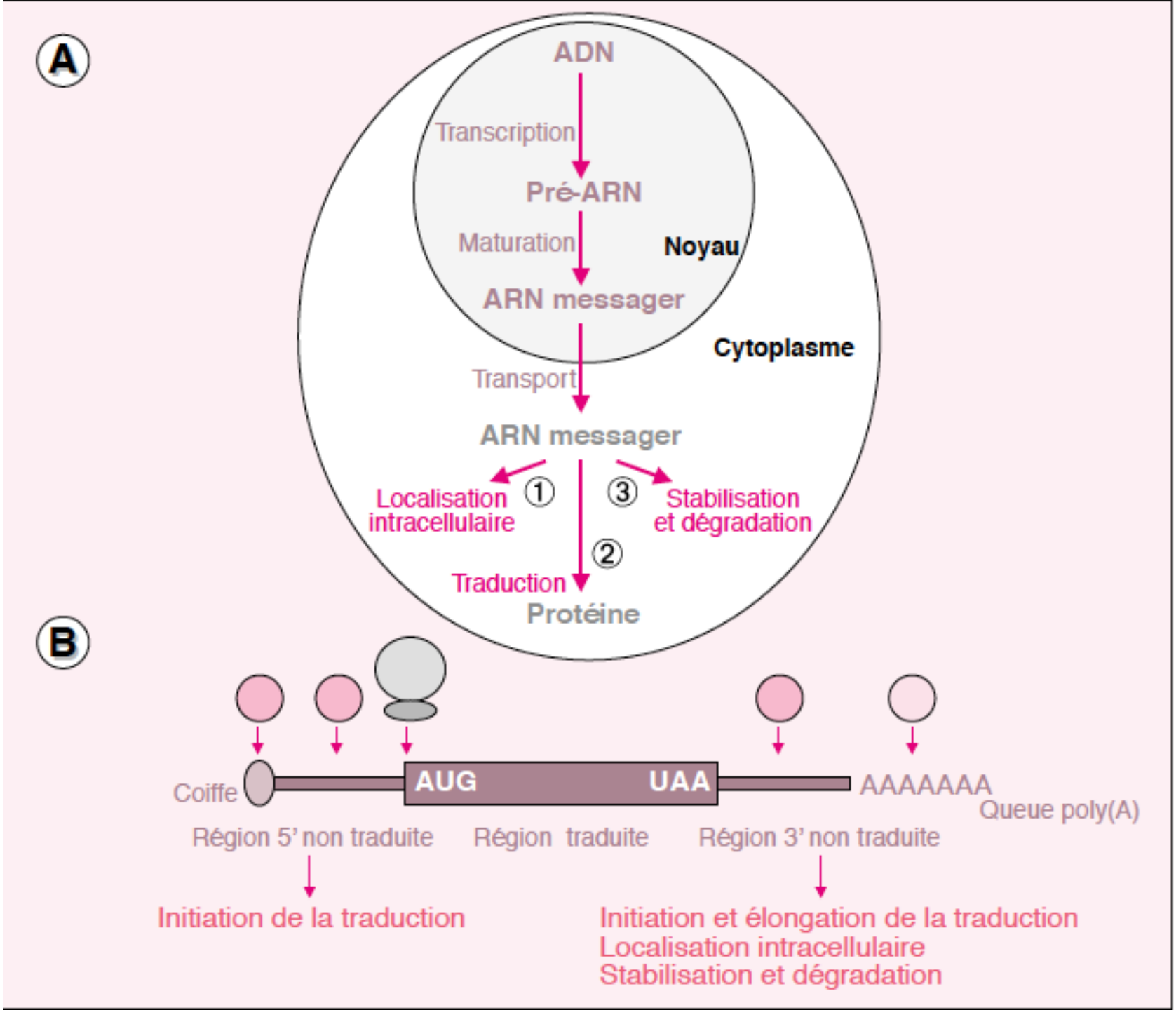
A
ADN
Transcription
Pré-ARN
Maturation
Noyau
ARN messager
Cytoplasme
Transport
ARN messager
Localisation intracellulaire
①
③
Stabilisation et dégradation
②
Traduction
Protéine
B
Coiffe
AUG
UAA
AAAAAAA
Queue poly(A)
Région 5' non traduite
Région traduite
Région 3' non traduite
Initiation de la traduction
Initiation et élongation de la traduction
Localisation intracellulaire
Stabilisation et dégradation

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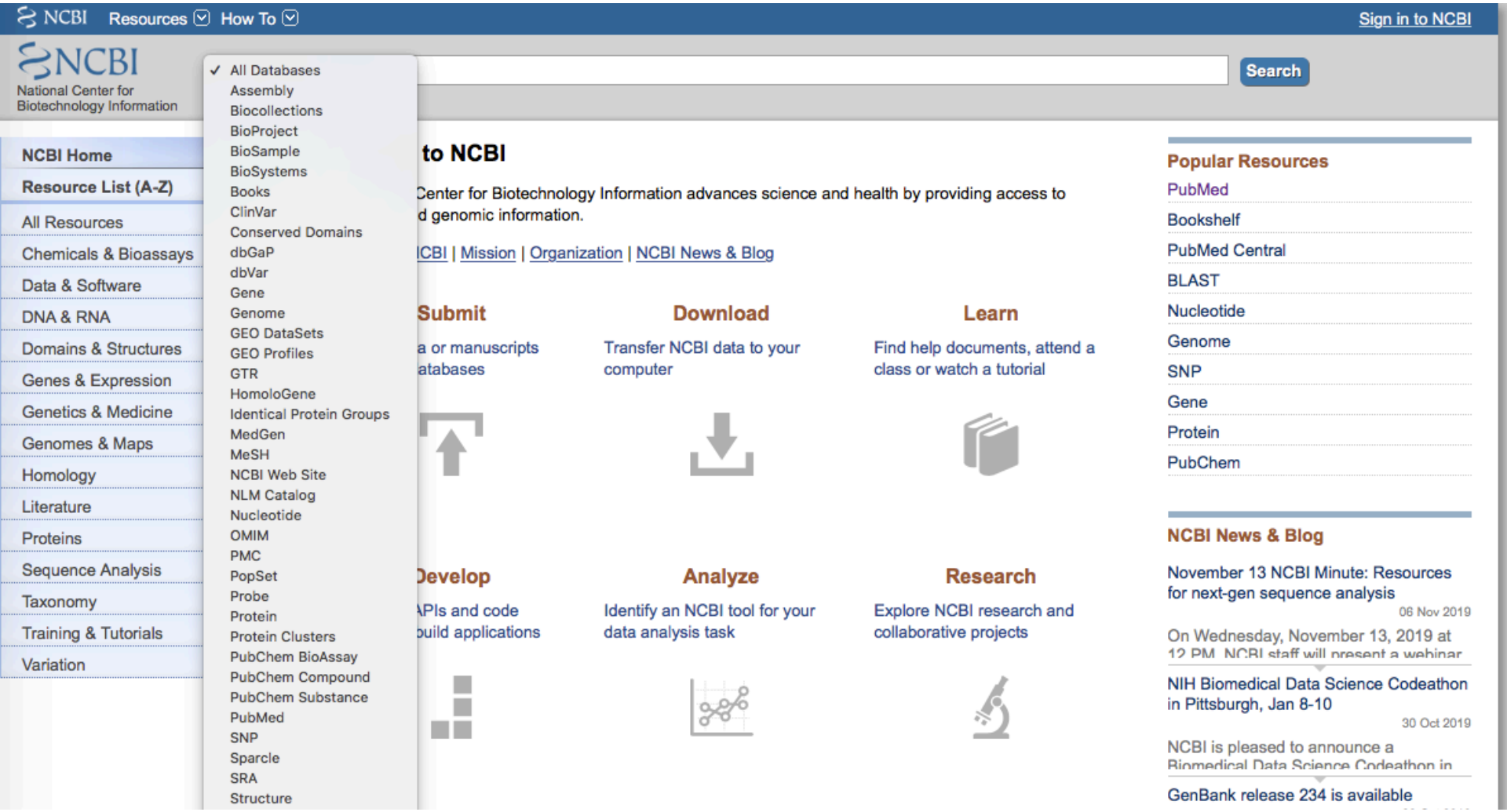
06 Nov 2019

On Wednesday, November 13, 2019 at 12 PM, NCBI staff will present a webinar

NIH Biomedical Data Science Codeathon in Pittsburgh, Jan 8-10

30 Oct 2019

NCBI is pleased to announce a Biomedical Data Science Codeathon in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Gene
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PubChem
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NIH Biomedical Data Science Codeathon in Pittsburgh, Jan 8-10
30 Oct 2019
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Gene KSRP

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Non-coding
Protein-coding

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Ensembl
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RefSeqGene

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✓ Current

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Show additional filters

Tabular 20 per page Sort by Relevance Send to:

See KHSRP (KSRP) KH-type splicing regulatory protein in the Gene database
ksrp in Homo sapiens Mus musculus Xenopus tropicalis All 5 Gene records

Search results

Items: 1 to 20 of 60

<< First < Prev Page 1 of 3 Next > Last >>

See also 3 discontinued or replaced items.

Name/Gene ID	Description	Location	Aliases	MIM
KHSRP ID: 8570	KH-type splicing regulatory protein [*Homo sapiens* (human)]	Chromosome 19, NC_000019.10 (6413102..6424811, complement)	FBP2, FUBP2, KSRP, p75	603445
Khsrp ID: 16549	KH-type splicing regulatory protein [*Mus musculus* (house mouse)]	Chromosome 17, NC_000083.6 (57021049..57031507, complement)	6330409F21Rik, Fbp2, Fubp2, Ksrp	
khsrp ID: 100170586	KH-type splicing regulatory protein [*Xenopus tropicalis* (tropical clawed frog)]	Chromosome 3, NC_030679.1 (130039451..130057575, complement)	VgRBP71, fbp2, fubp2, ksrp	
khsrp.S ID: 399189	KH-type splicing regulatory protein S homeolog [*Xenopus laevis* (African clawed frog)]		XELAEV_18000829mg, VgRBP71, fbp2, fubp2, khsrp-b, ksrp	
khsrp.L	KH-type splicing	Chromosome 3L,	XELAEV_18019123mg,	

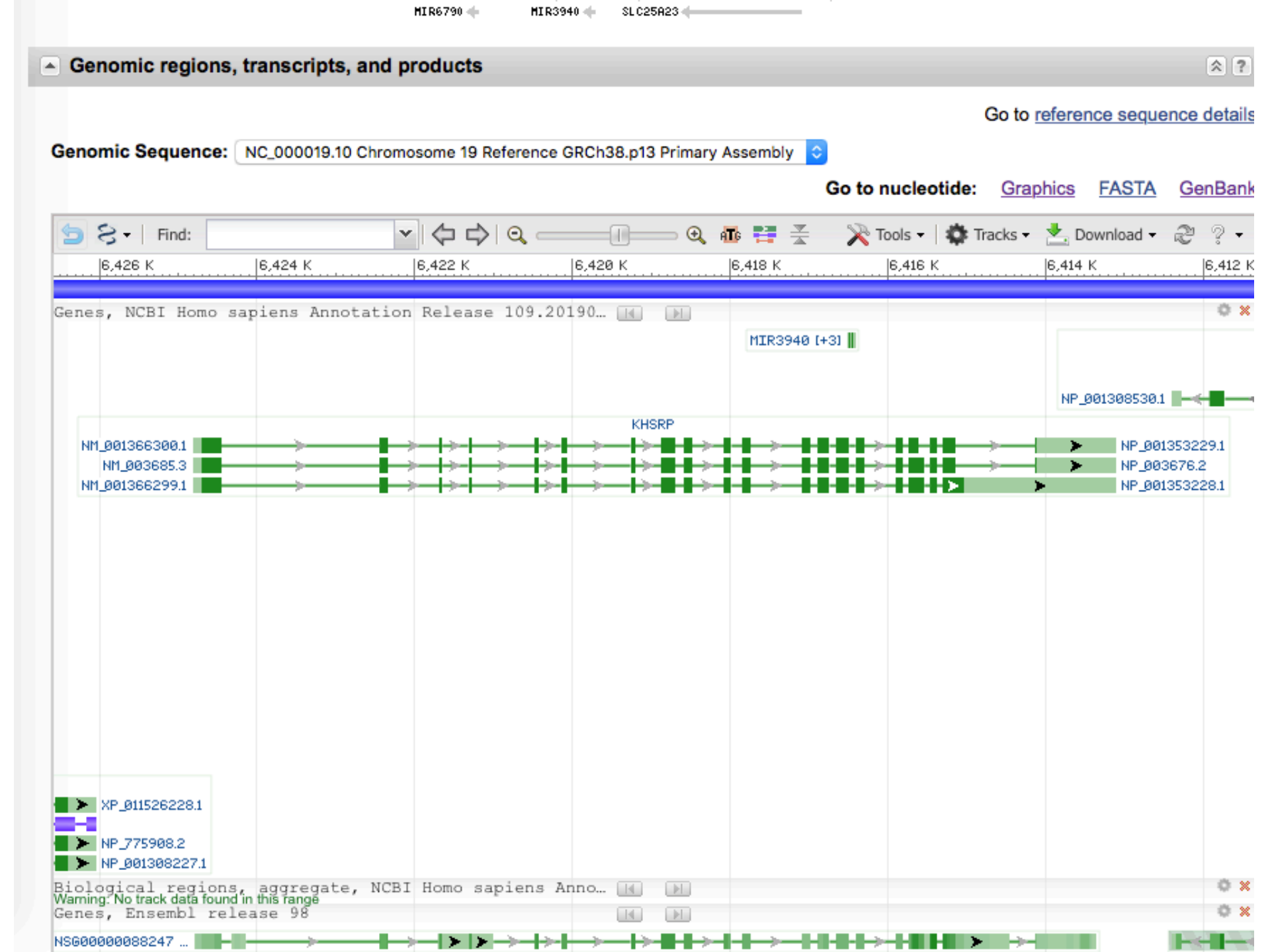
KHSRP KH-type splicing regulatory protein [*Homo sapiens* (human)]

Gene ID: 8570, updated on 3-Nov-2019

Summary

Official Symbol	KHSRP provided by HGNC
Official Full Name	KH-type splicing regulatory protein provided by HGNC
Primary source	HGNC:HGNC:6316
See related	Ensembl:ENSG00000088247 MIM:603445
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as	p75; FBP2; KSRP; FUBP2
Summary	The KHSRP gene encodes a multifunctional RNA-binding protein implicated in a variety of cellular processes, including transcription, alternative pre-mRNA splicing, and mRNA localization (Min et al., 1997 [PubMed 9136930]; Gherzi et al., 2004 [PubMed 15175153]).[supplied by OMIM, Apr 2010]
Expression	Ubiquitous expression in testis (RPKM 37.2), endometrium (RPKM 25.1) and 25 other tissues See more
Orthologs	mouse all

Genomic context


MIR6790
MIR3940
SLC25A23
Genomic regions, transcripts, and products
Go to reference sequence details
Genomic Sequence:
NC_000019.10 Chromosome 19 Reference GRCh38.p13 Primary Assembly
Go to nucleotide:
Graphics
FASTA
GenBank
Find:
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Tracks
Download
6,426 K
6,424 K
6,422 K
6,420 K
6,418 K
6,416 K
6,414 K
6,412 K
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NP_003676.2
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XP_011526228.1
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NP_001308227.1
Biological regions, aggregate, NCBI Homo sapiens Anno…
Warning: No track data found in this range
Genes, Ensembl release 98
NSG00000088247 …

Homo sapiens chromosome 19, GRCh38.p13 Primary Assembly

NCBI Reference Sequence: NC_000019.10

FASTA Graphics

```
LOCUS       NC_000019              11710 bp    DNA     linear   CON 09-SEP-2019
DEFINITION  Homo sapiens chromosome 19, GRCh38.p13 Primary Assembly.
ACCESSION   NC_000019 REGION: complement(6413102..6424811)
VERSION     NC_000019.10
DBLINK      BioProject: PRJNA168
            Assembly: GCF_000001405.39
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 11710)
  CONSRTM   International Human Genome Sequencing Consortium
  TITLE     Finishing the euchromatic sequence of the human genome
  JOURNAL   Nature 431 (7011), 931-945 (2004)
   PUBMED   15496913
REFERENCE   2  (bases 1 to 11710)
  AUTHORS   Grimwood,J., Gordon,L.A., Olsen,A., Terry,A., Schmutz,J.,
            Lamerdin,J., Hellsten,U., Goodstein,D., Couronne,O.,
            Tran-Gyamfi,M., Aerts,A., Altherr,M., Ashworth,L., Bajorek,E.,
            Black,S., Branscomb,E., Caenepeel,S., Carrano,A., Caoile,C.,
            Chan,Y.M., Christensen,M., Cleland,C.A., Copeland,A., Dalin,E.,
            Dehal,P., Denys,M., Detter,J.C., Escobar,J., Flowers,D.,
            Fotopulos,D., Garcia,C., Georgescu,A.M., Glavina,T., Gomez,M.,
            Gonzales,E., Groza,M., Hammon,N., Hawkins,T., Haydu,L., Ho,I.,
            Huang,W., Israni,S., Jett,J., Kadner,K., Kimball,H., Kobayashi,A.,
            Larionov,V., Leem,S.H., Lopez,F., Lou,Y., Lowry,S., Malfatti,S.,
            Martinez,D., McCready,P., Medina,C., Morgan,J., Nelson,K.,
```

FASTA Send to:

Homo sapiens chromosome 19, GRCh38.p13 Primary Assembly

NCBI Reference Sequence: NC_000019.10

GenBank Graphics

>NC_000019.10:c6424811-6413102 Homo sapiens chromosome 19, GRCh38.p13 Primary Assembly

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CGCCAGGCGCGGGGGACCGGGGCGGCGGCGGTCCCGGCGGCGGCGGCCCGGGCGGGGGGTCGGCCGGGGG
CCCCTCTCAGCCACCCGGCGGAGGCGGCCCGGGAATCCGCAAGGACGCTTTCGCCGACGCCGTGCAGCGG
GCCCGCCAGGTGAGGAGGCCGAGGGCCTGAGGGGCGCGCTCGCGCGCGCGCGCAGGCGGGGGAGGGGGCG
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ACAGTCTCAATATCACCCAGGCAGGGGTGCAGTGGCACGATCTCAGCACACCACAGCCTCCACCTCTCCA
GTTGAAGTGCTCCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTATAAGTGTGCACCACCACACCCAGCT

Change region shown

- Whole sequence
- Selected region

from: 6413102 to: 6424811

Update View

Customize view

Display options

- [x] Show reverse complement

Update View

Analyze this sequence

- Run BLAST
- Pick Primers
- Highlight Sequence Features

Related information

- Assembly
- BioProject
- Protein

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Primer-BLAST

A tool for finding specific primers

Finding primers specific to your PCR template (using Primer3 and BLAST).

Reset page | Save search parameters | Retrieve recent results | Publication | Tips for finding specific primers

PCR Template

Enter accession, gi, or FASTA sequence (A refseq record is preferred) Clear

NC_000019.10

Or, upload FASTA file Choisir le fichier aucun fichier sél.

Range

	From	To
Forward primer	6413102	
Reverse primer		6424811

Clear

Primer Parameters

Use my own forward primer (5'->3' on plus strand) Clear

Use my own reverse primer (5'->3' on minus strand) Clear

	Min	Max
PCR product size	70	1000
# of primers to return	10	

	Min	Opt	Max	Max Tm difference
Primer melting temperatures (Tm)	57.0	60.0	63.0	3

Exon/intron selection

A refseq mRNA sequence as PCR template input is required for options in the section

Exon junction span No preference

Exon junction match

Exon at 5' side	Exon at 3' side
7	4

Minimal number of bases that must anneal to exons at the 5' or 3' side of the junction

Intron inclusion Primer pair must be separated by at least one intron on the corresponding genomic DNA

Primer3web version 4.1.0 - Pick primers from a DNA sequence.

disclaimer | code | cautions

Select the Task for primer selection generic

Template masking before primer design (available species)

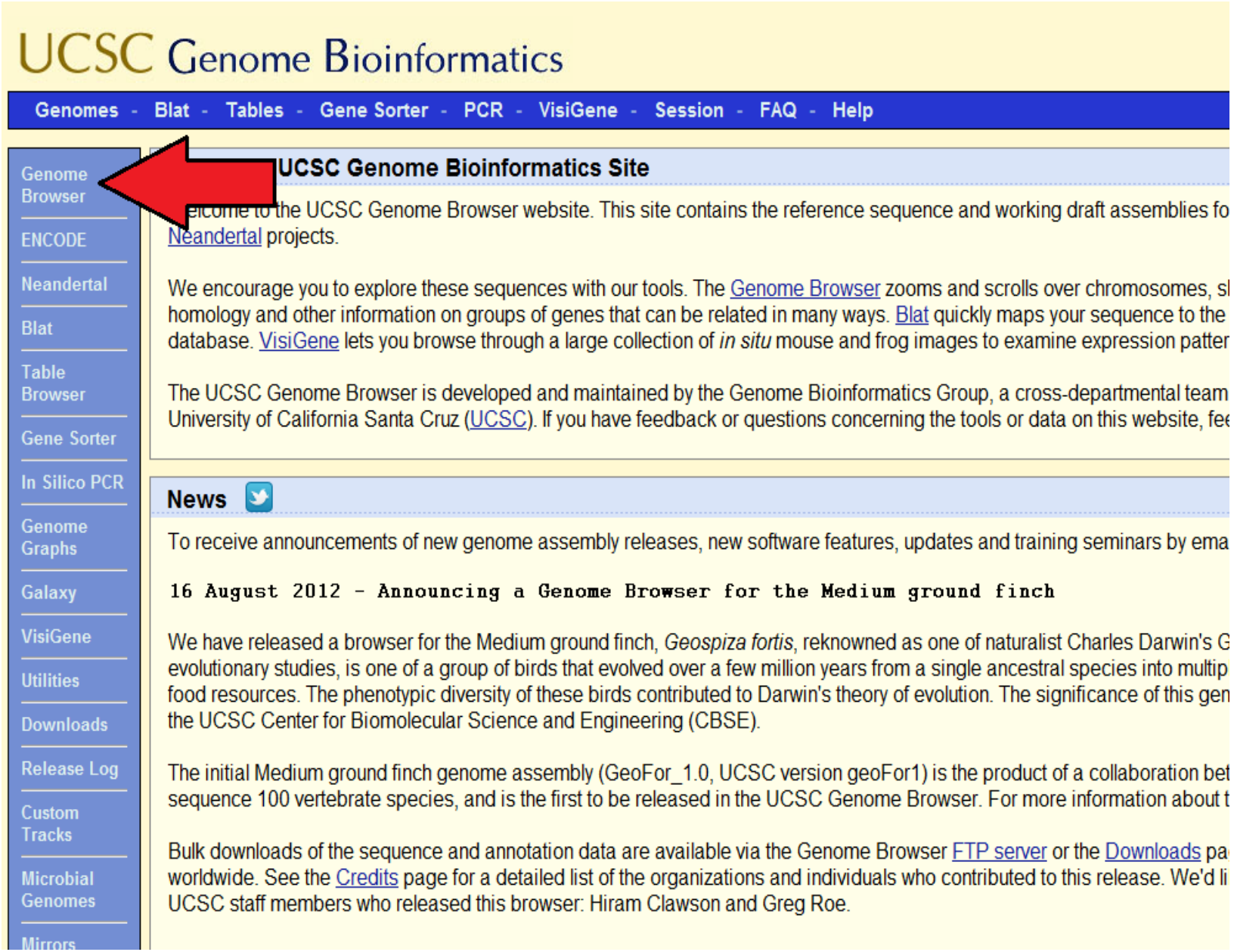
Select species Example: Mus musculus	Nucleotides to mask in 5' direction 1
Primer failure rate cutoff < 0.1	Nucleotides to mask in 3' direction 0

Paste source sequence below (5'->3', string of ACGTNacgtn -- other letters treated as N -- numbers and blanks ignored). FASTA format ok. Please N-out undesirable sequence (vector, ALUs, LINEs, etc.) or use a Mispriming Library (repeat library) NONE

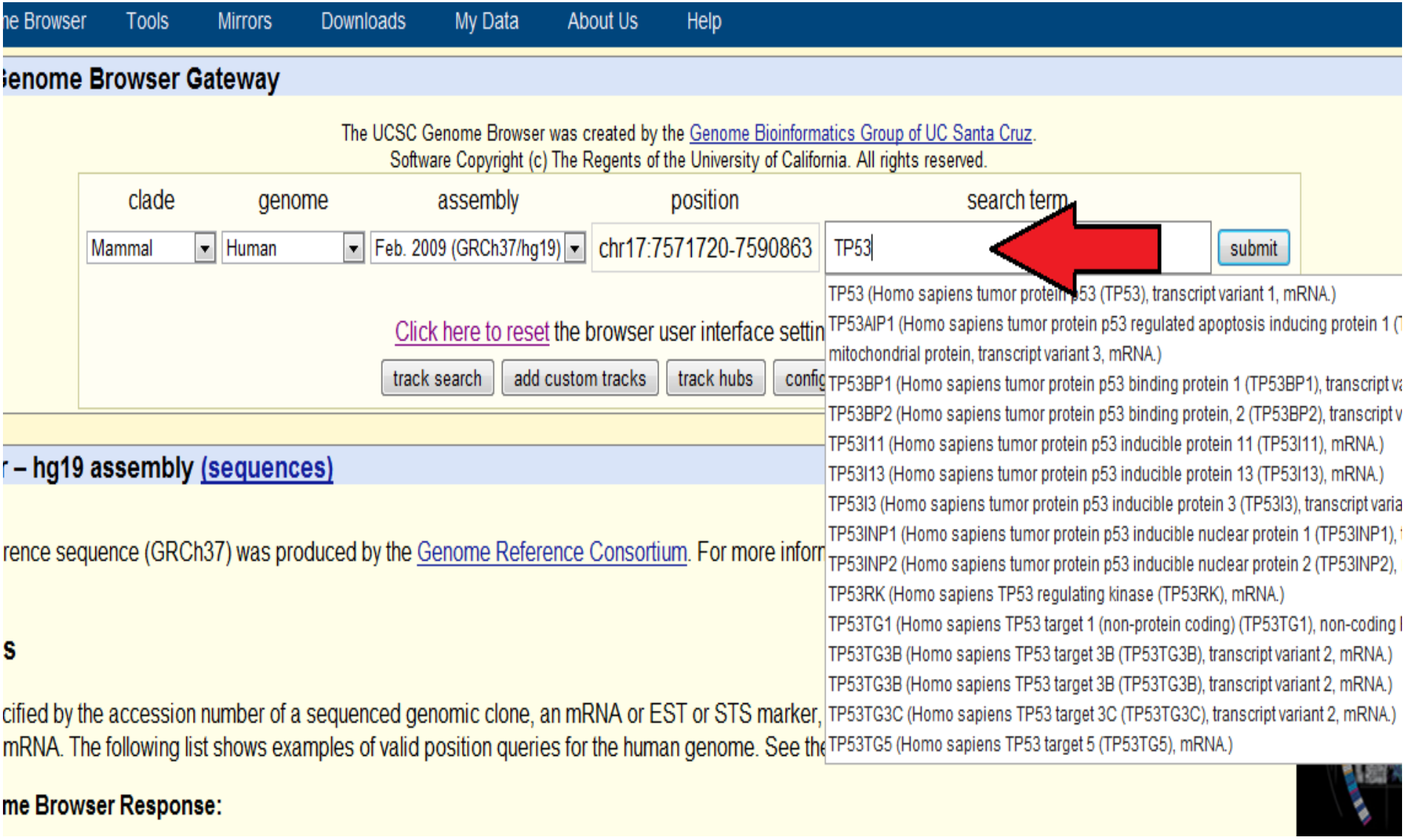
Pick left primer, or use left primer below	Pick hybridization probe (internal oligo), or use oligo below	Pick right primer, or use right primer below (5' to 3' on opposite strand)

Pick Primers | Download Settings | Reset Form

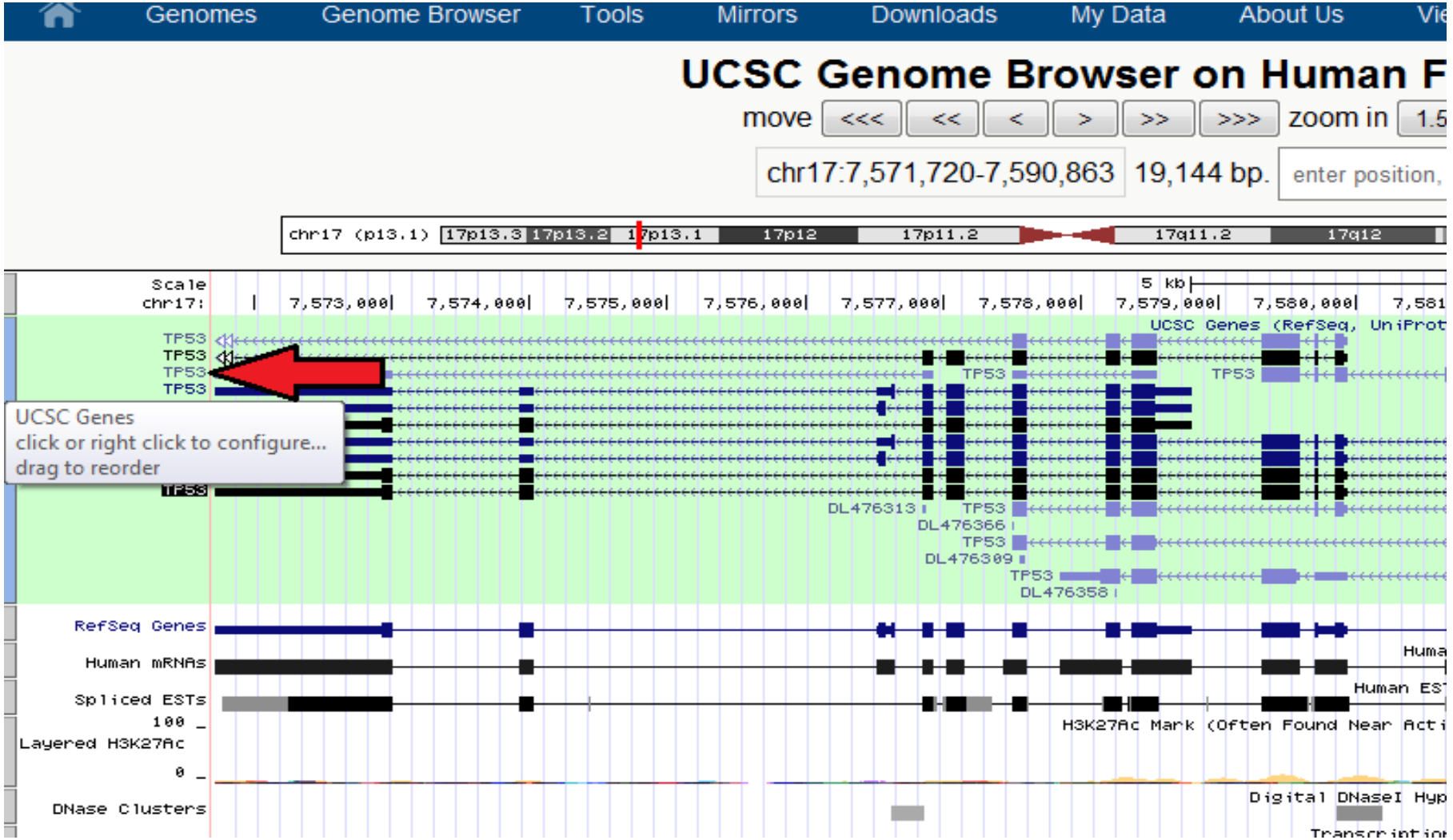
Go to http://genome.ucsc.edu/index.html click on Genome Browser



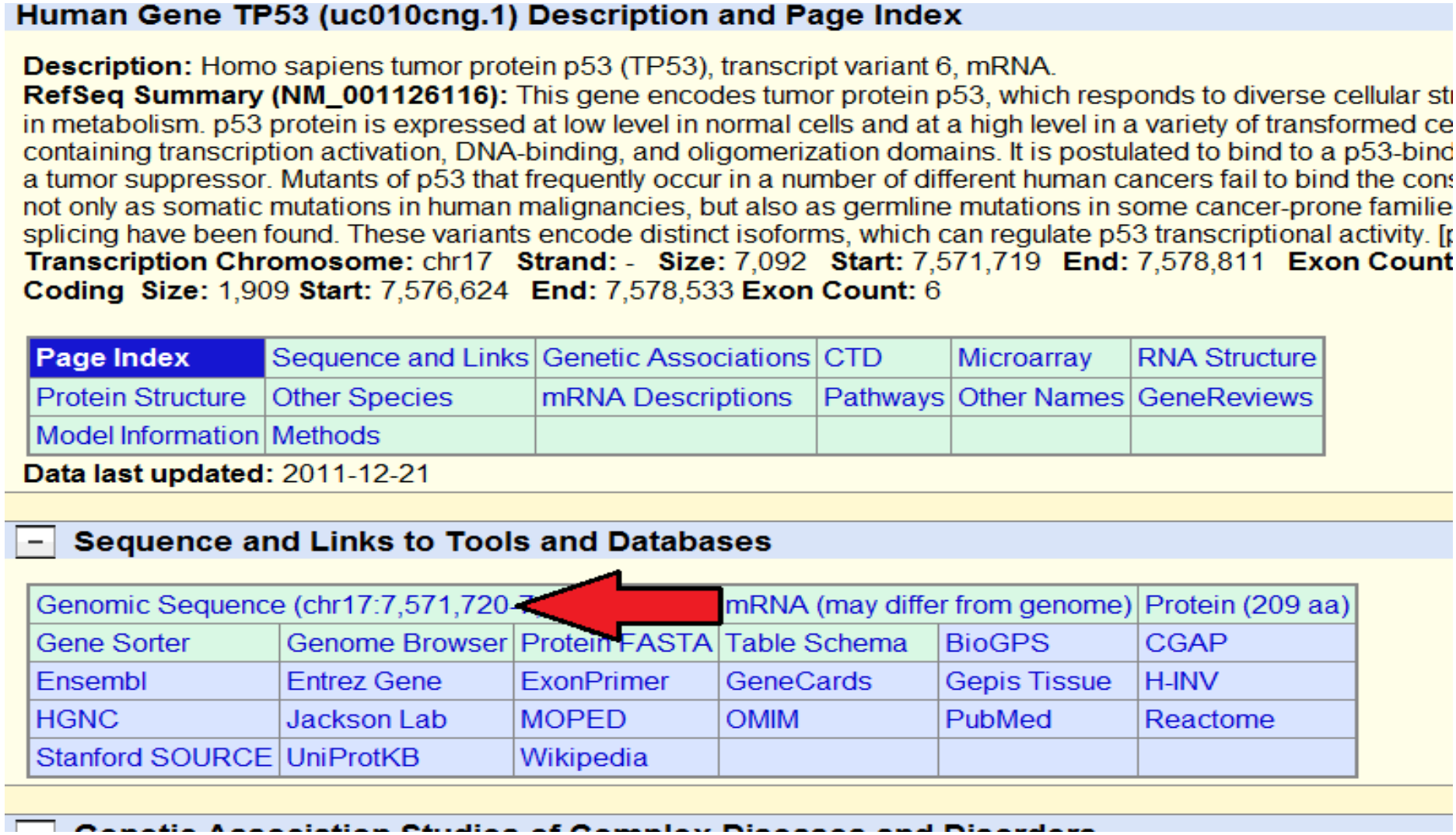
Begin typing the symbol of your gene into the “Search term” box. Select the most appropriate one from the autocomplete list



On the genome viewer, click on the symbol of your gene in the “UCSC Genes” track, in this case, I clicked on the TP53. Any of those will take you to the next page. Pease, note the direction of the arrows in the gene, since it indicates the direction of transcription. In this case, the 5’ end is to the right.



Click on the “Genomic sequence” link in the table called “sequence and Links to Tools and Databases”



Human Gene TP53 (uc010cng.1) Description and Page Index

Description: Homo sapiens tumor protein p53 (TP53), transcript variant 6, mRNA.
RefSeq Summary (NM_001126116): This gene encodes tumor protein p53, which responds to diverse cellular st
in metabolism. p53 protein is expressed at low level in normal cells and at a high level in a variety of transformed ce
containing transcription activation, DNA-binding, and oligomerization domains. It is postulated to bind to a p53-binc
a tumor suppressor. Mutants of p53 that frequently occur in a number of different human cancers fail to bind the cons
not only as somatic mutations in human malignancies, but also as germline mutations in some cancer-prone familie
splicing have been found. These variants encode distinct isoforms, which can regulate p53 transcriptional activity. [
Transcription Chromosome: chr17 **Strand:** - **Size:** 7,092 **Start:** 7,571,719 **End:** 7,578,811 **Exon Count**
Coding Size: 1,909 **Start:** 7,576,624 **End:** 7,578,533 **Exon Count:** 6

Page Index	Sequence and Links	Genetic Associations	CTD	Microarray	RNA Structure
Protein Structure	Other Species	mRNA Descriptions	Pathways	Other Names	GeneReviews
Model Information	Methods				

Data last updated: 2011-12-21

Sequence and Links to Tools and Databases

Genomic Sequence (chr17:7,571,720-		mRNA (may differ from genome)			Protein (209 aa)
Gene Sorter	Genome Browser	Protein FASTA	Table Schema	BioGPS	CGAP
Ensembl	Entrez Gene	ExonPrimer	GeneCards	Gepis Tissue	H-INV
HGNC	Jackson Lab	MOPED	OMIM	PubMed	Reactome
Stanford SOURCE	UniProtKB	Wikipedia			

Select the ” CDs in upper case, UTR in lower case” option.
Also (not indicated in the picture), you may want to select “One FASTA record per region (exon, intron, etc)” since it separates each region into different records.

Get Genomic Sequence Near Gene

Note: if you would prefer to get DNA for more than one feature of this track at a time, try

Sequence Retrieval Region Options:

- [ ] Promoter/Upstream by 1000 bases
- [x] 5' UTR Exons
- [x] CDS Exons
- [x] 3' UTR Exons
- [x] Introns
- [ ] Downstream by 1000 bases

- (•) One FASTA record per gene.
- ( ) One FASTA record per region (exon, intron, etc.) with 0 extra bases upstrea
  - [ ] Split UTR and CDS parts of an exon into separate FASTA records

Note: if a feature is close to the beginning or end of a chromosome and upstream/dow

Sequence Formatting Options:

- ( ) Exons in upper case, everything else in lower case.
- (•) CDS in upper case, UTR in lower case.
- ( ) All upper case.
- ( ) All lower case.
- [ ] Mask repeats: (•) to lower case ( ) to N

submit

>hg19 knownGene uc010cng.1 range=chr17:7571720-7578811 5'pad=0 3'pad=0 strand=- repeatMasking=nor

tgaggccaggagatggaggctgcagtgagctgtgatcacaccactgtgct
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