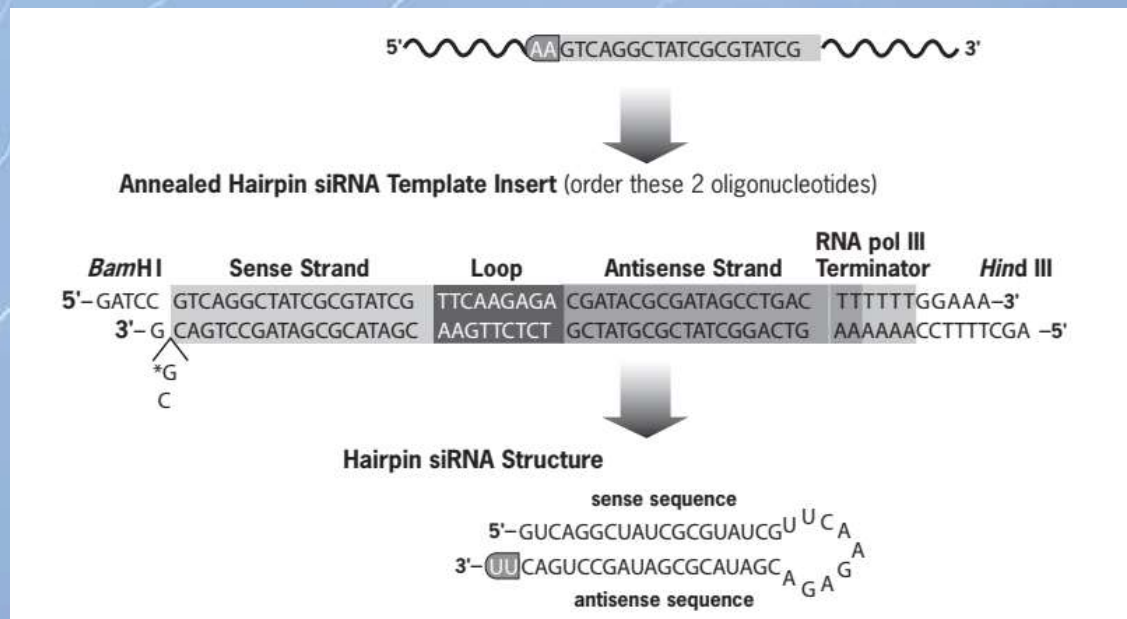




Молекулярна фізіологія: вісцеральні системи

Тема 9. Практикум: основи біоінформатики для дослідження експресії генів

Олексій Болдирєв

Інститут фізіології ім. О.О. Богомольця
НАН України
«Моя наука»



Що можна робити?

- Підбір праймерів
- Підбір shRNA (кшРНК)
- Аналіз фрагменту на сайти рестрикції
- Пошук послідовності для транскрипційних факторів

Пошук гена

Gene

Gene

trpm8

Search

Create RSS Save search Advanced

Gene sources

Genomic

Categories

Alternatively spliced

Annotated genes

Protein-coding

Pseudogene

Sequence content

CCDS

Ensembl

RefSeq

RefSeqGene

Status

Current

Clear all

Show additional filters

Tabular 20 per page Sort by Relevance

Send to

Filters: [Manage Filters](#)

Results by taxon

Top Organisms [\[Tree\]](#)

Homo sapiens (50)

Mus musculus (25)

Rattus norvegicus (14)

Micropterus salmoides (10)

Oreochromis aureus (10)

All other taxa (1448)

[More...](#)

Find related data

Database: [Select](#)

[Find items](#)

Search details

trpm8[All Fields] AND alive[prop]

GENE

Was this helpful?



[TRPM8 – transient receptor potential cation channel subfamily M member 8](#)

[Homo sapiens \(human\)](#)

Also known as: LTRPC8, LTrpC-6, TRPP8, trp-p8

Gene ID: 79054

[RefSeq transcripts \(5\)](#)

[RefSeq proteins \(5\)](#)

[PubMed \(171\)](#)

[Orthologs](#)

[Genome Data Viewer](#)

[BLAST](#)

[Download](#)

RefSeq Sequences



Search results

Items: 1 to 20 of 1557

[First](#) [Prev](#) Page 1 of 78 [Next](#) [Last](#)

See also 42 discontinued or replaced items

Пошук потрібного виду

Search results

Items: 1 to 20 of 1557

<< First < Prev Page 1 of 78 Next > Last >>

 See also 42 discontinued or replaced items.

Name/Gene ID	Description	Location	Aliases	MIM
☐ TRPM8 ID: 79054	transient receptor potential cation channel subfamily M member 8 [<i>Homo sapiens</i> (human)]	Chromosome 2, NC_000002.12 (233917373..234019522)	LTRPC6, LTrpC-6, TRPP8, trp-p8	606678
☐ Trpm8 ID: 171382	transient receptor potential cation channel, subfamily M, member 8 [<i>Mus musculus</i> (house mouse)]	Chromosome 1, NC_000067.7 (88234457..88316575)	CMR1, LTRPC6, LTrpC-6, TRPP8, Trp-p8	
☐ Trpm8 ID: 171384	transient receptor potential cation channel, subfamily M, member 8 [<i>Rattus norvegicus</i> (Norway rat)]	Chromosome 9, NC_051344.1 (88897039..88990167)	CMR1	
☐ TRPM8 ID: 424025	transient receptor potential cation channel subfamily M member 8 [<i>Gallus gallus</i> (chicken)]	Chromosome 7, NC_052538.1 (5594840..5670551)		
☐ TRPM8 ID: 101808218	transient receptor potential cation channel subfamily M member 8 [<i>Ficedula albicollis</i> (Collared flycatcher)]	Chromosome 7, NC_021679.1 (1008035..1042821, complement)		
☐ TRPM8 ID: 486170	transient receptor potential cation channel subfamily M member 8 [<i>Canis lupus familiaris</i> (dog)]	Chromosome 25, NC_051829.1 (45800006..45703702)		
☐ Trpm8 ID: 100337634	transient receptor potential cation channel subfamily M member 8 [<i>Cavia porcellus</i> (domestic guinea pig)]			
☐ TRPM8 ID: 100429414	transient receptor potential cation channel subfamily M member 8 [<i>Macaca mulatta</i> (Rhesus monkey)]	Chromosome 12, NC_041765.1 (121363089..121462405)		
☐ TRPM8 ID: 541151	transient receptor potential cation channel subfamily M member 8 [<i>Bos taurus</i> (cattle)]	Chromosome 3, NC_037330.1 (113586057..113677902)		
☐ TRPM8 ID: 480037	transient receptor potential cation channel subfamily M member 8 [<i>Oes troglodyes</i>]	Chromosome 2B, NC_036881.1 (420500085..420603050)	CK820_G0010776	

Rattus norvegicus transient receptor potential cation channel, subfamily M, member 8 (Trpm8), mRNA

NCBI Reference Sequence: NM_134371.3

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

Go to: ☒

LOCUS NM_134371 4165 bp mRNA linear ROD 12-JAN-2022

DEFINITION Rattus norvegicus transient receptor potential cation channel, subfamily M, member 8 (Trpm8), mRNA.

ACCESSION NM_134371

VERSION NM_134371.3

KEYWORDS RefSeq.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM [Rattus norvegicus](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 4165)

AUTHORS Huang Y, Li S, Jia Z, Li S, He W, Zhou C, Zhang R, Xu R, Sun B, Ali DW, Michalak M, Chen XZ and Tang J.

TITLE TRIM4 interacts with TRPM8 and regulates its channel function through K423-mediated ubiquitination

JOURNAL J Cell Physiol 236 (4), 2934-2949 (2021)

PUBMED [33037615](#)

REMARK GeneRIF: TRIM4 interacts with TRPM8 and regulates its channel function through K423-mediated ubiquitination.

REFERENCE 2 (bases 1 to 4165)

AUTHORS Luo QQ, Wang B, Chen X, Qiu HY, Li WT, Yan XJ and Chen SL.

TITLE Acute stress induces visceral hypersensitivity via glucocorticoid receptor-mediated membrane insertion of TRPM8: Involvement of a non-receptor tyrosine kinase Pyk2

JOURNAL Neurogastroenterol Motil 32 (10), 1514-1528 (2020)

PUBMED [32391653](#)

REMARK GeneRIF: Acute stress induces visceral hypersensitivity via glucocorticoid receptor-mediated membrane insertion of TRPM8: Involvement of a non-receptor tyrosine kinase Pyk2.

REFERENCE 3 (bases 1 to 4165)

AUTHORS Lai H, Liu C, Hou L, Lin W, Chen T and Hong A.

Transcript exon combination :: AY072788.2 [ECO:0000332]
 RNAseq introns :: mixed/partial sample support
 SAMD00132277, SAMD00132295
 [ECO:0000350]

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	230-386	JACYVU010000215.1	21994565-21994721	
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	1401-1691	JACYVU010000215.1	22017507-22017797	
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	2800-2977	JACYVU010000215.1	22033410-22033587	
	2978-3168	JACYVU010000215.1	22043606-22043796	
	3169-3268	JACYVU010000215.1	22048361-22048460	
	3269-3302	JACYVU010000215.1	22049878-22049911	
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ORIGIN

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Формат FASTA

transcription fac... glo376_Supp.pdf W Ukrainian dance... Contra v3 Molecular Biol... NEB Tm Calcula... NEBcutter V2.0 NM_134371.3 - Trpm8 transient... Rattus norvegicus

← → ↻ 🔒 https://www.ncbi.nlm.nih.gov/nuccore/NM_134371.3?report=fasta ☆

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An official website of the United States government Here's how you know

NIH National Library of Medicine
National Center for Biotechnology Information Log in

Nucleotide Nucleotide Search Advanced Help

FASTA = Send to: Change region shown Customize view

Rattus norvegicus transient receptor potential cation channel, subfamily M, member 8 (Trpm8), mRNA

NCBI Reference Sequence: NM_134371.3
[GenBank](#) [Graphics](#)

>NM_134371.3 Rattus norvegicus transient receptor potential cation channel, subfamily M, member 8 (Trpm8), mRNA
AGAGAAGCTCTTGGCTGTTTGAGCAGCTCCACGGCAAGATGCTCTCGAGGGAGCCAGGCTCAGCATGAG
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Analyze this sequence
Run BLAST
Pick Primers
Highlight Sequence Features

Articles about the Trpm8 gene
TRPM4 interacts with TRPM8 and regulates its channel function through K4 [J Cell Physiol. 2021]
TRPM8-regulated calcium mobilization plays a critical role in synergistic che [Theranostics. 2020]
Acute stress induces visceral hypersensitivity via glucocorticoid re [Neurogastroenterol Motil. 2020]
See all

Reference sequence information
RefSeq alternative splicing

11:23 11.05.2022 ENG

Пошук праймерів

transcription fac... glo376_Supp.pdf Ukrainian dance... Contra v3 Molecular Biol... NEB Tm Calcula... NEBcutter V2.0 NM_134371.3 - T... Tpm8 transient... Primer design: x

https://www.ncbi.nlm.nih.gov/tools/primer-blast/index.cgi?ORGANISM=NM_134371.3&LJ=

Статистика @my_sci... ВікіпедіяПрокт:Укра...

Primer-BLAST

A tool for finding specific primers

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

Primers for target on one template Primers common for a group of sequences

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

PCR Template

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

NM_134371.3

Or, upload FASTA file Огляд... Файл не вибрано.

Range ? Clear

Forward primer From To

Reverse primer From To

Primer Parameters

Use my own forward primer (5' to 3' on plus strand) ? Clear

Use my own reverse primer (5' to 3' on minus strand) ? Clear

PCR product size Min Max

70 1000

of primers to return

10

Primer melting temperatures (T_m) Min Opt Max Max T_m difference ?

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 Primer must span an exon-exon junction ?

Exon junction match Min 5' match Min 3' match Max 3' match

7 4 8

Minimal and maximal 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 ?

11:25 11.05.2022 ENG

Специфічність праймерів

transcription fac... glo376_Supp.pdf Ukrainian dance... Contra v3 Molecular Biol... NEB Tm Calcula... NEBcutter V2.0 NM_134371.3... Tpm8 transient... Primer design: x

← → ↺ https://www.ncbi.nlm.nih.gov/tools/primer-blast/index.cgi?ORGANISM=10116&INPUT_SEQUENCE=NM_134371.3&UI... Штатистика @my_sci... ВікіпедіяПродуктУкра... Інші закладки

Intron inclusion
Intron length range

7 4 8
Minimal and maximal number of bases that must anneal to exons at the 5' or 3' side of the junction
☐ Primer pair must be separated by at least one intron on the corresponding genomic DNA
Min 1000 Max 10000

Note: Parameter values that differ from the default are highlighted in yellow

Primer Pair Specificity Checking Parameters

Specificity check ☒ Enable search for primer pairs specific to the intended PCR template
Search mode Automatic
Database Refseq mRNA
Exclusion ☐ Exclude predicted Refseq transcripts (accession with XM, XR prefix) ☐ Exclude uncultured/environmental sample sequences
Organism 10116 Add organism
Enter an organism name (or organism group name such as enterobacteriaceae, rodents), taxonomy id or select from the suggest
Entrez query (optional)
Primer specificity stringency
Primer must have at least 2 total mismatches to unintended targets, including at least 2 mismatches within the last 5 bps at the 3' end
Ignore targets that have 6 or more mismatches to the primer
Max target amplicon size 4000
Allow splice variants ☐ Allow primer to amplify mRNA splice variants (requires refseq mRNA sequence as PCR template input)
Get Primers
Show results in a new window ☐ Use new graphic view
Note: Parameter values that differ from the default are highlighted in yellow
+ Advanced parameters

mispinned product size deviation
Splice variant handling
Get Primers
Advanced parameters

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11:26 11.05.2022

Є праймери!

Graphical view of primer pairs



Detailed primer reports

Primer pair 1

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	GAGAAGCTCTTGGCTGTTGA	Plus	21	2	22	58.50	47.62	4.00	1.00
Reverse primer	GACAGAGGTGTTGATGGCTTTC	Minus	22	998	977	59.51	50.00	3.00	2.00
Product length	997								
Exon junction	980/981 (reverse primer) on template NM_134371.3								

Products on intended targets

>NM_134371.3 Rattus norvegicus transient receptor potential cation channel, subfamily M, member 8 (Trpm8), mRNA

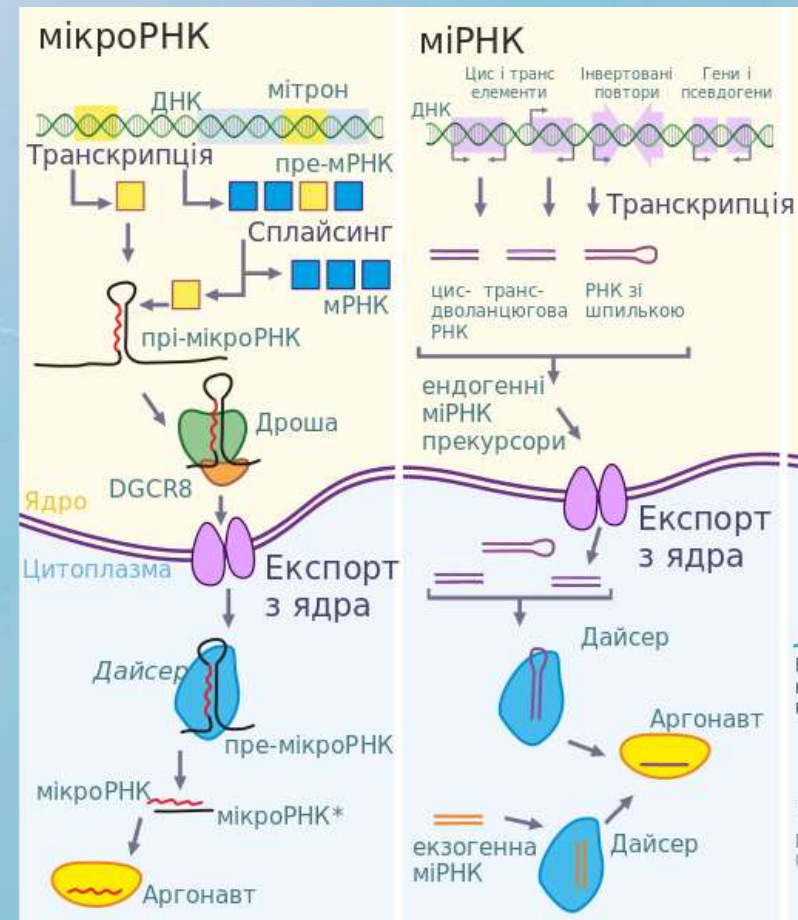
product length = 997

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Forward primer 1 GAGAAGCTCTTGGCTGTTGA 21
Template       2 ..... 22

Reverse primer 1 GACAGAGGTGTTGATGGCTTTC 22
Template       998 ..... 977
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Заглушення роботи гену

- РНК-інтерференція
- CRISPR-Cas



Малі шпилькові РНК (shRNA)

5' ~~~~~ AA GTCAGGCTATCGCGTATCG ~~~~~ 3'



Annealed Hairpin siRNA Template Insert (order these 2 oligonucleotides)

<i>Bam</i> HI	Sense Strand	Loop	Antisense Strand	RNA pol III Terminator	<i>Hind</i> III
5'–GATCC	GTCAGGCTATCGCGTATCG	TTCAAGAGA	CGATACGCGATAGCCTGAC	TTTTTTGGAAA–3'	
3'–G	CAGTCCGATAGCGCATAGC	AAGTTCTCT	GCTATGCGCTATCGGACTG	AAAAAACCTTTTCGA –5'	

$\swarrow$
 *G
 C



Hairpin siRNA Structure

sense sequence

5'–GUCAGGCUAUCGCGUAUCG^U^U^C^A

3'–^{UU}CAGUCCGAUAGCGCAUAGC^A^G^A^G

antisense sequence

Пошук послідовності

Journal List > PLoS One > PMC4366198

PLOS ONE



PLoS One, 2015; 10(3): e0118870.

Published online 2015 Mar 19. doi: [10.1371/journal.pone.0118870](https://doi.org/10.1371/journal.pone.0118870)

PMCID: PMC4366198

PMID: [25789740](https://pubmed.ncbi.nlm.nih.gov/25789740/)

Knockdown of Glutamate Cysteine Ligase Catalytic Subunit by siRNA Causes the Gold Nanoparticles-Induced Cytotoxicity in Lung Cancer Cells

Min Liu, Yunkue Zhao, and Xiumei Zhang*

Pedro V. Baptista, Academic Editor

• Author information • Article notes • C

Transfection of siRNA in A549 cell line

This article has been cited by other articles

Associated Data

• Supplementary Materials

Gene silencing of GCLC was performed using a siRNA knockdown system. A non-specific control siRNA duplex [5'-UUCUCCGAACGUGUCACGUTT-3'], GCLC siRNA-1 duplex [5'-GCUAAUGAGUCUGACCAUU (dTdT)-3'], GCLC siRNA-2 duplex [5'-CUAUGUGGUGU UUGUGGUA (dTdT)-3'] and GCLC siRNA-3 duplex [5'-GUAGUAUUCUGAACUACCU (dTdT)-3'] were purchased from the Sigma—Aldrich. In brief, A549 cells were plated into 6-well plates at a density of 1.5×10^5 per well. The next day, cells (~60–70% confluence) in each well were transfected with the negative control, GCLC siRNA (75pmol in free of FBS RPMI1640) using Thermo Scientific DharmaFECT Transfection Reagents (Thermo Scientific) according to the manufacturer's instructions. One day later, the medium was changed to normal growth medium and the cells were cultured for an additional 48 hours. The transfected cells were collected and used for PCR, western blot analysis, and GSH levels measurement [25–27].



GCLC [ред.]
Матеріал з Вікіпедії — вільної енциклопедії

GCLC (англ. *Glutamate-cysteine ligase catalytic subunit*) — білок, який кодується однойменним геном, розташованим у людей на короткому плечі 6-ї хромосоми.^[d] Довжина поліпептидного ланцюга білка становить 637 амінокислот, а молекулярна маса — 72 766^[d].

Кодований геном білок для функцій належить до **лигаз**, **фосфопротеїнів**. Задіяний у такому біологічному процесі, як ацетилювання. Білок має сайт для зв'язування з АТФ, нуклеотидами.

Література [ред.]

- Gipp J.J., Chang C., Mulcahy R.T. (1992) Cloning and nucleotide sequence of a full-length cDNA for human liver gamma-glutamylcysteine synthetase... *Biochem. Biophys. Res. Commun.* **185**: 29 — 35. *PubMed* DOI:10.1006/0250-0160(92)0537777g
- The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC)... *Genome Res.* **14**: 2121 — 2127. 2004. *PubMed* DOI:10.1101/gr.2596504g
- Mulcahy R.T., Gipp J.J. (1995) Identification of a putative antioxidant response element in the 5'-flanking region of the human gamma-glutamylcysteine synthetase heavy subunit gene... *Biochem. Biophys. Res. Commun.* **209**: 227 — 233. *PubMed* DOI:10.1006/brc.1995.1493g
- Misra I., Griffith O.W. (1998) Expression and purification of human gamma-glutamylcysteine synthetase. *Protein Expr. Purif.* **13**: 268 — 275. *PubMed* DOI:10.1006/prep.1998.0897g
- Hamilton D., Wu J.H., Alarou-Jamali M., Batist G. (2003) A novel missense mutation in the gamma-glutamylcysteine synthetase catalytic subunit gene causes both decreased enzymatic activity and glutathione production... *Blood* **102**: 725 — 730. *PubMed* DOI:10.1182/blood-2002-11-3622g
- Beutler E., Gelbart T., Kondo T., Matsunaga A.T. (1999) The molecular basis of a case of gamma-glutamylcysteine synthetase deficiency... *Blood* **94**: 2890 — 2894. *PubMed*

Примітки [ред.]

- ↑ Human PubMed Reference g.
- ↑ Mouse PubMed Reference g.
- ↑ HUGO Gene Nomenclature Committee. HGNC 43111g (англ.). Процитовано 6 вересня 2017.
- ↑ UniProt, P48506g (англ.). *Архів оригіналу* за 1 вересня 2017. Процитовано 6 вересня 2017.

Див. також [ред.]

- Хромосома 6

 Це незавершена стаття про білок.
Ви можете допомогти проекту, виправивши або дописавши її.

GCLC

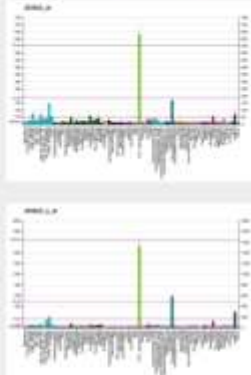
Ідентифікатори

Символи GCLC, GCL, GCS, GLCL, GLCLC, glutamate-cysteine ligase catalytic subunit

Зовнішні ID OMIM: 606857 MGI: 104990 HomoloGene: 1148 GeneCards: GCLC

Онтологія гена [показати]

Шаблон експресії



Більше даних

Ортологи

Види	Людина	Миша
Entrez	2720	14620
Ensembl	ENSG000000001084	ENSMUSG000000032386
UniProt	P48506	P67484

GCLC glutamate-cysteine ligase catalytic subunit [*Homo sapiens* (human)]

Gene ID: 2728, updated on 24-Apr-2022

[Download Datasets](#)

Summary

Official Symbol	GCLC provided by HGNC
Official Full Name	glutamate-cysteine ligase catalytic subunit provided by HGNC
Primary source	HGNC:HGNC:4311
See related	Ensembl:ENSG000000001084 MIM:606857 AllianceGenome:HGNC:4311
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominidae; Homo
Also known as	GCL; GCS; GLCL; GLCLC
Summary	Glutamate-cysteine ligase, also known as gamma-glutamylcysteine synthetase is the first rate-limiting enzyme of glutathione synthesis. The enzyme consists of two subunits, a heavy catalytic subunit and a light regulatory subunit. This locus encodes the catalytic subunit, while the regulatory subunit is derived from a different gene located on chromosome 1p22-p21. Mutations at this locus have been associated with hemolytic anemia due to deficiency of gamma-glutamylcysteine synthetase and susceptibility to myocardial infarction [provided by RefSeq, Oct 2010]
Expression	Ubiquitous expression in liver (RPKM 39.8), urinary bladder (RPKM 19.1) and 24 other tissues See more
Orthologs	mouse all
NEW	Try the new Gene table Try the new Transcript table

Table of contents

- Summary
- Genomic context
- Genomic regions, transcripts, and products
- Expression
- Bibliography
- Phenotypes
- Variation
- Pathways from PubChem
- Interactions
- General gene information
 - Markers, Homology, Gene Ontology
- General protein information
- NCBI Reference Sequences (RefSeq)
- Related sequences
- Additional links
 - Locus-specific Databases

Genome Browsers

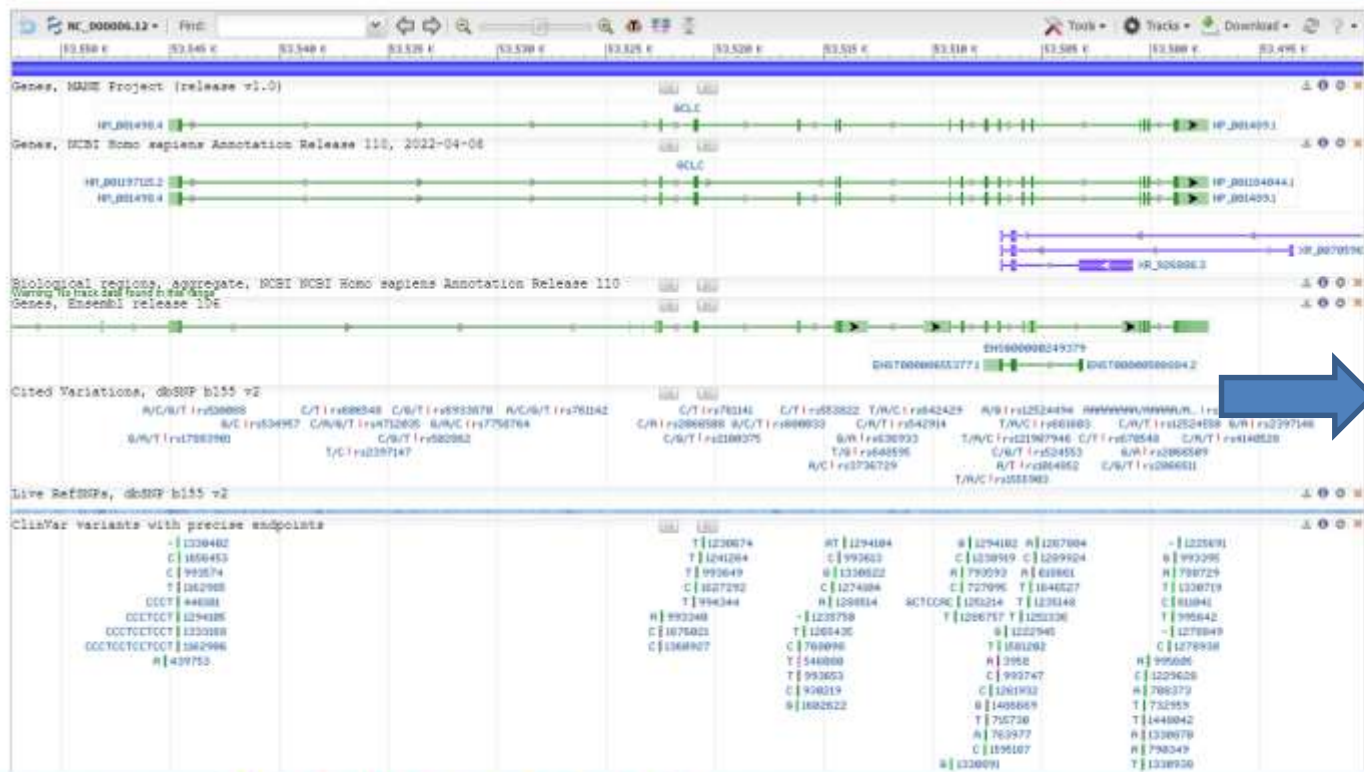
Genome Data Viewer

Genomic context

Genomic Sequence: NC_000006.12 Chromosome 6 Reference GRCh38 p14 Primary Assembly

Go to reference sequence details

Go to nucleotide: Graphics FASTA GenBank



- BioAssays, RNA Target, Active
- BioAssays, RNA Target, Tested
- BioProjects
- BioSystems
- CCDS
- ClinVar
- Conserved Domains
- dbVar
- Full text in PMC
- Full text in PMC_nucleotide
- Functional Class
- Gene neighbors
- Genes with a similar H3K4me3 profile
- Genome
- GEO Profiles
- GTR
- HomoloGene
- MedGen
- Nucleotide
- OMIM
- Probe
- Protein
- PubChem Compound
- PubChem Substance
- PubMed
- PubMed (GeneRIF)
- PubMed (OMIM)
- PubMed(nucleotide/PMC)

HomoloGene

HomoloGene

Search

Limits Advanced

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Display Settings: HomoloGene

Send to: +

Links from Gene

HomoloGene:1148. Gene conserved in Opisthokonta

Genes

Genes identified as putative homologs of one another during the construction of HomoloGene.

GCLC, *H.sapiens*
glutamate-cysteine ligase, catalytic subunit
GCLC, *P.troglodytes*
glutamate-cysteine ligase, catalytic subunit
GCLC, *M.musculus*
glutamate-cysteine ligase, catalytic subunit
GCLC, *C.lupus*
glutamate-cysteine ligase, catalytic subunit
GCLC, *B.taurus*
glutamate-cysteine ligase, catalytic subunit
Gcl, *M.musculus*
glutamate-cysteine ligase, catalytic subunit
Gcl, *R.norvegicus*
glutamate-cysteine ligase, catalytic subunit
GCLC, *G.gallus*
glutamate-cysteine ligase, catalytic subunit
gcl, *X.tropicalis*
glutamate-cysteine ligase, catalytic subunit
gcl, *D.rexo*
glutamate-cysteine ligase, catalytic subunit
Gcl, *D.melanogaster*
Glutamate-cysteine ligase catalytic subunit
AgAP_AGAP001512, *A.gambiae*
AgAP_AGAP001512
gcs-1, *C.elegans*
gcs-1
GSH1, *S.cerevisiae*
GSH1
XLA_AGAP001512, *A.gambiae*

Proteins

Proteins used in sequence comparisons and their conserved domain architectures.

NP_001489.1
637 aa
XP_001155030.1
637 aa
XP_001108943.1
637 aa
XP_852845.1
637 aa
NP_001077143.1
605 aa
NP_034425.1
637 aa
NP_036947.1
637 aa
XP_418910.3
583 aa
NP_001072803.1
637 aa
NP_954971.2
631 aa
NP_525005.2
717 aa
XP_321610.3
649 aa
NP_485027.2
654 aa
NP_012434.1
678 aa
XP_457311.1

Download Links

BLAST(n)

transcript... glx376_Su... W Ukrain... Contr... Molec... NEB T... NEBou... NM_1... Trpni... Rattus... Primer... W Flyra... Gcic g... Rattus... Nuc... Knock... + -

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=MegaBlast&PROGRAM=blastn&BLAST_PROGRAMS=megaBlast 90% ☆

Статистика @my_sci... ВікіпедіяПрокт.Укра... Інші закладки

BLAST blastn suite Home Recent Results Saved Strategies Help

blastn blastp blastx tblastn tblastx

Align Sequences Nucleotide BLAST

BLASTn program search nucleotide subjects using a nucleotide query, more... Reset page Bookmark

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) Clear Query subrange

NM_012815.2 From To

Or, upload file Огляд... Файл не вибрано

Job Title Enter a descriptive title for your BLAST search

Align two or more sequences

Enter Subject Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) Clear Subject subrange

>gi
GCTAATGAGCTGACCAIT From To

Or, upload file Огляд... Файл не вибрано

Program Selection

Optimize for

☒ Highly similar sequences (megablast)

☐ More dissimilar sequences (discontiguous megablast)

☐ Somewhat similar sequences (blastn)

Choose a BLAST algorithm

BLAST Search nucleotide sequence using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window



Nucleotide

Nucleotide ▾

Advanced

Search

Help

GenBank ▾

Send to: ▾

Change region shown ▾

Customize view ▾

Rattus norvegicus glutamate-cysteine ligase, catalytic subunit (Gclc), mRNA

NCBI Reference Sequence: NM_012815.2

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

Go to: ☒

LOCUS NM_012815 3079 bp mRNA linear ROD 1
DEFINITION Rattus norvegicus glutamate-cysteine ligase, catalytic subunit (Gclc), mRNA.
ACCESSION NM_012815
VERSION NM_012815.2
KEYWORDS RefSeq.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM [Rattus norvegicus](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 3079)
AUTHORS Zhang S, Li H, Zhang L, Li J, Wang R and Wang M.
TITLE Effects of troxerutin on cognitive deficits and glutamate cysteine ligase subunits in the hippocampus of streptozotocin-induced type 1 diabetes mellitus rats
JOURNAL Brain Res 1657, 355-360 (2017)
PUBMED [27998794](#)
REMARK GeneRIF: Study determined the effects of troxerutin on cognitive deficits and glutamate cysteine ligase subunits (GCLM and GCLC) in the hippocampus of streptozotocin-induced type 1 diabetes mellitus rat: troxerutin alleviates oxidative stress and promotes learning potential in STZ-induced diabetic rats likely through GCL

Find regions of similarity between this sequence and other sequences using BLAST.

Analyze this sequence ▴

Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

Articles about the Gclc gene ▴

Effects of troxerutin on cognitive deficits and glutamate cysteine ligase subunit [Brain Res. 2017]

Epigenetic modifications of Nrf2-mediated glutamate-cysteine ligase [Free Radic Biol Med. 2014]

Schisandra Chinensis Baillon regulates the gene expression of phase II antioxidant [Nutr Res Pract. 2014]

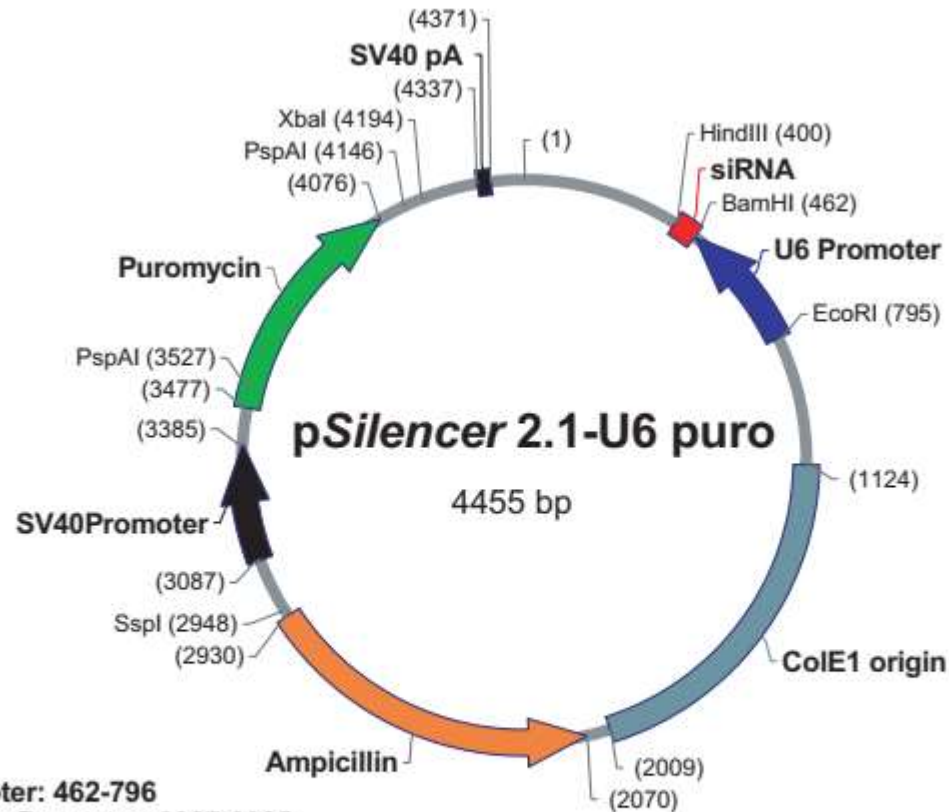
See all...

Reference sequence information ▴

RefSeq alternative splicing

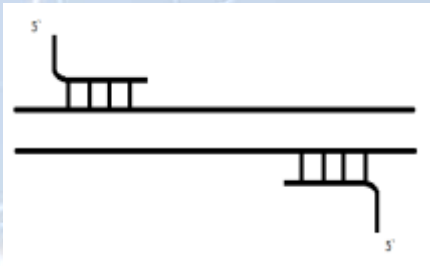
See the other reference mRNA sequence splice variants for Gclc (XM_039080870.1).

Клонування до вектору



U6 Promoter: 462-796
SV40 early Promoter: 3087-3385
Puromycin: 3477-4076
SV40 early pA signal: 4337-4371
Ampicillin: 2070-2930
ColE1 origin: 1124-2009

Можна клонувати й мікроРНК, але...



Constructs		Mature miR-223
miR-223(67)		—
miR-223(87)		—
miR-223(107)		—
miR-223(147)		+
miR-223(187)		+
miR-223(227)		+

- Розмір фрагменту геномної ДНК - 290bp
- for 5'-tatt/ aagctt/ TGTCAGTGGCCATTTTCTTGACAGT
- rev 5'- tatt /ggatcc /TGCACATGGTCCATTACTGCTCC

Інструмент для рестриктаз



NEBcutter V2.0

Try the updated [NEBcutter V3.0](#)

Program
Guide

Help

Comments

This tool will take a DNA sequence and find the large, non-overlapping open reading frames using the E.coli genetic code and the sites for all Type II and commercially available Type III restriction enzymes that cut the sequence just once. By default, only enzymes available from NEB are used, but other sets may be chosen. Just enter your sequence and "submit". Further options will appear with the output. **The maximum size of the input file is 1 MByte, and the maximum sequence length is 300 KBases.**

[What's new in V2.0](#) [Citing NEBcutter](#)

Local sequence file: Файл не вибрано.

GenBank number: [\[Browse GenBank\]](#)

or paste in your DNA sequence: *(plain or FASTA format)*

Standard sequences:
Plasmid vectors
Viral + phage

The sequence is: ☒ Linear ☐ Circular

Enzymes to use:
☒ NEB enzymes
☐ All commercially available specificities
☐ All specificities
☐ All + defined oligonucleotide sequences
☐ Only defined oligonucleotide sequences
[\[define oligos\]](#)

Minimum ORF length to display: a.a.

Name of sequence: *(optional)*

Earlier projects:

Note: Your earlier projects will be deleted 2 days after they were last accessed.
You need to have cookies enabled in your browser for this feature to work.

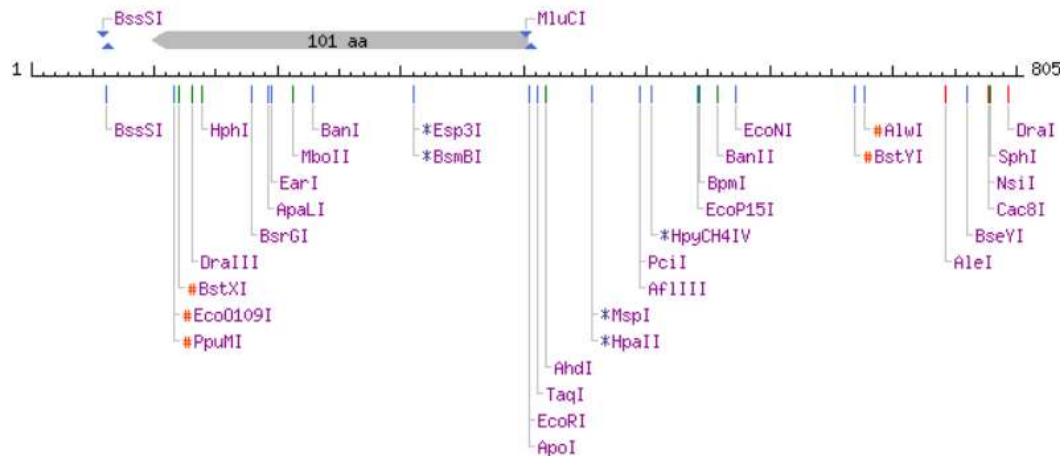
Результат

Linear Sequence: *unnamed sequence*

[Help](#)

[Comments](#)

Cleavage code	Enzyme name code
⌵ blunt end cut	Available from NEB
⌵ 5' extension	Has other supplier
⌵ 3' extension	Not commercially available
⌵ cuts 1 strand	*: cleavage affected by CpG meth.
	#: cleavage affected by other meth.
	(enz.name): ambiguous site



Main options

New DNA
Custom digest
View sequence
ORF summary
Save project
Print

Availability

All commercial
All

Display

2 cutters
3 cutters

Zoom

Zoom in
More...

List

0 cutters
1 cutters
All sites
Save all sites
Flanking enzymes

Minimum ORF length to display: 100 aa.

Пошук сайтів для транскрипційних факторів



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ConTra v3

Visualization and exploration of predicted transcription factor binding sites

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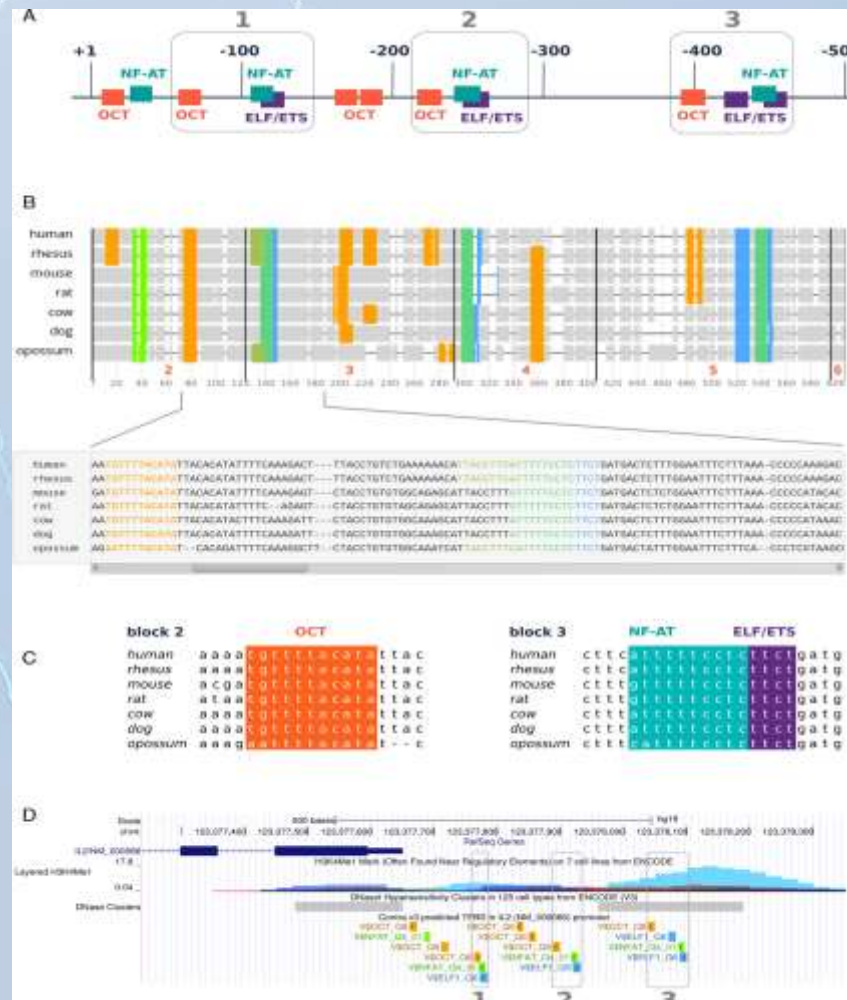
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Figure 1. Analysis of the human IL2 promoter with ConTra v3 in exploration mode followed by visualization of a ...



Як має виглядати

Type of analysis:	exploration
Reference organism:	Human (<i>Homo sapiens</i>)
Transcript:	GABARAPL1 chr12:10365488, number of introns: 3, NM_031412
Sequence parts:	promoter, upstream 1000bp
Motif database:	_all_
Email address:	none specified

Below you can find the results. You can also [download zip package](#).

Filter	Matrix ID	TF	PWM db	p-value	q-value	IC	Consensus	RP rank	HS rank	CE r
Select				<=	<= 0.25	>= 5		<=	<=	<=
☐	V\$ATF6_01	ATF6	TRANSFAC20113	7.45040e-4	0.0308757	8.997	TGACGTGG	1	24	3
☐	V\$CREBP1CJUN_01	ATF2:c-Jun	TRANSFAC20113	0.0027338	0.0377650	8.641	TGACGYA	2	25	4
☐	MA0967.1	BZIP60	JASPAR_CORE_2016	0.0058484	0.0484737	6.893	TGACGTCA	3	26	5
☐	MA0018.2	CREB1	JASPAR_CORE_2016	0.0101197	0.0698965	5.547	TGACGYCA	4	27	6
☐	V\$CREB_01	CREB	TRANSFAC20113	0.0155379	0.0919882	7.787	TGACGTMA	5	28	7

Як виглядає

bioinf2.irc.ugent.be/contrav3/#/results/2e102ca351f3ab52ed374aa77d0d351f

Inflammation Research Center
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ConTra v3

Visualization and exploration of predicted transcription factor binding sites

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Type of analysis: **exploration**
Reference organism: **Human (Homo sapiens)**
Transcript: **TRPM8 chr2:234826042, number of introns: 25, NM_024080**
Sequence parts: **promoter, upstream 1500bp**
Motif database: **_all_**
Email address: **none specified**

RE-RUN

Below you can find the results. You can also [download zip package](#).

Filter	Matrix ID	TF	PWM db	p-value	q-value	IC	Consensus	RP rank	HS rank	CE rank
Select				<=	<= 0,25	>= 5		<=	<=	<=
☐	V\$SP2_01	SP2	TRANSFAC20113	0.0010631	0.0807928	8.537	RGCGGGGAC	2	1	21

Select the stringency **core = 0.95, similarity matrix = 0.85**

RUN VISUALIZATION

Menu
[Parameters](#)
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