Primers/Amorces

› *Tumeur :*

Gène	*Séquence 5' - 3'*	*Référence GenBank®*	*Longueur de l'amplicon (pb)*
Glut1 (Slc2a1)	Fwd : TGC CTT GGA TGT CCT ATC TG Rev : ACC AGG GCC TAC TTC AAA GA	NM_011400.3	71
Hprt (Hprt)	Fwd : CAG GCC AGA CTT TGT TGG AT Rev : TTG CGC TCA TCT TAG GCT TT	NM_013556.2	147
Ppia (Ppia)	Fwd : AGC ATA CAG GTC CTG GCA TC Rev : TTC ACC TTC CCA AAG ACC AC	NM_008907.1	127
Tweak (Tnfsf12)	Fwd : GCT ACG ACC GCC AGA TTG GG Rev : GCC AGC ACA CCG TTC ACC AG	NM_011614.3	130
Vegfa (Vegfa)	Fwd : CAC CCA CGA CAG AAG GAG AG Rev : TCT CAA TCG GAC GGC AGT AG	NM_001025250.3	87

Dr AMIROUCHE A.

(2020/2021)

Dessin Des Couples d'amorces Références- Primer

Principe

Crée un couple d'amorces valide pour la quantification de l'expression d'un gène d'intérêt.

Comment?

1- NCBI (National Center for Biotechnology Information) (www.ncbi.nlm.nih.gov)

- Primer--BLAST (www.ncbi.nlm.nih.gov/tools/primer---blast))

2- Integrated DNA Technologies® (www.idtdna.com)

.

Protocole

› Obtenir la sequence nucléotidique du transcript du gene (sur NCBI)

:

1. Dans le menu déroulant, sélectionner «Gene». Dans la barre de recherche, taper le nom du gene d'intérêt, et cliquer sur «Search».

2. Sélectionner l'espèce désirée.

3. Cliquer sur «GenBank», puis sélectionner l'ARNm désiré dans «Features – mRNA».

4. Cliquer sur «FASTA», puis noter la sequence codante obtenue.

NCBI
National Center for Biotechnology Information

All Databases | Search

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

About the NCBI | Mission | Organization | NCBI News & Blog

Submit

Deposit data or manuscripts into NCBI databases

Download

Transfer NCBI data to your computer

Learn

Find help documents, attend a class or watch a tutorial

Develop

Use NCBI APIs and code libraries to build applications

Analyze

Identify an NCBI tool for your data analysis task

Research

Explore NCBI research and collaborative projects

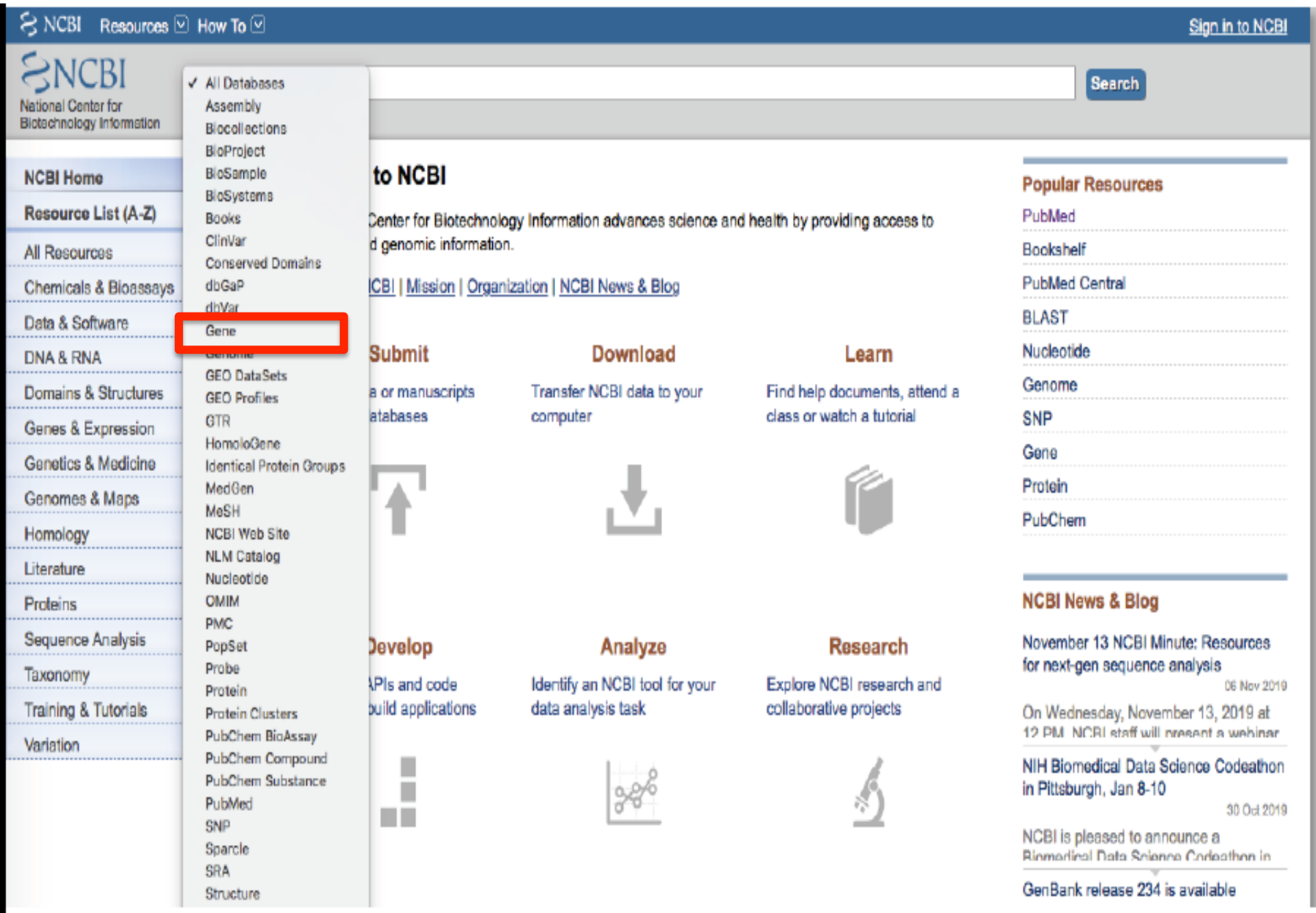
Popular Resources

PubMed
Bookshelf
PubMed Central
BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem

NCBI News & Blog

November 13 NCBI Minute: Resources for next-gen sequence analysis
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


NCBI Resources How To
Sign in to NCBI
NCBI
National Center for Biotechnology Information
All Databases
Assembly
Biocollections
BioProject
BioSample
BioSystems
Books
ClinVar
Conserved Domains
dbGaP
dbVar
Gene
GEO DataSets
GEO Profiles
GTR
HomoloGene
Identical Protein Groups
MedGen
MeSH
NCBI Web Site
NLM Catalog
Nucleotide
OMIM
PMC
PopSet
Probe
Protein
Protein Clusters
PubChem BioAssay
PubChem Compound
PubChem Substance
PubMed
SNP
Sparcle
SRA
Structure
Search
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
Training & Tutorials
Variation
to NCBI
Center for Biotechnology Information advances science and health by providing access to
d genomic information.
NCBI | Mission | Organization | NCBI News & Blog
Submit
a or manuscripts
atabases
Download
Transfer NCBI data to your computer
Learn
Find help documents, attend a class or watch a tutorial
Develop
APIs and code
build applications
Analyze
Identify an NCBI tool for your data analysis task
Research
Explore NCBI research and collaborative projects
Popular Resources
PubMed
Bookshelf
PubMed Central
BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem
NCBI News & Blog
November 13 NCBI Minute: Resources for next-gen sequence analysis
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
GenBank release 234 is available

NCBI Resources How To

Gene

Gene KSRP

Un exemple d'un gène d'intérêt

Create RSS Save search Advanced

Gene sources
Genomic

Categories
Alternatively spliced
Annotated genes
Non-coding
Protein-coding

Sequence content
CCDS
Ensembl
RefSeq
RefSeqGene

Status clear
✓ Current

Clear all

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

Selectionner une espèce

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 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

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.,
```

› Dessiner les couples d'amorces sur Primer - Blast):

1. Copier la sequence codante obtenue précédemment.

2. Dans la section «Primer Parameters»,fixer les paramètres suivants: taille de l'amplicon, temperature d'hybridation de l'amorce (Tm).

3. Dans la section «Exon/intron selection», fixer le parameter suivant: presence ou non d'un saut d'exon.

4. Cliquer sur «Get Primers» pour lancer la recherche.

5. Dans la section «Graphical view of primer pairs», verifier que l'amorce se trouve à cheval sur 2 exons.

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

AGAGTGCTCCGCGGCCGTGTGGAGCGAGGCCTTGTTCCCGCGTTGAGCCGCCGCCGCCGCCGCCGCCTCC
TCAGCTTCAGCCTCCGCGCCAGGCCCGGCCCCGCCGCGCCATGTCGGACTACAGCACGGGAGGACCCCCG
CCCGGGCCGCCGCCGCCCGCCGGCGGGGGCGGGGGAGCCGGAGGCGCCGGGGGAGGCCCTCCGCCGGGCC
CGCCAGGCGCGGGGGACCGGGGCGGCGGCGGTCCCGGCGGCGGCGGCCCGGGCGGGGGGTCGGCCGGGGG
CCCCTCTCAGCCACCCGGCGGAGGCGGCCCGGGAATCCGCAAGGACGCTTTCGCCGACGCCGTGCAGCGG
GCCCGCCAGGTGAGGAGGCCGAGGCCCTGAGCGCCCCGCTCGCGCGCGCGCGCGCAGGCGGGGCGAGGGGCG
GGGGTCACGTGCGCGCGCGCGCGCAGGGTCGCGGAGGGGGGCCGGGGCCGTCGCGGGGTCACGTGGCGG
TAGGCGGGGGCCTGGCCCTCCCGCTGCGCCTCGAGTGGGATCCCAACGGGTGACCCCCCTGCAGGGAGTA
GGGGCGCACTGGGGGTCACCAGGAGCGGCGCCTGGGTGTGCAGGCGCCCCGGAGCTCGGAGACGCACTTT
TGGGACCCCCCCCTTAGCCCCCCGGCCTTAGGACATGCCTGGAGGCAGGGGTCCACCTTCCCGGGCGGAG
GGCCTTTACTCTCCCCTCCATATCAGGGCAAAGGGCAGTGTTTGCCCCCAACCCAGTCCCATTTCTGTCC
CCTCTCTAGGAGAAAGGGACATTGTGGGGCTGGGAGGGACAGTCCTTCCTCTTCAGTCGGGAAAGTGGAT
GGGGACCTGTCTAGGGCTGAGCACTTGGGCGAAATGGGGAAGACGAGCATGGGGACTGGCTCTTGGATGC
TTTGGTGGCTTGAAAGCGTGGTCTGTCTCTTTGGGGGAAAGAAGGGAGGGTCTCCCACCCCCGTGTATTG
AGGCGTAATGACAAGGAAGTGTCACATGCTGCTAGGACTGACCTCTCCAGCTCCATTTGCAGCCTCCCCA
TGGCCTGGAGGGGTGGGGGTCGGTAGAATGGGAGGACTTTGCCGCCGACCGGCTCCTGGGCTGTCCCAAT
GCCTCCGGGGCTAGAGACTGGCTCCTCCCAAGGTGGGAGGTCCCGTTAAGTGAACGCCTGTGTTCTGGCC
CTCTGTCGTCTCTCTCACCCTTGGAGTTGGGTGGGTTCTAGCGTGCATTTGGTCTTATTGCCCATGGAAC
CGTCTGATTCTGGGACAGCTTGAAGGGAGGAAGCTGGTGCTGTCAGTTGGTGGGGACAGGCCCCCTGTGG
GCATCCCATGAGTTTTGGCTCTAGGGCAGCGTAGAAAAATGGAGACTGGTGGAAAGGGAGATTCTTAACA
TGGTTTGGGTTTCTAAACCCCAGACTCTGATCCTAAGTTTGCTGGGTTGAGGTTTCTTTAAAGTTGCTCT
TCACGTGTCTGAGATGTAACTTGTGTCCCATAGAGTCTTGGTTTTTTGTTTGTTTGTTTGTTTTTTGGAA
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

6. Dans la section «Detailed primer reports», verifier que:

- Les amerces aient une taille d'environ 20 paires de bases (pb).
- La taille de l'amplicon soit comprise entre 70 et 120 (voire 150) pb.
- La temperature d'hybridation de l'amorce (Tm) à la sequence codante soit le plus proche de 60°C (temperature optimale).
- La difference de Tm des amerces forward et reverse n'excède pas 4°C.
- L'amorce se termine par une base forte (G ou C) en 3'.
- Il n'y ait pas:
- Plus de 2 bases fortes (G ou C) dans les 3 dernières bases en 3'.
- Plus de 3 bases fortes (G ou C) dans les 6 dernières bases en 3'
- Ou de G en 5'.
- Il y ait plus de C que de G dans l'amorce.
- Le pourcentage de GC soit inférieur à 60%.
- Le pourcentage de GC soit approximativement le meme dans les amorces
forward et reverse.

U.S. National Library of Medicine | NCBI National Center for Biotechnology Information

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

Amorces PCR

› *Tumeur :*

Gène	*Séquence 5' - 3'*	*Référence GenBank®*	*Longueur de l'amplicon (pb)*
Glut1 (Slc2a1)	Fwd : TGC CTT GGA TGT CCT ATC TG Rev : ACC AGG GCC TAC TTC AAA GA	NM_011400.3	71
Hprt (Hprt)	Fwd : CAG GCC AGA CTT TGT TGG AT Rev : TTG CGC TCA TCT TAG GCT TT	NM_013556.2	147
Ppia (Ppia)	Fwd : AGC ATA CAG GTC CTG GCA TC Rev : TTC ACC TTC CCA AAG ACC AC	NM_008907.1	127
Tweak (Tnfsf12)	Fwd : GCT ACG ACC GCC AGA TTG GG Rev : GCC AGC ACA CCG TTC ACC AG	NM_011614.3	130
Vegfa (Vegfa)	Fwd : CAC CCA CGA CAG AAG GAG AG Rev : TCT CAA TCG GAC GGC AGT AG	NM_001025250.3	87