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Basic Local Alignment Search Tool

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BLAST finds regions of similarity between biological sequences. [more...](#)

New DELTA-BLAST, a more sensitive protein-protein search

**BLAST Assembled RefSeq Genomes**

Choose a species genome to search, or [list all genomic BLAST databases](#).

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☐ [Arabidopsis thaliana](#)

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☐ [Microbes](#)

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**Basic BLAST**

Choose a BLAST program to run.



[nucleotide blast](#)

Search a **nucleotide** database using a **nucleotide** query  
*Algorithms:* [blastn](#), [megablast](#), [discontiguous megablast](#)

[protein blast](#)

Search **protein** database using a **protein** query  
*Algorithms:* [blastp](#), [psi-blast](#), [phi-blast](#), [delta-blast](#)

[blastx](#)

Search **protein** database using a **translated nucleotide** query

[tblastn](#)

Search **translated nucleotide** database using a **protein** query

[tblastx](#)

Search **translated nucleotide** database using a **translated nucleotide** query

**Specialized BLAST**

**News**

[BLAST 2.2.28+ released](#)

A new version of the stand-alone BLAST applications is available.  
Tue, 02 Apr 2013 09:00:00 EST  
[More BLAST news...](#)

**Tip of the Day**

[More tips...](#)

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NCBI/BLAST/blastn suite **Standard Nucleotide BLAST**

blastn blastp blastx tblastn tblastx

Enter Query Sequence BLASTN programs search nucleotide databases using a nucleotide query. [more...](#) [Reset page](#) [Bookmark](#)

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) Query subrange [From](#) [To](#)

1 atggcgagcg tcttggtcc ctacagaaag gggcggagcc tggactgggg ggcaggctca  
61 gattcaggtt aaattgtgga ttgagctgc agttacagac agctgacct ggaagcgaat  
121 gggttgggac ctacgggttt tccggagctg aagaatgaca cattcctcg agcagcctgg  
181 ggagaggaaa cagactacac tcccgtttg tgcattgcgc aggcaggccg ttacttacca  
241 gagttaggg aaaccgggc tgccaggac ttttcagca cgtgtcgtc tctgaggcc

Or, upload file [Choose File](#) no file selected

Job Title [porphyria](#)  
Enter a descriptive title for your BLAST search

☐ Align two or more sequences

**Choose Search Set**

Database ☐ Human genomic + transcript ☐ Mouse genomic + transcript ☒ Others (nr etc.):  
[Nucleotide collection \(nr/nt\)](#)

Organism [Optional](#) [Exclude](#) [+](#)  
Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude [Optional](#) ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Entrez Query [Optional](#) [Enter an Entrez query to limit search](#)

**Program Selection**

Optimize for ☐ Highly similar sequences (megablast)  
☐ More dissimilar sequences (discontiguous megablast)  
☒ Somewhat similar sequences (blastn)  
[Choose a BLAST algorithm](#)

**BLAST** Search database [Nucleotide collection \(nr/nt\)](#) using [Blastn](#) (Optimize for somewhat similar sequences)  
☒ Show results in a new window

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### porphyria

Query ID: Id|45063  
 Description: None  
 Molecule type: nucleic acid  
 Query Length: 660

Database Name: nr  
 Description: Nucleotide collection (nt)  
 Program: BLASTN 2.2.28+ [Citation](#)

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#)

### Graphic Summary

Distribution of 132 Blast Hits on the Query Sequence

Mouse-over to show details and scores, click to show alignments

Color key for alignment scores

| Score Range | Color |
|-------------|-------|
| <40         | Black |
| 40-50       | Blue  |
| 50-80       | Green |
| 80-200      | Pink  |
| >=200       | Red   |

Query: 1 100 200 300 400 500 600

### Descriptions

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

| Description                                                                                                     | Max score | Total score | Query cover | E value | Max ident | Accession                      |
|-----------------------------------------------------------------------------------------------------------------|-----------|-------------|-------------|---------|-----------|--------------------------------|
| <input type="checkbox"/> Homo sapiens uroporphyrinogen decarboxylase (UROD), transcript variant 1, mRNA         | 1191      | 1191        | 100%        | 0.0     | 100%      | <a href="#">NM_000374.4</a>    |
| <input type="checkbox"/> PREDICTED: Gorilla gorilla gorilla uroporphyrinogen decarboxylase-like (LOC1011462)    | 1177      | 1177        | 100%        | 0.0     | 99%       | <a href="#">XM_004025677.1</a> |
| <input type="checkbox"/> PREDICTED: Pan troglodytes uroporphyrinogen decarboxylase, transcript variant 9 (UROD) | 1177      | 1177        | 100%        | 0.0     | 99%       | <a href="#">XM_513127.4</a>    |
| <input type="checkbox"/> PREDICTED: Pan paniscus uroporphyrinogen decarboxylase (UROD), mRNA                    | 1177      | 1177        | 100%        | 0.0     | 99%       | <a href="#">XM_003812795.1</a> |
| <input type="checkbox"/> PREDICTED: Gorilla gorilla gorilla uroporphyrinogen decarboxylase-like (LOC1011465)    | 1171      | 1171        | 100%        | 0.0     | 99%       | <a href="#">XM_004025678.1</a> |
| <input type="checkbox"/> PREDICTED: Papio anubis uroporphyrinogen decarboxylase (UROD), mRNA                    | 1135      | 1135        | 100%        | 0.0     | 98%       | <a href="#">XM_003891779.1</a> |
| <input type="checkbox"/> PREDICTED: Macaca mulatta uroporphyrinogen decarboxylase-like (UROD), mRNA             | 1113      | 1113        | 100%        | 0.0     | 97%       | <a href="#">XM_002808215.1</a> |

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Nucleotide

Nucleotide

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## Homo sapiens uroporphyrinogen decarboxylase (UROD), transcript variant 1, mRNA

NCBI Reference Sequence: NM\_000374.4

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

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|            |                                                                                                                                                                                             |         |      |        |                 |
|------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------|------|--------|-----------------|
| LOCUS      | NM_000374                                                                                                                                                                                   | 1408 bp | mRNA | linear | PRI 17-APR-2013 |
| DEFINITION | Homo sapiens uroporphyrinogen decarboxylase (UROD), transcript variant 1, mRNA.                                                                                                             |         |      |        |                 |
| ACCESSION  | NM_000374                                                                                                                                                                                   |         |      |        |                 |
| VERSION    | NM_000374.4 GI:302393547                                                                                                                                                                    |         |      |        |                 |
| KEYWORDS   | .                                                                                                                                                                                           |         |      |        |                 |
| SOURCE     | Homo sapiens (human)                                                                                                                                                                        |         |      |        |                 |
| ORGANISM   | <a href="#">Homo sapiens</a><br>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo. |         |      |        |                 |
| REFERENCE  | 1 (bases 1 to 1408)                                                                                                                                                                         |         |      |        |                 |

Analyze this sequence

Run BLAST

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Highlight Sequence Features

Find in this Sequence

Articles about the UROD gene

A census of human soluble protein complexes. [Cell. 2012]

A high-throughput approach for measuring temporal [Nat Methods. 2012]

Molecular analysis of the UROD gene in

 COMMENT

REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [DB462002.1](#), [AK291877.1](#), [AL359473.22](#) and [AF104423.1](#). This sequence is a reference standard in the [RefSeqGene](#) project. On Aug 10, 2010 this sequence version replaced gi:[71051615](#).

Summary: This gene encodes an enzyme in the heme biosynthetic pathway. This enzyme is responsible for catalyzing the conversion of uroporphyrinogen to coproporphyrinogen through the removal of four carboxymethyl side chains. Mutations and deficiency in this enzyme are known to cause familial porphyria cutanea tarda and hepatoerythropoetic porphyria.[provided by RefSeq, Aug 2010].

Transcript Variant: This variant (1) represents the longer transcript and encodes the functional protein.

---

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[imaGenes](#)

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| FEATURES                     | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                                                                                                                                                        |
|------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <a href="#">source</a>       | 1..1408<br>/organism="Homo sapiens"<br>/mol_type="mRNA"<br>/db_xref="taxon:9606"<br>▶ /chromosome="1"<br>/map="1p34"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | <a href="#">Protein</a>                                                                                                                                                                                                                |
| <a href="#">gene</a>         | 1..1408<br>/gene="UROD"<br>/gene_synonym="PCT; UPD"<br>/note="uroporphyrinogen decarboxylase"<br>/db_xref="GeneID:7389"<br>/db_xref="HGNC:12591"<br>/db_xref="MIM:613521"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | <a href="#">PubMed</a><br><a href="#">PubMed (RefSeq)</a><br><a href="#">PubMed (Weighted)</a><br><a href="#">SNP</a><br><a href="#">Taxonomy</a><br><a href="#">UniGene</a><br><a href="#">UniSTS</a><br><a href="#">GEO Profiles</a> |
| <a href="#">exon</a>         | 1..153<br>/gene="UROD"<br>/gene_synonym="PCT; UPD"<br>/inference="alignment:Splign:1.39.8"<br>/number=1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                                        |
| <a href="#">misc feature</a> | 107..109<br>/gene="UROD"<br>/gene_synonym="PCT; UPD"<br>/note="upstream in-frame stop codon"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                                                                                                                                                        |
| <a href="#">CDS</a>          | 134..1237<br>/gene="UROD"<br>/gene_synonym="PCT; UPD"<br>/EC_number="4.1.1.37"<br>/note="uroporphyrinogen III decarboxylase"<br>/codon_start=1<br>/product="uroporphyrinogen decarboxylase"<br>/protein_id="NP_000365.3"<br>/db_xref="GI:71051616"<br>/db_xref="CCDS:CCDS518.1"<br>/db_xref="GeneID:7389"<br>/db_xref="HGNC:12591"<br>/db_xref="MIM:613521"<br>▶ /translation="MEANGLGPQGFPPELKNDTFLRAAWGEETDYTPVWCMRQAGRYLP<br>EFRETRAQQDFFSTCRSPEACCELTLQPLRRFPLDAAIIFSDILVVPQALGMEVTMVP<br>GKGPSFPEPLREEQDLERLRDPEVVASELGYVVFQAITLTRQRLAGRVPLIGFAGAPWT<br>LMTYMEGGSSSTMAQAKRWLYQRPQASHQLLRILTALVPYLVGQVQVAGAALQLFE<br>SHAGHLGPQLFNKFALPYIRDVAKQVKARLREAGLAPVPMIIFAKDGHFALEELAQAG<br>YEVVGLDWTVAPKKARECVGKTVTLQGNLDPCALYASEEEIGQLVKQMLDDFGPHRYI<br>ANLGHGLYPDMDPEHVGAFFVDAVHKHSRLLRQN" |                                                                                                                                                                                                                                        |

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Homo sapiens uroporphyrinogen decarboxylase (UROD), trar Nucleotide

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A new version of the stand-alone BLAST applications is available.

Tue, 02 Apr 2013 09:00:00 EST

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**Mus musculus (house mouse) Protein BLAST**

[blastp](#) [blastx](#) [tblastn](#) [tblastx](#)

BLASTP programs search protein databases using a protein query. [more...](#) [Reset page](#) [Bookmark](#)

**Enter Query Sequence**

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#)

MEANGLGPQGFPKNDTFLRAAWGEETDYTPVWCMRQAGRYLP  
EFRETRAAQDFFSTCRSPEACCELTLQPLRRFPLDAAIIFSDILVVPQALGMEVTMVP  
GKGPSFPEPLREEQDLERLRDPEVVASELGYVFQAITLTRQLAGRVPLIGFAGAPWT  
  
LMTYMVEGGGSSTMAQAKRWLYQRPQASHQLRLTLDALVPYLVGQVVAGAQAQLQFE

Query subrange [?](#)

From

To

Or, upload file  no file selected [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

**Choose Search Set**

Database [?](#)  29281 sequences [?](#)

Exclude [Optional](#) ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Entrez Query [Optional](#)

Enter an Entrez query to limit search [?](#)

**Program Selection**

Algorithm [?](#) ☒ blastp (protein-protein BLAST)

☐ PSI-BLAST (Position-Specific Iterated BLAST)

☐ PHI-BLAST (Pattern Hit Initiated BLAST)

☐ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm [?](#)

**BLAST** ☒ Show results in a new window

Search database **Build proteins - Mus musculus** using **Blastp (protein-protein BLAST)**

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### Protein Sequence (367 letters)

|                      |            |                      |                                              |
|----------------------|------------|----------------------|----------------------------------------------|
| <b>Query ID</b>      | Id 34094   | <b>Database Name</b> | Build proteins                               |
| <b>Description</b>   | None       | <b>Description</b>   | Mus musculus Annotation Release 103 proteins |
| <b>Molecule type</b> | amino acid | <b>Program</b>       | BLASTP 2.2.28+ <a href="#">Citation</a>      |
| <b>Query Length</b>  | 367        |                      |                                              |

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#)

### Graphic Summary

[Show Conserved Domains](#)

Putative conserved domains have been detected, click on the image below for detailed results.

The graphic summary displays a horizontal bar representing the query sequence of 367 letters. Above the bar, a scale from 1 to 367 is shown. Below the bar, several domains are highlighted: 'active site' (red triangle), 'substrate binding site' (red triangle), 'URO-D' (red bar), 'URO-D\_CIMS\_like superfamily' (pink bar), and 'PRK06252' (black bar). The 'URO-D' domain is the most prominent, spanning from approximately position 100 to 350. The 'URO-D\_CIMS\_like superfamily' domain is a larger, lighter pink bar that encompasses the 'URO-D' domain. The 'PRK06252' domain is a black bar at the bottom, spanning from approximately position 100 to 350. The 'active site' and 'substrate binding site' are marked with red triangles at the beginning of the sequence.

Query seq. 1 50 100 150 200 250 300 350 367

active site

substrate binding site

Specific hits

Superfamilies

Multi-domains

URO-D

URO-D\_CIMS\_like superfamily

PRK06252

### Distribution of 4 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments

Color key for alignment scores

|     |       |       |        |       |
|-----|-------|-------|--------|-------|
| <40 | 40-50 | 50-80 | 80-200 | >=200 |
|-----|-------|-------|--------|-------|

Query 1 70 140 210 280 350

The distribution of 4 blast hits is shown as a horizontal bar with segments of different colors representing different alignment score ranges. The segments are: black (<40), blue (40-50), green (50-80), pink (80-200), and red (>=200). The bar is labeled 'Query' and has a scale from 1 to 350. The segments are positioned along the bar, with the red segment being the longest and most prominent, spanning from approximately position 100 to 350. The other segments are shorter and positioned at the beginning of the sequence.

## Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

|                          | Description                                            | Max score | Total score | Query cover | E value | Max ident | Accession                      |
|--------------------------|--------------------------------------------------------|-----------|-------------|-------------|---------|-----------|--------------------------------|
| <input type="checkbox"/> | <a href="#">unnamed protein product [Mus musculus]</a> | 702       | 702         | 100%        | 0.0     | 93%       | <a href="#">NP_033504.2</a>    |
| <input type="checkbox"/> | <a href="#">unnamed protein product [Mus musculus]</a> | 31.6      | 31.6        | 36%         | 0.98    | 25%       | <a href="#">NP_001025158.1</a> |
| <input type="checkbox"/> | <a href="#">unnamed protein product [Mus musculus]</a> | 31.2      | 31.2        | 26%         | 1.6     | 28%       | <a href="#">NP_852060.2</a>    |
| <input type="checkbox"/> | <a href="#">unnamed protein product [Mus musculus]</a> | 30.8      | 30.8        | 21%         | 1.8     | 32%       | <a href="#">NP_853626.1</a>    |

## Alignments

Download ▾ GenPept Graphics

Sequence ID: [ref|NP\\_033504.2|](#) Length: 367 Number of Matches: 1

Range 1: 1 to 367 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match

| Score          | Expect | Method                      | Identities   | Positives    | Gaps      |
|----------------|--------|-----------------------------|--------------|--------------|-----------|
| 702 bits(1811) | 0.0    | Compositional matrix adjust | 341/367(93%) | 351/367(95%) | 0/367(0%) |

|       |     |                                                               |     |
|-------|-----|---------------------------------------------------------------|-----|
| Query | 1   | MEANGLPQGFPELKNDTFLRAAWGEETDYPVWCMRQAGRYLPEFRETRAADFFSTCR     | 60  |
| Sbjct | 1   | MEANG G Q FPELKNDTFLRAAWGEETDYPVWCMRQAGRYLPEFRETRAADFFSTCR    | 60  |
| Query | 61  | SPEACCELTLQPLRRFPLDAAIIFSDILVVPQALGMEVTMVPKGPSFPEPLREEQDLER   | 120 |
| Sbjct | 61  | SPEACCELTLQPLRRFPLDAAIIFSDILVVPQALGMEVTMVPKGPSFPEPLREE+DLER   | 120 |
| Query | 121 | LRDPEVVASSELGYVFQAITLTRQRLAGRVPLIGFAGAPWTLMTYMVEGGSSSTMAQAKRW | 180 |
| Sbjct | 121 | LRDPAAASELGYVFQAITLTRQRLAGRVPLIGFAGAPWTLMTYMVEGGSSSTMAQAKRW   | 180 |
| Query | 181 | LYQRPQASHQLLRILTDLVPLYVGQVAGAAQALQLFESHAGHLGPFKFNKALPYIRDV    | 240 |
| Sbjct | 181 | LYQRPQASHKLLGILTDVLVPLYLGVAAGAQAALQLFESHAGHLGTELFKFPALPYIRDV  | 240 |
| Query | 241 | AKQVKARLREAGLAPVPMIIFAKDGHFALEELAQAQYEVVGLDWTVPKKARECVGKTVT   | 300 |
| Sbjct | 241 | AKRVKAGLQKAGLAPVPMIIFAKDGHFALEELAQAQYEVVGLDWTVPKKARERVGKAVT   | 300 |
| Query | 301 | LQGNLDPICALYASEEEIGQLVKQMLDDFGPHRYIANLGHGLYPMDPEHVGAFFDAVHKH  | 360 |
| Sbjct | 301 | LQGNLDPICALYASEEEIGRLVQQLDDFGPQRYIANLGHGLYPMDPEVGAFFDAVHKH    | 360 |

Related Information

[Gene](#) - associated gene details

[UniGene](#) - clustered expressed sequence tags

[Map Viewer](#) - aligned genomic context

## Related Information

[Gene](#) - associated gene details  
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Map Viewer Home Help

The Map Viewer provides a wide variety of genome mapping and sequencing data. [More..](#)

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**News**

**Mouse annotation release 103** Apr3  
Mouse annotation release 103 has been released to Mapviewer.... [more](#)

**Ovis aries annotation release 100** Jan 29  
Ovis aries annotation release 100 has been released to mapvi... [more](#)

**Rattus norvegicus build 5.1 released** Jan 9  
Rattus norvegicus build 5.1 has been released to mapviewer. ... [more](#)

**Human annotation release 104** Dec3, 2012  
Human annotation release 104 released to mapviewer. The chro... [more](#) [Show all](#)

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- Taxonomy
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- BLAST
- Map Viewer FTP

**Vertebrates** (28)

**Mammals** (21)

**Primates** (6)

| Scientific name            | Common name                   | Build                                                                | Tools |
|----------------------------|-------------------------------|----------------------------------------------------------------------|-------|
| <i>Callithrix jacchus</i>  | white-tufted-ear marmoset     | <a href="#">Build 1.1</a>                                            |       |
| <i>Homo sapiens</i>        | human                         | <a href="#">Annotation Release 104</a><br><a href="#">Build 36.3</a> |       |
| <i>Macaca mulatta</i>      | rhesus macaque                | <a href="#">Build 1.2</a>                                            |       |
| <i>Nomascus leucogenys</i> | northern white-cheeked gibbon | <a href="#">Build 1.1</a>                                            |       |
| <i>Pan troglodytes</i>     | chimpanzee                    | <a href="#">Build 3.1</a><br><a href="#">Build 2.1</a>               |       |
| <i>Pongo abelii</i>        | Sumatran orangutan            | <a href="#">Build 1.2</a>                                            |       |

**Rodents** (4)

| Scientific name          | Common name         | Build                                                                           | Tools |
|--------------------------|---------------------|---------------------------------------------------------------------------------|-------|
| <i>Cavia porcellus</i>   | domestic guinea pig | <a href="#">Build 1.1</a>                                                       |       |
| <i>Cricetus griseus</i>  | Chinese hamster     | <a href="#">Build 1.1</a>                                                       |       |
| <i>Mus musculus</i>      | laboratory mouse    | <a href="#">Annotation Release 103</a><br><a href="#">Build 37.2</a>            |       |
| <i>Rattus norvegicus</i> | rat                 | <a href="#">Build 5.1 (Annotation Release 103)</a><br><a href="#">RGSC v3.4</a> |       |

**Monotremes** (1)

**Marsupials** (1)

**Other Mammals** (9)

**Other Vertebrates** (7)

**Invertebrates** (17)

**Protozoa** (19)

**Plants** (118)

**Fungi** (17)

| Scientific name                 | Common name | Build                     | Tools |
|---------------------------------|-------------|---------------------------|-------|
| <i>Aspergillus clavatus</i>     |             | <a href="#">Build 1.1</a> |       |
| <i>Aspergillus fumigatus</i>    |             | <a href="#">Build 2.1</a> |       |
| <i>Aspergillus niger</i>        |             | <a href="#">Build 1.1</a> |       |
| <i>Candida glabrata</i>         |             | <a href="#">Build 1.1</a> |       |
| <i>Cryptococcus neoformans</i>  |             | <a href="#">Build 2.1</a> |       |
| <i>Debaryomyces hansenii</i>    |             | <a href="#">Build 1.1</a> |       |
| <i>Encephalitozoon cuniculi</i> |             | <a href="#">Build 1.1</a> |       |

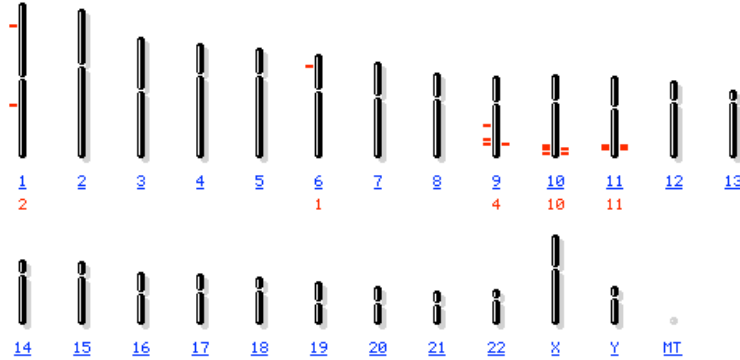
NCBI  NCBI Map Viewer

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Search for  on chromosome(s)  assembly  Find Advanced Search

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Annotation Release 104 statistics [Switch to previous build](#)



Hits:

**Search results for query "Porphyria": 28 hits**

| Chr | Assembly  | Match                                                                      | Map element                                    | Type     | Maps                   |
|-----|-----------|----------------------------------------------------------------------------|------------------------------------------------|----------|------------------------|
| 1   | reference | <a href="#">all matches</a>                                                |                                                |          |                        |
|     |           | <b>Porphyria variegata, 176200</b>                                         | <a href="#">Porphyria variegata, 176200</a>    | MIM      | <a href="#">Morbid</a> |
|     |           | <b>Porphyria cutanea tarda, 176100; Porphyria, hepatoerythropoietic...</b> | <a href="#">Porphyria cutanea tarda, 17610</a> | MIM      | <a href="#">Morbid</a> |
| 6   | reference | <b>Hemochromatosis, 235200; Microvascular complications of diabetes...</b> | <a href="#">Hemochromatosis, 235200; Micro</a> | MIM      | <a href="#">Morbid</a> |
| 9   | reference | <a href="#">all matches</a>                                                |                                                |          |                        |
|     |           | <b>Porphyria, acute hepatic, 612740; Lead poisoning, susceptibility...</b> | <a href="#">Porphyria, acute hepatic, 6127</a> | MIM      | <a href="#">Morbid</a> |
|     |           | <b>Production of rhPBGD and novel...porphyria (AIP) and other...</b>       | <a href="#">BD292563.1</a>                     | SEQUENCE | <a href="#">gbDNA</a>  |

Quick Filter

☐ Gene

Transcript :

☐ all

☐ RefSeq

Filter



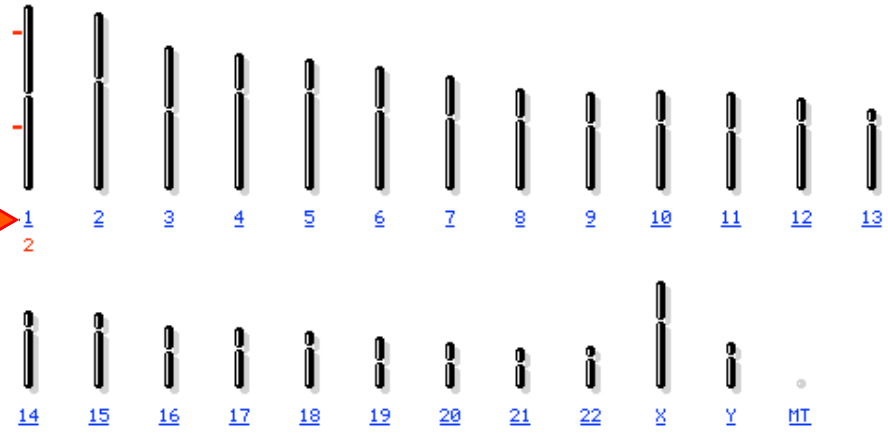
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Hits:

**Search results for query "Porphyria": 2 hits**

| Chr | Match                                                                      | Map element                                    | Type | Maps                      |
|-----|----------------------------------------------------------------------------|------------------------------------------------|------|---------------------------|
| 1   | <a href="#">all matches</a>                                                |                                                |      |                           |
|     | <b>Porphyria variegata, 176200</b>                                         | <a href="#">Porphyria variegata, 176200</a>    | MIM  | <a href="#">Morbidity</a> |
|     | <b>Porphyria cutanea tarda, 176100; Porphyria, hepatoerythropoietic...</b> | <a href="#">Porphyria cutanea tarda, 17610</a> | MIM  | <a href="#">Morbidity</a> |

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Human genome overview page (Build 36.3)  
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Map Viewer Help  
Human Maps Help  
FTP  
Data As Table View  
[Maps & Options](#)

Region Shown:  
1p36.11  
1q25.3  
Go

out  
zoom  
in

You are here:

Ideogram

default  
master

[Homo sapiens \(human\)](#) [Annotation Release 104 \(Current\)](#)

Chromosome: [1] 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT

Query: **Porphyria** [clear]

Master Map: OMIM Morbid

Region Displayed: 1p36.11-1q25.3

[Summary of Maps](#) [Maps & Options](#)

| Hs         | Unig  | Genes_seq | Morbid | MIM Number | GeneID    | Disease                                                                                                                                                      |
|------------|-------|-----------|--------|------------|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Hs.656915  | LCK   | HDAC1     |        | 130500     | 2035      | Elliptocytosis-1, <a href="#">611804</a>                                                                                                                     |
| Hs.472475  | YBX1  | SLC28A1   |        | 609919     | 100033389 | Gallbladder disease 3                                                                                                                                        |
| Hs.4403972 | YBX1  | SLC28A1   |        | 605425     | 127534    | Erythrokeratoderma variabilis with erythema gyratum repens, <a href="#">133200</a>                                                                           |
| Hs.646365  | MUTYH |           |        | 606713     | 171012    | van der Woude syndrome 2                                                                                                                                     |
| Hs.679809  | PCSK9 |           |        | 613521     | 7389      | Porphyria cutanea tarda, <a href="#">176100</a> ; Porphyria, hepatoerythropoietic, <a href="#">176100</a>                                                    |
| Hs.444301  | JUN   |           |        | 603615     | 8438      | Breast cancer, invasive ductal, <a href="#">114480</a> ; Lymphoma, non-Hodgkin, somatic, <a href="#">605027</a> ; Adenocarcinoma, colonic, somatic           |
| Hs.191911  | JRK1  | LEPR      |        | 610805     | 100034704 | Renal hypodysplasia, nonsyndromic, 1                                                                                                                         |
| Hs.470125  | LEPR  |           |        | 604566     | 29929     | Congenital disorder of glycosylation, type Ic, <a href="#">603147</a>                                                                                        |
| Hs.654491  | LEPR  |           |        | 611539     | 27022     | Autoimmune disease, susceptibility to, 1, <a href="#">607836</a>                                                                                             |
| Hs.198072  | LEPR  |           |        | 607562     | 149233    | Inflammatory bowel disease 17, protection against, <a href="#">612261</a> ; Psoriasis, protection against, <a href="#">605606</a>                            |
| Hs.479650  | LEPR  |           |        | 612779     | 1806      | Dihydropyrimidine dehydrogenase deficiency, <a href="#">274270</a> ; 5-fluorouracil toxicity, <a href="#">274270</a>                                         |
| Hs.146542  | LEPR  |           |        | 602458     | 6272      | Low density lipoprotein cholesterol level QTL6, <a href="#">613589</a>                                                                                       |
| Hs.654821  | LEPR  |           |        | 139340     | 2780      | Achromatopsia-4, <a href="#">613856</a>                                                                                                                      |
| Hs.337040  | LEPR  |           |        | 609245     | 29899     | Deafness, autosomal recessive 82, <a href="#">613557</a>                                                                                                     |
| Hs.744625  | LEPR  |           |        | 606014     | 257       | Frontonasal dysplasia 1, <a href="#">136760</a>                                                                                                              |
| Hs.649282  | LEPR  |           |        | 193000     | 54113     | Vesicoureteral reflux                                                                                                                                        |
| Hs.24212   | LEPR  |           |        | 600716     | 26191     | Diabetes, type 1, susceptibility to, <a href="#">222100</a> ; Rheumatoid arthritis, susceptibility to, <a href="#">180300</a> ; Systemic lupus erythematosus |
| Hs.699516  | LEPR  |           |        | 161900     | 59331     | Nephropathy-hypertension                                                                                                                                     |
| Hs.732392  | ABCR4 |           |        | 608781     | 449015    | Asperger syndrome susceptibility 3                                                                                                                           |
| Hs.732666  | ABCR4 |           |        | 176310     | 5087      | Leukemia, acute pre-B-cell                                                                                                                                   |
| Hs.335034  | DPYD  | UCRM1     |        | 600923     | 5498      | Porphyria variegata, <a href="#">176200</a>                                                                                                                  |
| Hs.267659  | GSTM1 |           |        | 146790     | 2212      | Lupus nephritis, susceptibility to                                                                                                                           |
| Hs.732334  | CSF1  |           |        | 605205     | 55811     | Hypercalciuria, absorptive, susceptibility to, <a href="#">143870</a>                                                                                        |
| Hs.568247  | FLG   |           |        | 601652     | 4653      | Glaucoma 1A, primary open angle, juvenile-onset, <a href="#">137750</a> ; Glaucoma 1A, primary open angle, recessive; Glaucoma, e                            |