAGATGGCATCCAGTCTCCATCAAGATTGCTTGTGTC
TATAATTACCTCTCTGTGGTTAGGGCAGAAGGGAATTGCTCAAAGTAAACAATGGCCGAGGGACTAACT
TGTTTAGCAGTTAGCAGTTAGCTAAAGCCTGTTTATGATACATCCTGGTTTCAATTACTGTGCAGTGACT
GACATGGCGCCAGGGGTTGGCTCTCAGCTCTTTCTGTCTGTACACAGCACACCCAGGTCTCTGGGA
AAGGAATTTTAAACAGATCTCCGTCTCATTCTTTCTATTTCTTTTTTTTTTAAATCGAAATAAATGAAT
ACATCACACATC

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-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]

See all...

Pathways for the Nqo1 gene

Regulation of ornithine decarboxylase (ODC)

Metabolism of amino acids and derivatives

fasta

Select CDS → in brown (FASTA bottom right corner)

[illegible]

NCBI/coding sequence (CDS)

 [Resources](#) [How To](#)

[jostovap](#) [My NCBI](#) [Sign Out](#)

Nucleotide

Nucleotide

Search

[Limits](#) [Advanced](#)

[Help](#)

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](#)

[Send:](#)

Change region shown

☐ Whole sequence

☒ Selected region

from: 1600 to: 1680

Update View

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-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]

See all...

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
AGGCTCAGCTCTTACTAGCCTAGCCTGTAGCCAGCCCTAAGGATCTCTCCGAAGAGCTTTAGGGTCGTCT
TGGCAACCAGCTGCTCAGCCAATCAGCGTTTCGGTATTACGATCCTCCCTCAACATCTGGAGCCATGGCGG
CGAGAAGAGCCCTGATTGTACTGGCCCATTCAGAGAAGACATCATTCAACTACGCCATGAAGGAGGCTGC
TGTAGAGGCTCTGAAGAAGAGAGGATGGGAGGTACTCGAATCTGACCTCTATGCTATGAACCTCAACCCC
ATCATTTCCAGAAATGACATCACAGGTGAGCTGAAGGACTCGAAGAAGCTTTCAGTATCCTTCCGAGTCAT
CTCTAGCATATAAGGAAGGACGCCCTGAGCCCAGATATTGTGGCCGAACACAAGAAGCTGGAAGCTGCAGA
CCTGGTGATATTTCACTTCCCATTCAGTGGTTTGGGGTGCCAGCCATTCTGAAAGGCTGGTTTGAGAGA
GTGCTCGTAGCAGGATTTGCCTACACATATGCTGCCATGTACGACAACGGTCCTTTCAGAAATAAGAAGA
CCTTGCTTTCTATCACCACCTGGGGGTAGCGGCTCCATGTACTCTCTTCAGGGTGTCCACGGGGACATGAA
CGTCATTCTCTGGCCGATTGAGAGTGGCATCCTGCGTTTCTGTGGCTTCCAGGTCTTAGAACCTCAACTG
GTTTACAGCATTGGCCACACTCCACCAGATGCCCGCATGCAGATCCTGGAAGGATGGAAGAAACGTCCTGG
AAACCGTCTGGGAGGAGACCCCACTCTATTTTGCTCCAAGCAGCCTGTTTGACCTAAACTTTCAGGCAGG
ATTCTTAATGAAAAGGAAGTTCAAGAGGAGCAGAAGAAGAACAAGTTTGGCCTCTCTGTGGGCCATCAC
CTGGGCAAGTCCATTCCAGCTGACAACCAGATCAAAGCTAGAAAATAAGGATTTTTTCTTAACATATAG
TTAGACGCAGCTTTCTTTTCCCAGCTTGTCTGACTTGCTTTTCAATTTTTTCTTTGCTCCACGAGGAT
GGGAAAAGGAGTAAGTTTGCTTCATGCTTTTTTTTTTTTGTAGTCTGCCATAACAACAAATGAA
TGAAGTCAGATTAGGAGCCTCAGGGCAAGGTGCAGAAGCGAGCTGGAATACTCTTCTAGGTCATTATG
CAATATTCGCCATTTCTTCGGGCTAGTCCAGTTAGATGGCATCCAGTCCCTCCATCAAGATTCGTTGTC
```

In the bottom line:

Nucleotide

Nucleotide ▾

Search

Advanced

Help



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>.

FASTA ▾

Send to: ▾

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

NCBI Reference Sequence: NM_008706.5

[GenBank](#) [Graphics](#)

>NM_008706.5:141-305 Mus musculus NAD(P)H dehydrogenase, quinone 1 (Nqo1), mRNA
CGAGAAGAGCCCTGATTGTACTGGCCCATTCAGAGAAGACATCATTCAACTACGCCATGAAGGAGGCTGC
TG TAGAGGCTCTGAAGAAGAGAGGATGGGAGGTACTCGAATCTGACCTCTATGCTATGAACTTCAACCCC
ATCATTTCAGAAATGACATCACAG

Change region shown

- ☐ Whole sequence
☒ Selected region

from: to:

Update View

Customize view

Analyze this sequence

[Run BLAST](#)[Pick Primers](#)[Highlight Sequence Features](#)[Find in this Sequence](#)[Show in Genome Data Viewer](#)

Articles about the Nao1 gene

Practical part

Find „your“ nucleotide sequence.

look for CDS

[BLAST](#)
[Align](#)
[Peptide search](#)
[ID mapping](#)
[SPARQL](#)

UniProtKB ▾

[Advanced](#) | [List](#)

[Search](#)

[Help](#)

→ Sequence & Isoforms

Link to nucleotides from UniProt

UniProt

BLAST Align Peptide search ID mapping SPARQL UniProtKB

Advanced | List Search

Help

Function

Names & Taxonomy

Subcellular Location

Disease & Variants

PTM/Processing

Expression

Interaction

Structure

Family & Domains

Sequence & Isoforms

Similar Proteins

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]
	CCDS32472.1 [P15559-2]		NP_001020605.1 NM_001025434.1 [P15559-3]
PIR	A41135 A30879		

Length 274

Mass (Da) 30,868

Last updated 1990-04-01 v1

Checksumⁱ A4010462AD00F3FE

10 20 30 40 50 60 70 80 90 100

MVGRRLIVL AHSERTSFNY AMKEAAAAAL KKKGWEVVES DLYAMNFNPI ISRKDITGKL KDPANFQYPA ESVLAYKEGH LSPDIVAEQK KLEAADLVIF

110 120 130 140 150 160 170 180 190 200

Scroll down↓

Practical part

Find „your“ nucleotide sequence.

Try to link through Uniprot

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



Nucleotide

Nucleotide ▾

[Limits](#) [Advanced](#)

Search

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

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

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.,

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 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

Graphics ▾

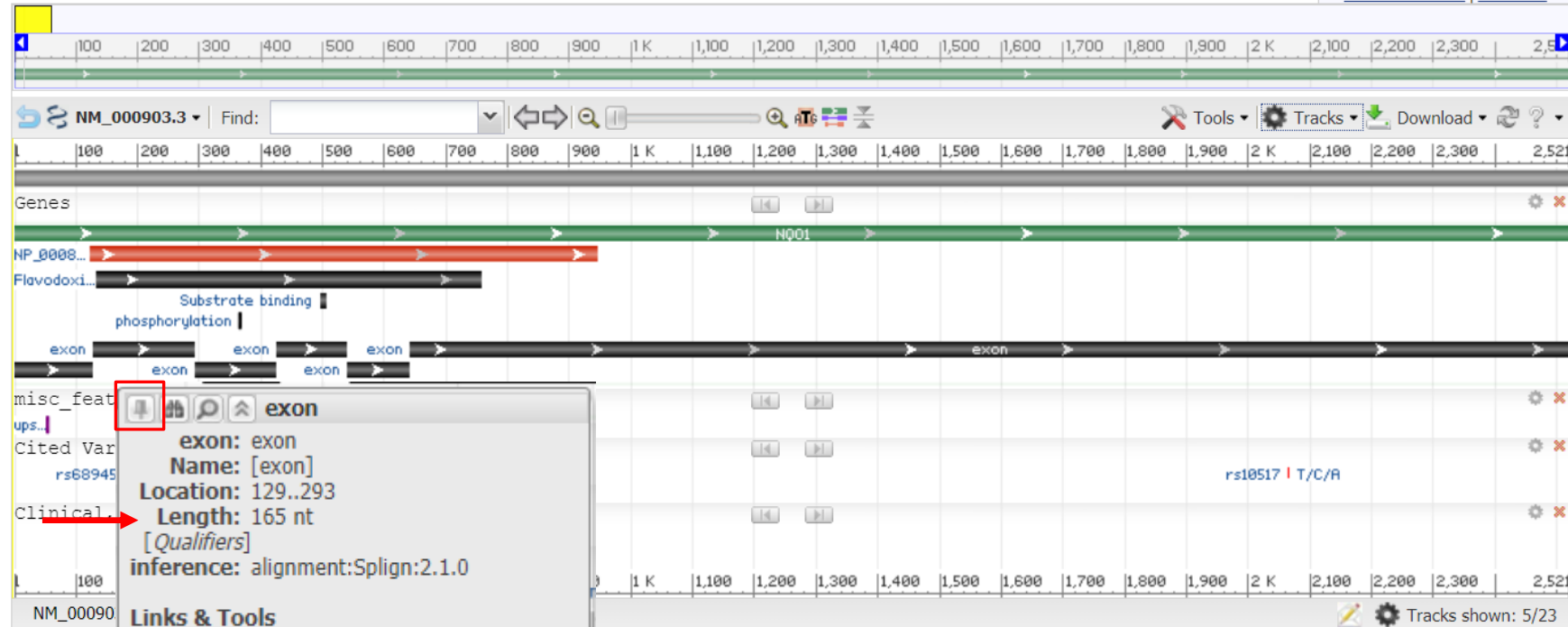
Send to: ▾

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

NCBI Reference Sequence: NM_000903.3

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

[Link To This View](#) | [Feedback](#)



Nucleotide

Nucleotide ▾

[Limits](#) [Advanced](#)

Search

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

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

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.,

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 iso](#) [J Biol Chem. 2013][See all...](#)[Pathways for the Nqo1 gene](#) ▴[Regulation of ornithine decarboxylase \(ODC\)](#)[Metabolism of amino acids and derivatives](#)[Metabolism](#)[See all...](#)[Reference sequence information](#) ▴

Practical part

Find „your“ nucleotide sequence.

Explore the graphic view

NCBI/Gene (secondary database)

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:

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

database GENE

GENE

Was this helpful?

👍

👎

NQO1 – NAD(P)H quinone dehydrogenase 1

Homo sapiens (human)

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

Gene ID: 1728

RefSeq transcripts (4)

RefSeq proteins (4)

RefSeqGene (1)

PubMed (580)

Orthologs

Genome Browser

BLAST

Download

RefSeq Sequences

+

Items: 1 to 20 of 9424

<< First

< Prev

Page 1

of 472

Next >

Last >>

NCBI/Gene (secondary database)

NQ01 - NAD(P)H quinone dehydrogenase 1 BETA

[Homo sapiens](#)

[Summary](#) [Transcripts and proteins](#) [Orthologs](#) [Gene ontology](#)

[Download](#) [datasets](#) [API](#)

Gene name	NAD(P)H quinone dehydrogenase 1
Symbol	NQ01
Gene ID	1728
Organism	Homo sapiens (human)
Gene type	protein-coding
Synonym	DTD, QR1, DHQU, DIA4, NMOR1, NMORI
Proteins	4

Scroll down

[View the legacy Gene page](#)

NCBI/Gene (secondary database)

 NCBI [Resources](#) [How To](#)

[jostovap](#) [My NCBI](#) [Sign Out](#)

Gene

[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](#)

NCBI/Gene

NCBI

Resources

How To

Sign in to NCBI

Gene

Gene

nqo1

Search

Create RSS Create alert Advanced

Help

Gene sources

Genomic

Categories

Alternatively spliced

Annotated genes

Protein-coding

Pseudogene

Sequence content

CCDS

Ensembl

RefSeq

RefSeqGene

Status

Current

Chromosome locations

more...

Clear all

Show additional filters

Tabular

20 per page

Sort by Relevance

Send to

Hide sidebar >>

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
☐ 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
☐ Nqo1 ID: 24314	NAD(P)H quinone dehydrogenase 1 [<i>Rattus norvegicus</i> (Norway rat)]	Chromosome 19, NC_005118.4 (38422210..38437103)	Dia4	
☐ 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	
☐ nqo1 ID: 322506	NAD(P)H dehydrogenase, quinone 1 [<i>Danio rerio</i>	Chromosome 7, NC_007118.7 (56703254..56722320)	wu:fb63c10, zgc:77191	

Find related data

Database: Select

Find items

Search details

nqo1[All Fields] AND alive[prop]

NCBI/Gene

NCBI Resources How To Sign in to NCBI

Gene Gene Search

Advanced Help

Full Report Send to: Hide sidebar >>

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

Table of contents

Summary

Genomic context

Genomic regions, transcripts, and products

Expression

Bibliography

Phenotypes

Variation

HIV-1 interactions

Pathways from BioSystems

Interactions

General gene information

Markers, Homology, Gene Ontology

General protein information

NCBI Reference Sequences (RefSeq)

Related sequences

Additional links

NCBI/Gene

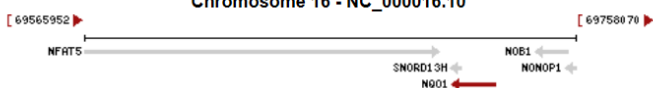
Genomic context

Location: 16q22.1

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

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

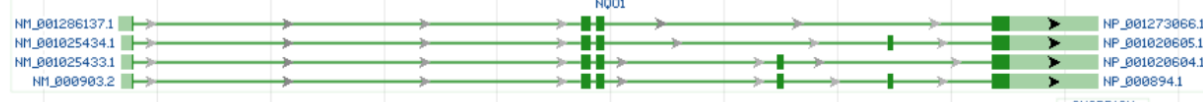
NC_000016.10

Find:

Tools

Tracks

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



SNORD13H NR_145753.1

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

[Full Report](#)

Send to:

Hide sidebar >>

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

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

Summary

Official Symbol NQO1 provided by HGNC

Official Full Name NAD(P)H quinone dehydrogenase 1 provided by [HGNC](#)

Primary source [HGNC:HGNC:2874](#)

See related [Ensembl:ENSG00000181019](#) [MIM:125860](#); [Vega:OTTHUMG00000137575](#)

Gene type protein coding

RefSeq status REVIEWED

Organism *Homo sapiens*

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

Iso known as DTD; QR1; DHQU; DIA4; NMOR1; NMORI

Summary This gene is a member of the NAD(P)H dehydrogenase (quinone) family and encodes a cytoplasmic 2-electron reductase. This FAD-binding protein forms homodimers and reduces quinones to hydroquinones. This protein's enzymatic activity prevents the one electron reduction of quinones that results in the production of radical species. Mutations in this gene have been associated with tardive dyskinesia (TD), an increased risk of hematotoxicity after exposure to benzene, and susceptibility to various forms of cancer. Altered expression of this protein has been seen in many tumors and is also associated with Alzheimer's disease (AD). Alternate transcriptional splice variants, encoding different isoforms, have been characterized. [provided by RefSeq, Jul 2008]

Orthologs [mouse](#) [all](#)

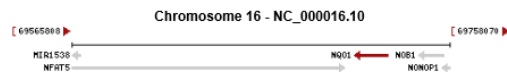
 Genomic context

Location: 16q22.1

See NQO1 in [Genome Data Viewer](#) [Map Viewer](#)

Exon count: 6

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



 Genomic regions, transcripts, and products

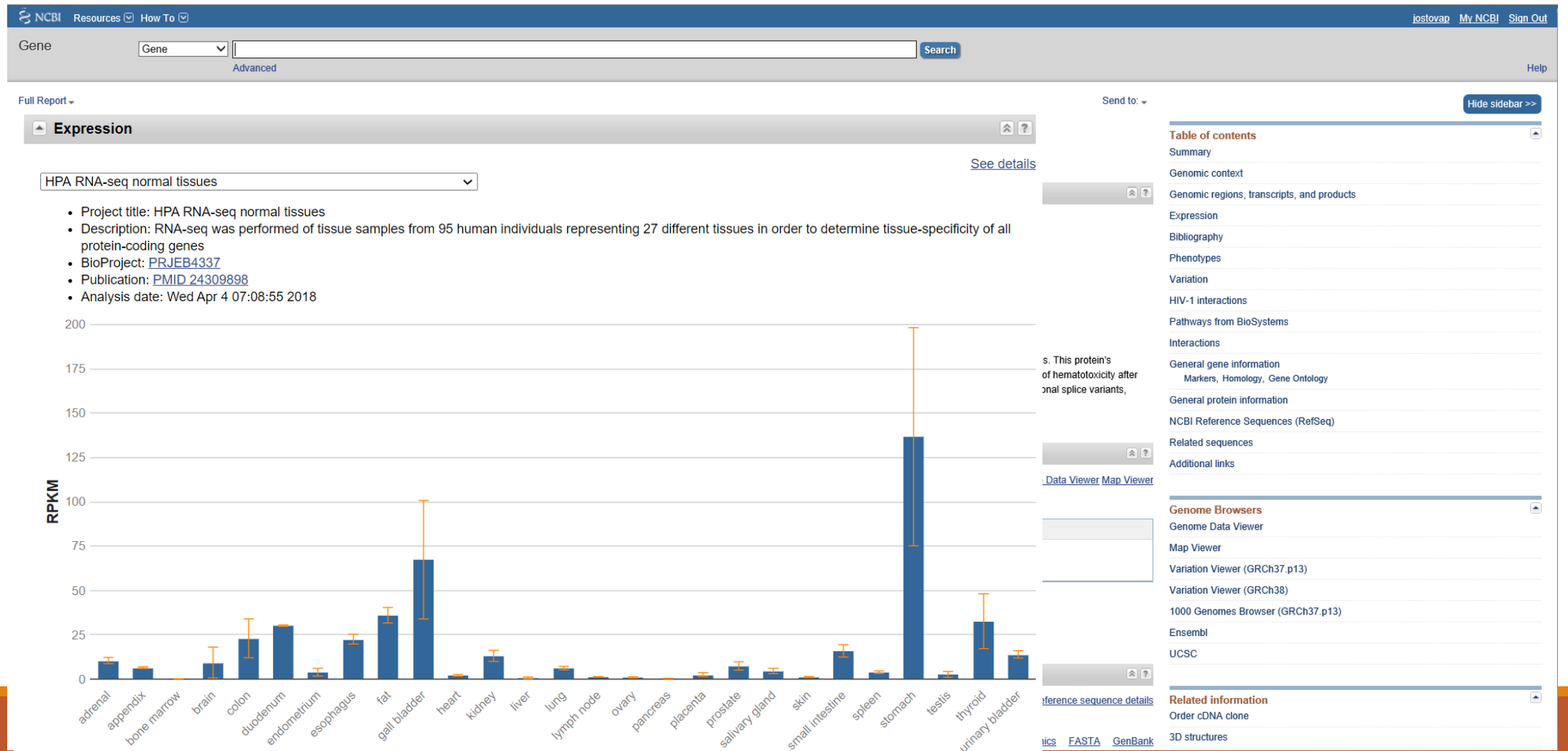
Genomic Sequence: [NC_000016.10 Chromosome 16 Reference GRCh38.p7 Primary Assembly](#)

Go to [reference sequence details](#)

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

Table of contents	
Summary	
Genomic context	
Genomic regions, transcripts, and products	
Expression	
Bibliography	
Phenotypes	
Variation	
HIV-1 interactions	
Pathways from BioSystems	
Interactions	
General gene information	
Markers, Homology, Gene Ontology	
General protein information	
NCBI Reference Sequences (RefSeq)	
Related sequences	
Additional links	
Genome Browsers	
Genome Data Viewer	
Map Viewer	
Variation Viewer (GRCh37.p13)	
Variation Viewer (GRCh38)	
1000 Genomes Browser (GRCh37.p13)	
Ensembl	
UCSC	
Related information	
Order cDNA clone	
3D structures	

NCBI/Gene - expression



NCBI/Gene – whole gene sequence

Genomic context

Location: 16q22.1

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)

See NQO1 in [Genome Data Viewer](#) [Map Viewer](#)

Genome Browsers

[Genome Data Viewer](#)

[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](#) Chromosome 16 Reference GRCh38.p12 Primary Assembly

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 ▾

Send to: ▾

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: 69709401 to: 69726560

Update View

Customize view

Analyze this sequence

[Run BLAST](#)

[Pick Primers](#)

[Highlight Sequence Features](#)

[Find in this Sequence](#)

Related information

[Assembly](#)

[BioProject](#)

[Protein](#)

[PubMed](#)

[Taxonomy](#)

GenBank ▼

Send to: ▼

Change region shown

- Whole sequence (abbreviated view)

☒ Selected region

from: 69709401 to: 69726560

Update View

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](#)

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa;
Mammalia; Eutheria;
Catarrhini; Hominidae

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

CDS

```
/db_xref
```

/db_xref

compleme

17033..1

/gene="M

/gene_sy

```
/note=";
```

Derived

prediction

/codon s

/product

/protein

1201	ataaactaca	gagagggtgat	taataagaaca	tgggagagtt	gaatgatacc	tagcacaact
1261	gtacctctaaa	acttttaggcc	taaaagaagag	aattaaatgt	tgtgatagctc	tttaagaagac
1321	attttttctag	catctttttca	catctttttcc	taagtggcctc	cttgagagccc	gtgaggtattt
1381	ggtttatatgc	catctagatga	atcataagaag	cttgatataaa	atgatccaaa	aatgcacgaa
1441	tacagtcgat	tcctctctcat	ttattctctg	tgggaaaaaga	aaaaacacaaa	tcttaaaaaac
1501	taaaagcagat	caggggaagcc	tggaaaagata	cccgagattga	ataacatgtt	aggaaggaaa
1561	ccagctcaag	gaatctcatt	tcttagctttt	gattctgttgc	tcaattggga	tgaattgtcc
1621	caagtgtatgg	cccacagaaa	ggccaaattt	cttgtttttc	tcctcatctc	gtactctctt
1681	tttctattaag	aattctgcct	ggaagtttag	gtccaaaggg	ctgcttggag	caaaatcacg
1741	tggtgtctca	tcaccaaatc	ttccagagct	ttttctcat	ctctccagga	tttgaattgc
1801	ggcgtctgct	ggagtgtgcc	caatgctata	tgtcagttga	ggttctaaga	cttgggaagcc
1861	acagaaatgc	agaattgccac	cttgaggata	caggaagcac	agagagagtaa	gtcaaccaat
1921	tcattgcagc	tgtactataca	acacagaaga	tgtgtctggg	ctttcagta	agacactctc
1981	ataagcagct	ctcaggcaca	ctagagaatc	agttcagagc	tagctctctc	cttcttacct
2041	ctacctagct	gttaccaatt	tagcctttgc	cagagtgtgt	ctctctttaa	tgcataaacc
2101	tgtaaactgt	gccaaacttg	atctctttgc	aaagaagcgt	gaagttctgt	tacttttagg
2161	agttctcagtt	tcttgccagg	tgaactacca	agaactcgct	gggtgcattt	ctctgcctct
2221	ccatatcaat	agatgatctc	tttttttctt	tttttttttt	tttttttttt	tgaggcagag
2281	ctctcgtcgg	tcgtcaggc	tgggagtgcca	tggcagatc	tcggctcatt	gcggcttcca
2341	cttctctgggt	tcaagcggtt	ctctctcgct	agcctccga	gtagctggga	tacaggacct
2401	gcgccaccat	gccagataaa	tttttgtatc	tttagtagag	acaggggttc	actgtgttga
2461	ccaggttggt	ctcgaactcc	tgaacctaa	tgatcgctct	cgctcagctc	cccaaatgic
2521	tgggagtaga	ggccccagatg	agttctgata	aatgatattc	aagctggcc	acctactggc
2581	tcttctcttc	aacctctctc	tttatagaaa	ttatctttag	ggtttggtaa	caccaataac
2641	ccccaccagc	gcttcagttt	tatccatgta	taaacctggc	ggactaaatt	atttctcttt
2701	cttgcgaaac	aggggtctgc	ctgttatccc	agggctggcat	cgagtgtgtg	gatcatagct
2761	tatttcagcc	tgcgaactct	gggtctctgc	ctttagatct	ccaaagtgtc	ggagaccagc
2821	gtgatgatct	acacccctac	aattttgttt	tttttttttt	tagagatgag	gtcttataatg
2881	tgtcccaggc	tgtgtctcaa	gtctctggct	caagcgatcc	ttctgcctca	gctcccagct
2941	aaatcatttc	ttaattgttc	tggggctctc	atagctctat	ggagctgac	agcaactctg
3001	agaaggacag	gaaggctgga	gagagatgtc	agtcactctg	tgagaccagg	gccacaggct
3061	atcacatcaac	agagtatgta	ttcacacagc	ctcttggctg	ggacagaatg	ctgtttgaac
3121	acatgcacac	cagagttatg	ttcacacagc	gcaactggga	agcagcagag	gtttcttaaaa

```
complement(join(1576..1881,8723..
17033..17039))
/gene="NQO1"
/gene_synonym="DHQU; DIA4; DTD; I
/note="isoform d is encoded by tr
Derived by automated computation:
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="MVGRRALVLVLAHSETSF
MNFNPIISRKIDITGKLKDPANFYQPAESVLAY
GILFHCGFQVLQPTYSIGTIPADARIKQLE
FOAGL MKKEDEVDFEKNKIGT SVGHM GKS
```

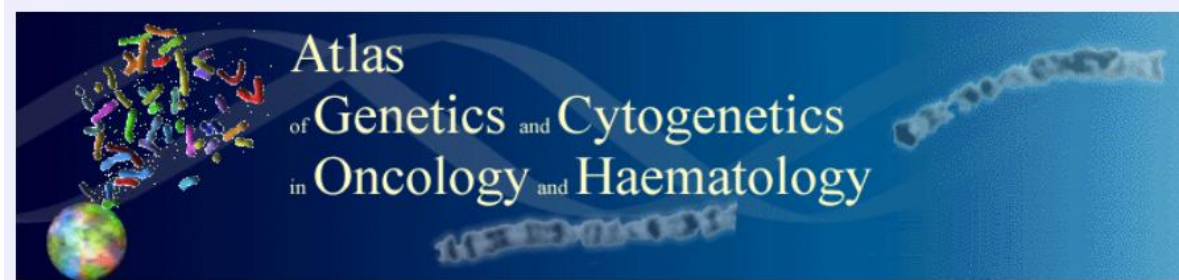
CDS Feature 1 of 4 NC_000016 : 4 segments (minus strand)

Details

Practical part

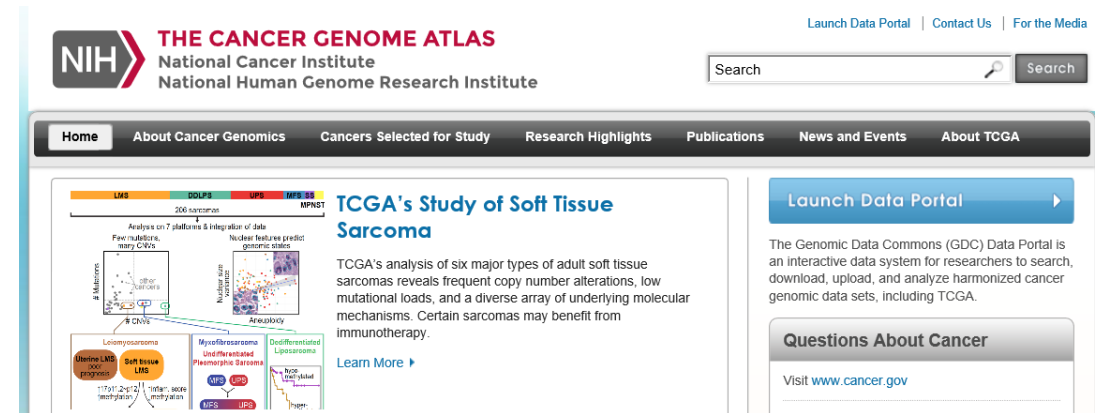
Explore „your“ nucleotide sequence
in Gene.

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



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

Launch Data Portal | Contact Us | For the Media

Search

Home About Cancer Genomics Cancers Selected for Study Research Highlights Publications News and Events About TCGA

TCGA's Study of Soft Tissue Sarcoma

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

Launch Data Portal

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

Questions About Cancer

Visit www.cancer.gov



GeneCardsSuite GeneCards MalaCards LifeMap Discovery PathCards TGex VarElect GeneAnalytics GeneAlaCart GenesLikeMe

Free for academic non-profit institutions. Other users need a [Commercial license](#)

WEIZMANN INSTITUTE OF SCIENCE LifeMap SCIENCES

Keywords Search Term Advanced

Home User Guide Analysis Tools News And Views About My Genes Log In / Sign Up



Ensembl BLAST/BLAT | BioMart | Tools | Downloads | Help & Documentation | Blog | Mirrors

Search all species...



Search: All species for Go

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

Browse a Genome

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

Find a Data Display



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

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

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

[Full details](#) | [All web updates, by release](#) | [More news on our blog](#)

Practical part

Explore „your“ nucleotide sequence
in database GeneCards.

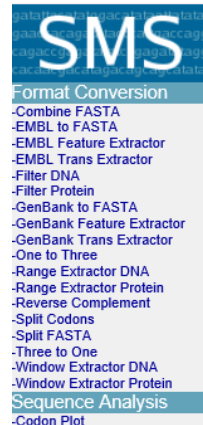
Sequence analysis

Filter DNA

DNA stats

Range Extractor DNA

Reverse complement



Sequence Manipulation Suite:

Filter DNA

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

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

```
1 ttaagatttg cgctttgcc aactgtacac caacctcggt
41 ttattgtcga acctcccgct tgtgcgcga tctgcatata
81 gatcccggtc agtccgtcac attctgcaa ttgagtatcc
121 tcgaagtctt attccacgtg ctcaaagcaa gggatatcga
161 cagtataaac cgctcgtg 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.
ttaagatttgcctttgccactgtacacccaactcgtttattgtcgaacctccgct
tgtgcccatctcatatagatcccggtcagtcctgacattctgcnaattgagtatcc
tcgaagcttattccacgtctcaangcagggtatctgacagtgataacccgctcgtgc
agatccaaattctcgattacacacacgactgattttatcatcaggtacactaaaact
cacaatttgaagcaccagcaggaatcgttctattctctagcttgcacacacgacgttg
taattggcataactcggcatcatagtggtcgtgtagcggactaagcgaaaactggt
cgttgatctctcaccatgattttacaagaagggtgaactcaatttgacgcggttaa
gttagatggctacgcgcagacagctctcgtatcgtatgaattagcgaagaggtatgg
caangcttggtacgatacagcagcgcgtggtgattacagtaggtgtagcgaaga
acgttcaacgtgtagatctcttctgcacacacgacatgcttccnagggtccaaag
cgattactagggtgcacagacgacgacgacgacgacgacgacgacgacgacgacgac
cactgttcaaaagctccgatacagcagcagcagcagcagcagcagcagcagcagcagc

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
aaaaaaaaaaaaa

>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.

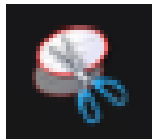
(HW: How many cytosins and contains 2. exon?)

Homework 5

Work with „your“ abbreviation.

- 1) Find your nucleotide sequence, what is your accession number?
- 2) Download the **CDS** of your sequence, and save it in FASTA format.
- 3) Which chromosome contains your sequence? How many exons does your sequence have?
- 4) How long is the second exon? How many cytosines have the second exon?
- 5) Where is your sequence mostly expressed?

E.g use „výstřižky“



„snipping tool“

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

DÚ5

1) NQO1:

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

NM_000903.2

2) >CDS

ATGTGTCGGCAGAAAGACACTGATCGTACTGGCTCACTCAGAGAGGACGTCCTTCAAATATGCCATGAAGG
AGGCTCGCTGCAGCGGCTTTGAAGAAGAAAGGATGGAGGGTGGTGGAGCTCGGACCTCTATGCCATGAACCT
CAATCCCTCATCTTCCGAAAGGACATCAGGTAAGTAACTGAAGGACCTCGGAACCTTTAGTATCTGCTGCC
GAGTCTGTCTGGCTTATAAAGAAAGGCCATCTGAGCCACAGATATGTGGCTGAACAAAGAAAGCTGGAAAG
CCGACGACCTTTGTATATTTCCAGTTCCCCCTCGAGTGGTTTGGAGTCCCTGCCATTTGAAAGGCTGGTT
TGAGCGAGTGTTCTATAGAGAGTTTGTCTACACTACGCTGCCATGTATGACAAGGACCTTCGCGAGT
AAGAAGCGAGTGCTTTCCATACCACCTGGTGCGCATGGCTCCATGTACTCTCGAAGGGATCCACGGGG
ACATGAATGTCACTTCTGCGCCAACTCAGATGGGCATCTGCATTTCTGTGGCTTCCAAGTCTTAGAAG
TCAACTGACATATGACATTTGGGCACACTCCAGCAGACGCGGAATTCAAATCTCGGAAGGATGGAAGAAA
CGCCTTGGAAGAAATATTTGGGATGAGACCACTGTAATTTGTCTCAAAGCAGACTCTTTGACCTTAACTTCC
AGGCAGGATTTCTAATGAAAAAAGAGGTACAGGATGAGGAGAAAAACAGAAATTTGGCCTTTCTGTGGG
CCATCACTTTGGGCAAGTCCATCCCAACTGACAACAGATCAAAGCTGGAATATGA

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

GCACAAGAGCACTGATCGTACTGGCTCACTCAGAGGACGTCCTTCAACTATGCCATGAAGGAGGCTGC
TCGACCGCGCTTTGAGAAGAAAGGATGGGAGGTGGTGGAGTCGGACCTCTATGCCATGAACCTTCAATCCC
ATCATTTCCAGAAAGGACATCACAG

ANO, jeden (rs689453)



Exon obsahuje: 38 cytosinů a 4 dinukleotidy CG

DNA Stats results

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

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

5)

