



NCBI Gene

A portal to gene-centered information from different sources

<https://www.ncbi.nlm.nih.gov/gene/>

National Center for Biotechnology Information • National Library of Medicine • National Institutes of Health • Department of Health and Human Services

Scope and Access

The Gene database [1, 2] provides detailed information for known and predicted genes defined by nucleotide sequence or map position. Currently, Gene contains over 17 million entries and includes data from all major taxonomic groups. Each record in the database corresponds to a single gene and is derived from processing by the NCBI Reference Sequence [3, 4] and genome annotation groups [5]. You can access data from the Gene database on the web through the Gene homepage, programmatically through the Entrez Programming Utilities, or by file transfer through its FTP site.

- Gene Homepage: www.ncbi.nlm.nih.gov/gene/
 - Entrez Programming Utilities: www.ncbi.nlm.nih.gov/books/NBK25501
 - Gene Data Files: ftp.ncbi.nlm.nih.gov/gene/DATA/
 - Gene Records in ASN.1 format: ftp.ncbi.nlm.nih.gov/gene/DATA/ASN_BINARY/
- You can obtain technical details on the Gene database from the NCBI Bookshelf:
- Gene Help: www.ncbi.nlm.nih.gov/books/NBK3841/
 - Gene FAQ: www.ncbi.nlm.nih.gov/books/NBK3840/

The screenshot shows the NCBI Gene search results for 'hemochromatosis'. The search bar (A) contains the term 'hemochromatosis'. The left sidebar (B) shows filters for Gene sources, Categories, and Status. The top navigation includes 'Items per page' (D), 'Format' (D), and 'Sort by' (D) menus. The main results table (E) lists genes like HFE, HJV, Hfe, and Tf. A 'Send to' dropdown (F) is open, showing options like 'File', 'Clipboard', and 'Summary (text)'. A vertical 'SIDEBAR' (C) is visible on the right.

Searching Gene

Enter a set of query terms and click the **Search** button (A) to find gene records of interest. Select filters in the left column (B) to narrow down the retrieved list according to chosen criteria. Click the “SIDEBAR” (C) to expand and access functions listed in the right-hand column. Use the pull-down menus (D) at the top to change the display format or sorting order. From left to right, the default tabular display (E) provides information on the official symbol and NCBI Gene ID, gene name and source organism, chromosome location, alias symbols known to be associated with the gene, and MIM id’s if available. You can save retrieved Gene records in various formats using the “File” option available under the “Send to” link (F). Click the official symbol to open the full report of that Gene record.

Advanced Search Builder

This tool (right) makes indexed fields accessible through a pull-down menu under the arrow (H), and terms indexed through the **Show index list** link (I). Select a term to enter it in the query box above (J) with the selected Boolean operator. Click **Add to history** link (K) to preview and save a search to the History. Click the number under the **Items found** column (L) to retrieve these records. Unlock the query box by clicking the **Edit** link to customize the query terms, such as combining searches (M). With a My NCBI account, you can save your gene search results permanently and customize the display format using options under the “NCBI Site Preferences” [9].

The screenshot shows the 'Gene Advanced Search Builder' interface. The search query is '#5 AND rodentia[organisms]'. The 'Builder' section (H) shows the query construction. The 'Show index list' link (I) is visible. The 'Items found' column (L) shows 386 results. The 'Add to history' link (K) is present. The 'Edit' link (M) is also visible.

Contents of a Gene record

Information found in a Gene record depends on publicly available data. All records, like the well-studied human HFE gene (right), contain a **Summary** section (A), which provides an overview of the gene. The HFE gene record also contains links to corresponding records from HUGO Gene Nomenclature Committee (B), other external links such as OMIM [7] (C). It also provides a list of unofficial symbols associated with this gene (D) and a brief summary of the gene and its product (E). For ease of navigation, the **Table of Contents** (F) provides direct links to individual sections of a Gene report. For example, click **Bibliography** (G) to scroll the display to that section

where a collection of publications relevant to the Gene record is listed. Similarly, click the **Reference sequences** (H) to bring the NCBI Reference Sequences section to focus and access individual sequences relevant to this gene. Click the "all" link next to **Orthologs** (I) to see orthologs of the gene derived from NCBI Eukaryotic Genome Annotation pipeline.

Full Report - Send to: ▾

HFE homeostatic iron regulator [*Homo sapiens* (human)]

Gene ID: 3077, updated on 12-Mar-2019

Summary

Official Symbol HFE provided by [HGNC](#)

Official Full Name homeostatic iron regulator provided by [HGNC](#)

Primary source [HGNC:HGNC:4886](#)

See related [Ensembl:ENSG0000010704](#) [MIM:613609](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Homo sapiens](#)

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

Also known as HH; HFE1; HLA-H; MVCD7; TFQTL2

Summary The protein encoded by this gene is a membrane protein that is similar to and associates with beta2-microglobulin (beta2M). It is thought that this protein is involved in iron absorption by regulating the interaction of the transferrin receptor with transferrin. Defects in this gene, hereditary haemochromatosis, is a recessive genetic disorder. Additional variants have been found but their full-length nature has not been determined. [MIM:234400] [RefSeq, Jul 2008]

Expression Ubiquitous expression in thyroid (RPKM 5.0), gall bladder (RPKM 4.6) and testis (RPKM 4.6)

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

Table of contents

- Summary
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Graphical presentation of the gene on the genome

The Sequence Viewer (SV) panel presents the RefSeqs for a Gene record in an interactive and customizable graphical display. This panel (below) depicts the genomic structure of the human HFE gene, its size, and single nucleotide polymorphisms (SNPs) mapped to it. The ruler provides the chromosome mapping information (J). The display lists alternatively spliced transcripts and their protein products and depicts them as bars (exons) linked by thin lines (introns, K). Mouseover the accession of a transcript to get the summary information in a popup window (L). Click the arrow (M) in the upper left-hand to pop the SV display into a full-screen mode for optimal results and more functionality. Features available in this mode allow you to customize the display, import data in various formats, view and download of subsequences, as well as select a region to BLAST, and bring the alignment results back into the display. See SV document linked off the full-screen mode for more details.

Genomic Sequence: [NC_000006.12](#) Chromosome 6 Reference GRCh38.p12 Primary Assembly

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

26,886 K | 26,888 K | 26,890 K | 26,892 K | 26,894 K | 26,896 K

Genes, NCBI Homo sapiens Annotation Release 109

HFE

NP_000410.3
NP_000410.3
NP_000410.1

NP_001390749.1
NP_1390806.2
NP_1390804.2
NP_1390803.2
NP_1390809.2
NP_1390807.2
NP_1390808.2
NP_1390810.2
NP_1390811.2
XP_011514543.3
XR_241893.4

LOC108783645

NR_144383.1

Cited Variations, dbSNP b152 v2

rs2794719 T/C/G	rs28934889 G/A	rs907289 C/G/T	rs1572982 G/A/T	rs707889 G/A/T
rs9366637 C/T	rs11833557 G/A	rs140080192 G/R/C	rs1800582 G/A	rs18455
	rs1799945 C/G	rs1800738 A/T	rs11833583 A/C	
	rs28934537 G/C	rs28934596 T/C	rs1800758 G/A	
	rs2071303 T/C	rs28934595 A/C	rs11833558 G/C/T	
	rs146519482 G/C/T	rs797045145 G/A	rs2858996 G/R/C/T	
	rs2032451 G/T			

RNA-seq exon coverage, aggregate (filtered), NCBI Homo sapiens Annotation Release 109 - log

RNA-seq intron-spanning reads, aggregate (filtered), NCBI Homo sapiens Annotation Release 109

26,886 K | 26,888 K | 26,890 K | 26,892 K | 26,894 K | 26,896 K

Summary

mRNA: [NM_000410.3](#)

Title: mRNA-homeostatic iron regulator transcript variant 1

Location: [26,087,281..26,095,241](#)

[Length]

Span on [NC_000006.12](#): 7,961 nt

Aligned length: 2,222 nt

Sequence length: 2,222 nt

[Positional Info]

[NC_000006.12](#) position: 26,094,564

mRNA position: 1,545

mRNA sequence: [TTTTGGGAAGAGGACT\[C\]CTTAAATTTGGGGG](#)

Download: [NM_000410.3](#)

Links & Tools

View GeneID: [3077](#) (HFE)

View HGNC: [4886](#)

View MIM: [613609](#)

BLAST Genome-specific: [NC_000006.12](#) ([26,087,281..26,095,241](#)), [NM_000410.3](#)

BLAST Genomic: [NC_000006.12](#) ([26,087,281..26,095,241](#))

BLAST mRNA: [NM_000410.3](#)

FASTA View: [NC_000006.12](#) ([26,087,281..26,095,241](#)), [NM_000410.3](#)

GenBank View: [NC_000006.12](#) ([26,087,281..26,095,241](#)), [NM_000410.3](#)

Graphical View: [NM_000410.3](#)

Expression

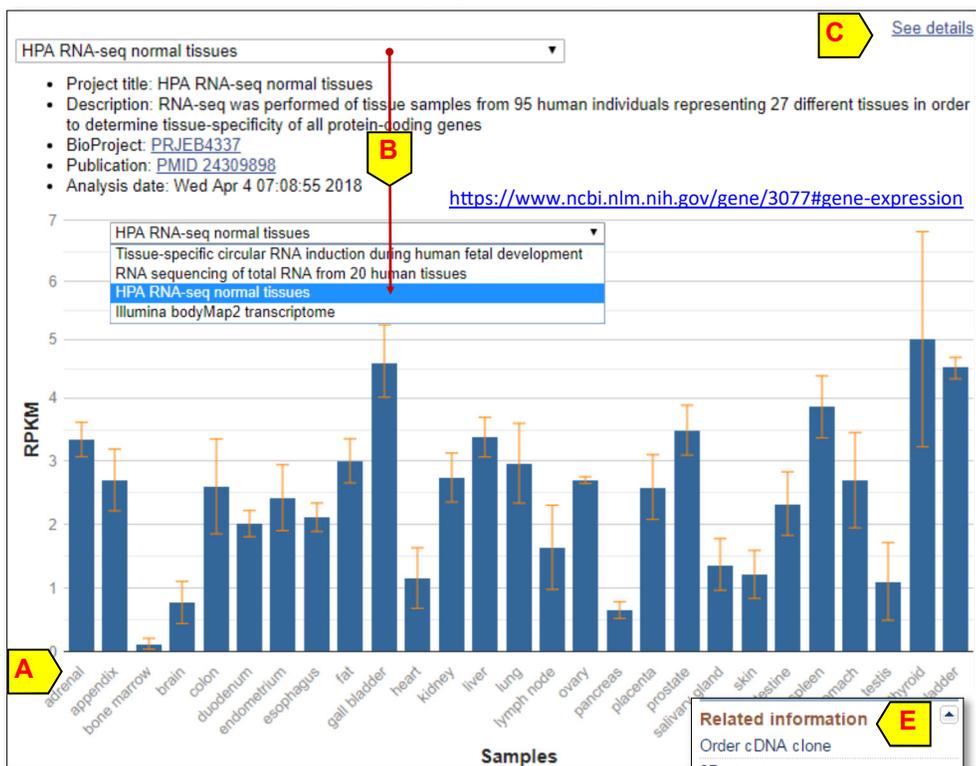
This newly added section sums up level of gene expression across various tissues (A), with information derived from alignment of Body Map 2 RNA-seq data (<https://www.ncbi.nlm.nih.gov/bioproject/144517>). You can use the pull-down menu to select source data from different studies (B). Click “See details” link (C) to see this report in a new window, along with the underlying data table and detailed counts from individual samples.

Phenotype Information

The “Phenotypes” section summarizes available information from OMIM, NHGRI, and PubMed as a list of links. The Phenotype and Genotype Integrator (PheGenI, D) tool, linked at the top, provides a user-friendly interface to collect genotype/phenotype data from available GWAS.

Related Records

A powerful feature of the Gene database is its integration with other gene-related resources at NCBI and elsewhere, via links in the “Related information” section (E). For the human HFE gene, this section contains genetic testing information from GTR (F), protein, RNA and genomic Reference Sequence records for the gene (G), various subsets of SNPs for the gene in dbSNP [6] (H), and Information on genetic disorders from/through OMIM [7] (I). For genes involved in known biologic pathways, links to BioSystems and outside resource like Kyoto Encyclopedia of Genes and Genomes (KEGG) are also available. Certain records also have links to databases outside NCBI to provide disease information or other details. The NCBI genome annotation process also analyzes and collects homologs for available genes and makes them available as the Ortholog link in the Summary section (p. 2).



- Related information**
- Order cDNA clone
 - 3D structures
 - BioAssay
 - BioAssay by Target (List)
 - BioAssay by Target (Summary)
 - BioAssay, by Gene target
 - BioAssays, RNAi Target, Tested
 - BioProjects
 - Books
 - CCDS
 - ClinVar
 - Conserved Domains
 - dbVar
 - Full text in PMC
 - Full text in PMC_nucleotide
 - Gene neighbors
 - Genome
 - GEO Profiles
 - GTR
 - HomoloGene
 - Map Viewer
 - MedGen
 - Nucleotide
 - OMIM
 - Probe
 - Protein
 - PubChem Compound
 - PubChem Substance
 - PubMed
 - PubMed (GeneRIF)
 - PubMed (OMIM)
 - PubMed(nucleotide/PMC)
 - RefSeq Proteins
 - RefSeq RNAs
 - RefSeqGene
 - SNP
 - SNP: GeneView
 - Taxonomy
 - UniGene
 - Variation Viewer

Phenotypes

[Find tests for this gene in the NIH Genetic Testing Registry \(GTR\)](#)
[Review eQTL and phenotype association data in this region using PheGenI](#)

Associated conditions

Description	Tests
<p>Alzheimer's disease</p> <p>MedGen: C0002395, OMIM: 104300 GeneReviews: Alzheimer Disease Overview, Early-Onset Familial Alzheimer Disease</p>	<p>Compare labs</p>
<p>Familial porphyria cutanea tarda</p> <p>MedGen: C0268323, OMIM: 176100 GeneReviews: Familial Porphyria Cutanea Tarda, Hepatoerythropoietic Porphyria</p>	<p>Compare labs</p>

NHGRI GWAS Catalog

Items 1 - 10 of 24 << First < Prev Page 1 of 3 Next > Last >>

Description

A genome-wide association study of red blood cell traits using the electronic medical record.

NHGRI GWA Catalog
[NHGRI GWA Catalog](#), [PubMed](#)

A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium.

NHGRI GWA Catalog
[NHGRI GWA Catalog](#), [PubMed](#)

Displaying and downloading gene records

Using the pull-down menu (A), you can change the display of a Gene record to other formats. Selecting a format from the list browser will automatically switch the display. The “Tabular_(text)” option provides more values (such as exon counts) than visible in the “Tabular” display itself, and the Gene Table format provides transcript-specific exon details.

You can save a gene record to a local file using the “Send to” link (B) using the following steps: Check the “File” radio button (C), select file format from the pull-down list (D), and click the “Create File” button. Doing so from a summary display of multiple gene records saves all the records in the list.

Special Gene Table display

HFE homeostatic iron regulator [*Homo sapiens* (human)]
Gene ID: 3077, updated on 12-Mar-2019

Genomic Sequence **NC_000006** Coordinate System **Genomic-based**

Reference GRCh38.p12 Primary Assembly NC_000006.12 from: 26087281 to: 26096216
Go to nucleotide: [Graphics](#) [FASTA](#) [GenBank](#)

Exon table for RefSeq mRNA NM_000410.3 and protein NP_000401.1 Interval (exons 5' to 3')

mRNA transcript variant 1 NM_000410.3, 6 exons, total annotated spliced exon length: 2222
protein isoform 1 precursor NP_000401.1 (CCDS4578.1), 6 coding exons, annotated AA length: 348

Interval (exons 5' to 3')		Length (bp)		
Exon	Coding	Exon	Coding	Intron
26087281-26087516	26087441-26087516	236	76	3324
26090841-26091104	26090841-26091104	264	264	209
26091314-26091589	26091314-26091589	276	276	1095
26092685-26092960	26092685-26092960	276	276	158
26093119-26093232	26093119-26093232	114	114	953
26094186-26095241	26094186-26094226	1056	41	

Exon table for RefSeq mRNA NM_001300749.1 and protein NP_001287678.1 Interval (exons 5' to 3')

Homo sapiens chromosome 6, GRCh38.p7 Primary Assembly
NCBI Reference Sequence: NC_000006.12
[GenBank](#) [Graphics](#)

```
>gi|568815592:26087281-26087516 Homo sapiens chromosome 6, GRCh38.p7 Primary Assembly
CTAAAGTTCGAAAGACCTGTTGCTTTTCACCCAGGAAGTTTACTGGGCATCTCCTGAGCCTAGGCAATA
GCTGTAGGGTGACTTCTGGAGCCATCCCCGTTTCCCGGCCCCCAAAGAAGCGGAGATTTAACGGGGAC
GTGCGGCCAGAGCTGGGGAAATGGGCCCGGAGCCAGGCCGGCGCTTCTCCTCTGATGCTTTTCAGAC
CGCGTCTGCAGGGGCGCTTGCTGC
```

When genome annotation is available, the “Gene Table” format will be available to display genomic coordinates of exons and introns for all annotated transcript variants of the gene record (E). Clicking a set of numerical coordinates (F) retrieves the subsequence for that element in FASTA format. Default coordinates are based on the highest level reference assembly for that genome, such as the reference assembly for the chromosome. If needed, you can also select to use coordinates on other RefSeq records through options in the pull-down menus (G). One of the

splicing variants for human HFE displayed under “Gene Table” format is NM_000410.3 encoding a protein product NP_000401.1 (H). This variant has six exons, all of which are coding (I). Columns under the Length (bp) heading (J) contain the exon lengths and the length of the intervening introns.

References

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- Gene Help Manual [www.ncbi.nlm.nih.gov/books/NBK3841/](#)
- MyNCBI help manual. [https://www.ncbi.nlm.nih.gov/books/NBK3842/](#)