

Search NCBI databases - NCBI x National Center for Biotechnol... x

https://www.ncbi.nlm.nih.gov/search/all/?term=BRCA 1%20 90%

NIH U.S. National Library of Medicine National Center for Biotechnology Information shamim_cst

Search NCBI BRCA 1 x Search

NCBI Databases

Results found in 23 databases for **BRCA 1**

Did you mean [brca1](#) ?

Literature	Genes	Genetics
Bookshelf 0	Gene 579	ClinVar 427
MeSH 1	GEO DataSets 1,238	dbGaP 0
NLM Catalog 1	GEO Profiles 14,896	dbSNP 0
PubMed 2,290	HomoloGene 0	dbVar 0
PubMed Central 14,037	PopSet 6	GTR 40
	UniGene 1	MedGen 2
		OMIM 18

https://www.ncbi.nlm.nih.gov/uniGene/?term=BRCA 1

Nucleotide is selcted

Search NCBI databases - NCBI x BRCA 1 - Nucleotide - NCBI x DNA & RNA - Site Guide - NCBI x National Center for Biotechnol... x

https://www.ncbi.nlm.nih.gov/nuccore/?term=BRCA 1 110%

NCBI Resources How To shamim_cst My NCBI Sign Out

Nucleotide Nucleotide BRCA 1 Search Create alert Advanced Help

The Nucleotide database will include EST and GSS sequences in early 2019. [Read more.](#)

Species: Animals (955), Plants (264), Fungi (233), Protists (101), Bacteria (237), Customize ...

Molecule types: genomic, DNA/RNA (1,305), mRNA (833), Customize ...

Source databases: INSDC (GenBank), GenBank, FASTA, Graphics

Summary 20 per page Sort by Default order Send to: Filters: [Manage Filters](#)

See [BRCA1 \(BRCA 1\) BRCA1, DNA repair associated in the Gene database](#)
[brca 1 reference sequences](#) Genomic (1) Transcript (6) Protein (5)

Items: 1 to 20 of 2213

Found 2215 nucleotide sequences. Nucleotide (2213) EST (2)

[Arabidopsis thaliana chromosome 4 sequence](#)

1. 18,585,056 bp linear DNA
 Accession: CP002687.1 GI: 332656411
[Assembly](#) [BioProject](#) [BioSample](#) [Protein](#) [PubMed](#) [Taxonomy](#)

Results by taxon

Top Organisms [Tree](#)

- synthetic construct (414)
- Escherichia coli (225)
- Homo sapiens (151)
- Eothenomys melanogaster (62)
- Crocidura beccarii (23)
- All other taxa (1338)

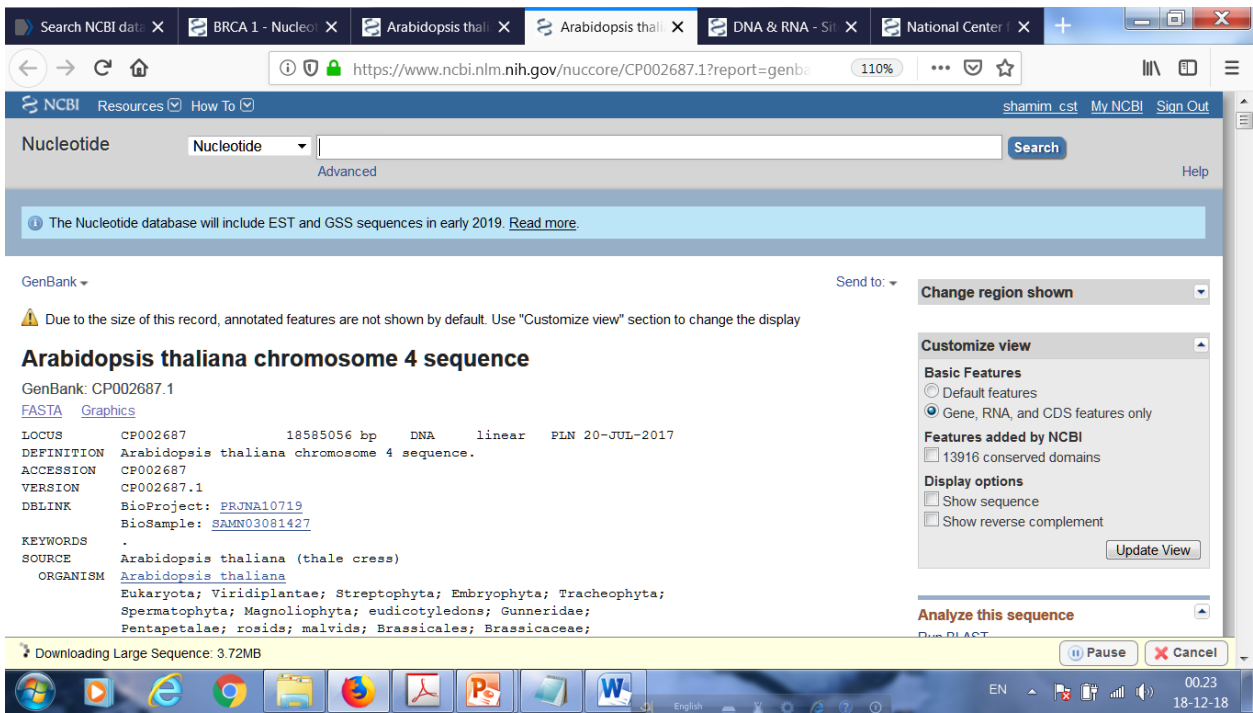
More...

Find related data

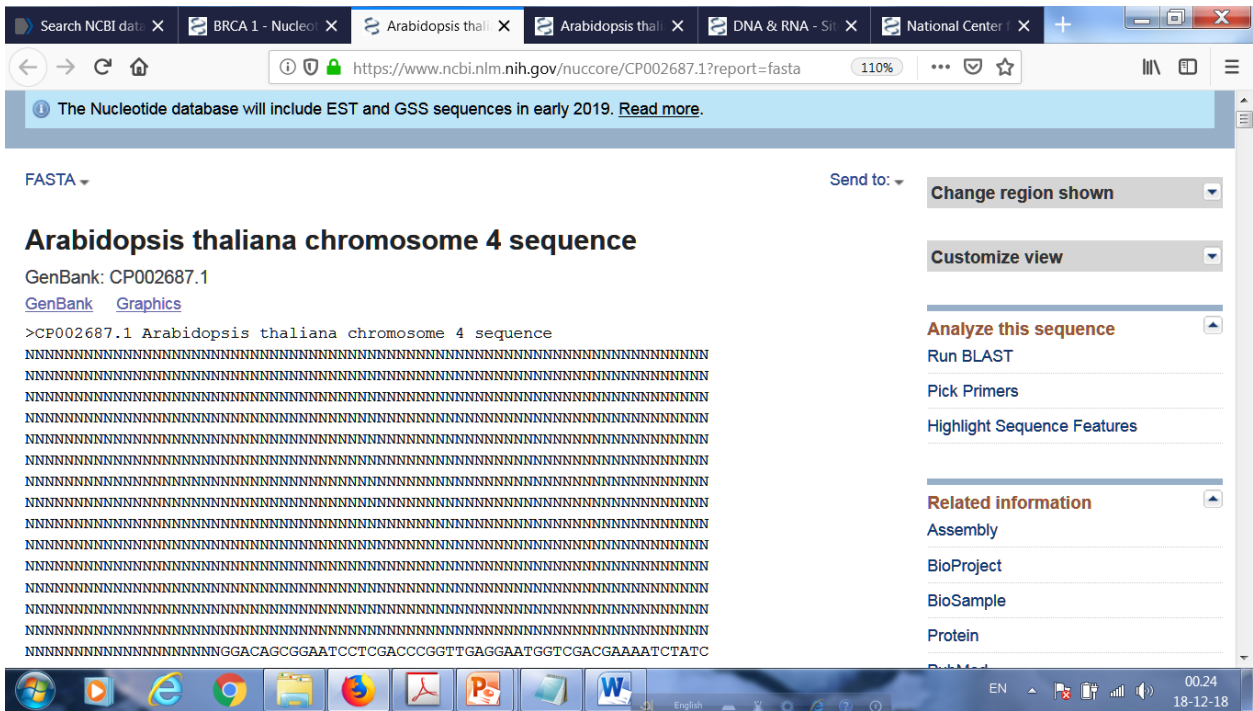
Database: Select

00:18 18-12-18

Genbank is selected



FASTA is selected



Search NCBI | BRCA 1 - Nuc | Arabidopsis | Arabidopsis | DNA & RNA | g1p3 - Nuc | Synthetic con | g1p3 gene

https://www.ncbi.nlm.nih.gov/nuccore/?term=g1p3

Viruses (1)
Customize ...

Molecule types
genomic
DNA/RNA (12)
mRNA (17)
Customize ...

Source databases
INSDC (GenBank) (15)
RefSeq (15)
Customize ...

Sequence length
Custom range

See [IFI6 \(G1P3\) interferon alpha inducible protein 6](#) in the Gene database
g1p3 reference sequences [Transcript \(4\)](#) [Protein \(4\)](#)

Items: 1 to 20 of 30

<< First < Prev Page 1 of 2 Next > Last >>

1 Found 99 nucleotide sequences. Nucleotide (30) EST (67) GSS (2)

1. [Synthetic construct Homo sapiens clone FLH141188.01L interferon alpha-inducible protein \(G1P3\) mRNA, partial cds](#)
393 bp linear mRNA
Accession: AY892940.1 GI: 60654332
[Protein](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

Results by taxon

Top Organisms []

- Homo sapiens (1)
- synthetic constru
- Pan troglodytes (
- Macaca fascicula
- Pan paniscus (1)
- All other taxa (4)

More...

Find related data

Database:
Select

Find items

Search NCBI | BRCA 1 - Nuc | Arabidopsis | Arabidopsis | DNA & RNA | g1p3 - Nuc | Synthetic | g1p3 gene

https://www.ncbi.nlm.nih.gov/nuccore/AY892940.1?report=fasta

Synthetic construct Homo sapiens clone FLH141188.01L interferon alpha-inducible protein (G1P3) mRNA, partial cds

GenBank: AY892940.1

[GenBank](#) [Graphics](#)

>AY892940.1 Synthetic construct Homo sapiens clone FLH141188.01L interferon alpha-inducible protein (G1P3) mRNA, partial cds

```

ATGCGGCAGAAGGCGGTATCGCTTTTCTTGTGCTACCTGCTGCTCTTCACTTGCAGTGGGGTGGAGGCAG
GTAAGAAAAGTGCFCGGAGAGCTCGGACAGCGGCTCCGGGTTCTGGAAGGCCCTGACCTTCATGGCGGT
CGGAGGAGGACTCGCAGTCGCCGGGCTGCCCGCGCTGGGCTTCACCGCGCCCGCATCGCGGCCAACTCG
GTGGCTGCCTCGCTGATGAGCTGGTCTGCGATCCTGAATGGGGCGCGGCTGCCCGCCGGGGGCTAGTGG
CCACGCTGCAGAGCCTCGGGGCTGGTGGCAGCAGCGTCGTCATAGGTAATATTGGTGCCCTGATGGGCTA
CGCCACCCACAAGTATCTCGATAGTGAGGAGGATGAGGAGTTG

```

Slected blstx

Gip3 sequence found from FASTA

BLAST Results

Job title: Nucleotide Sequence (393 letters)

RID: 1FV5FGGD01R (Expires on 12-19 01:36 am)

Query ID	Ic Query_324479	Database Name	nr
Description	None	Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	nucleic acid	Program	BLASTX 2.8.1+ Citation
Query Length	393		

Other reports: [Search Summary](#) [Taxonomy reports](#)

Graphic Summary

Show Conserved Domains

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

RF +1 Specific hits

Tr1-6-16

Questions/comments

Select first red line

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

RF #1
Specific hits
Superfamilies

Ifi-6-16
Ifi-6-16 superfamily

Distribution of the top 100 Blast Hits on 100 subject sequences

Mouse over to see the title, click to show alignments

Color key for alignment scores

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

Query

1 70 140 210 280 350

Homo sapiens interferon, alpha-inducible protein (clone..
Score:224 Evalue:1.9e-73
Accession:AAP36492.1
Alignment

Questions/comments

Download GenPept Graphics

Homo sapiens interferon, alpha-inducible protein (clone IFI-6-16), partial [synthetic construct]
Sequence ID: [AAP36492.1](#) Length: 131 Number of Matches: 1
[See 3 more title\(s\)](#)

Range 1: 1 to 131

Score	Expect	Method	Identities	Positives	Gaps	Frame
224 bits(571)	2e-73	Compositional matrix adjust.	131/131(100%)	131/131(100%)	0/131(0%)	+1

Query 1 MRQKAVSLFLCYLLLF TCSGVEAGKKKCESSESDSGSFWKALTFMavggglavaglpalg 180
Sbjct 1 MRQKAVSLFLCYLLLF TCSGVEAGKKKCESSESDSGSFWKALTFMavggglavaglpalg 60

Query 181 FTGAGIAANSVAASLMSWSAILNGGGVPAGGLVATLQSLGAGGSSVVIIGNIGALMGYATH 360
Sbjct 61 FTGAGIAANSVAASLMSWSAILNGGGVPAGGLVATLQSLGAGGSSVVIIGNIGALMGYATH 120

Query 361 KYLDSEDEEL 393
Sbjct 121 KYLDSEDEEL 131

Download GenPept Graphics

interferon alpha-inducible protein 6 isoform a precursor [Homo sapiens]
Sequence ID: [NP_002029.3](#) Length: 130 Number of Matches: 1
[See 12 more title\(s\)](#)

Questions/comments

BLAST » blastx » RID-1FV5FGGD01R [Home](#) [Recent Results](#) [Saved Strategies](#) [Help](#)

BLAST Results

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#) [YouTube](#) [How to read this page](#) [Blast report description](#)

Job title: Nucleotide Sequence (393 letters)

RID [1FV5FGGD01R](#) (Expires on 12-19 01:36 am)
Query ID Icl|Query_324479
Description None
Molecule type nucleic acid
Query Length 393

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTX 2.8.1+ [Citation](#)

Other reports: [Search Summary](#) [Taxonomy reports](#)

Graphic Summary

Show Conserved Domains

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

RF +1
Specific hits



[Questions/comments](#)

Search NCBI databases - NCBI X Genes & Expression - Site Guide X

https://www.ncbi.nlm.nih.gov/guide/genes-expression/

NCBI Resources How To shamim_cst My NCBI Sign Out

NCBI National Center for Biotechnology Information

All Databases 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

Genes & Expression

All Databases Downloads Submissions Tools How To

Databases

BioProject (formerly Genome Project)
A collection of genomics, functional genomics, and genetics studies and links to their resulting datasets. This resource describes project scope, material, and objectives and provides a mechanism to retrieve datasets that are often difficult to find due to inconsistent annotation, multiple independent submissions, and the varied nature of diverse data types which are often stored in different databases.

BioSystems
Database that groups biomedical literature, small molecules, and sequence data in terms of biological relationships.

ClinVar
A resource to provide a public, tracked record of reported relationships between human variation and observed health status with supporting evidence. Related information

Quick Links

- BioProject (formerly Genome Project)
- BioSystems
- Database of Genotypes and Phenotypes (dbGaP)
- Gene
- Gene Expression Omnibus (GEO) Database
- Gene Expression Omnibus (GEO) Datasets
- Gene Expression Omnibus (GEO) Profiles
- Online Mendelian Inheritance in Man (OMIM)

23.24 17-12-18

Search NCBI databases - NCBI X DNA & RNA - Site Guide - NCBI X Home - Gene - NCBI X Home - BioSystems - NCBI X

https://www.ncbi.nlm.nih.gov/guide/dna-rna/

NCBI Resources How To shamim_cst My NCBI Sign Out

NCBI National Center for Biotechnology Information

All Databases 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

DNA & RNA

All Databases Downloads Submissions Tools How To

Databases

Assembly
A database providing information on the structure of assembled genomes, assembly names and other meta-data, statistical reports, and links to genomic sequence data.

BioCollections
A curated set of metadata for culture collections, museums, herbaria and other natural history collections. The records display collection codes, information about the collections' home institutions, and links to relevant data at NCBI.

BioProject (formerly Genome Project)
A collection of genomics, functional genomics, and genetics studies and links to their resulting datasets. This resource describes project scope, material, and objectives and provides a mechanism to retrieve datasets that are often difficult to find due to inconsistent annotation, multiple independent submissions, and the varied nature of diverse data types

Quick Links

- BioProject (formerly Genome Project)
- Database of Short Genetic Variations (dbSNP)
- GenBank
- Nucleotide Database
- PopSet
- RefSeqGene
- Reference Sequence (RefSeq)
- Sequence Read Archive (SRA)
- Trace Archive

23.29 17-12-18

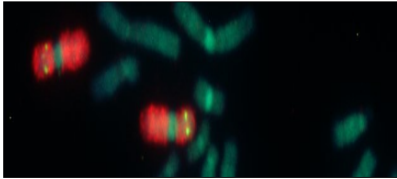
Search NCBI databases - NCBI | DNA & RNA - Site Guide - NCBI | Home - Gene - NCBI | Home - BioSystems - NCBI

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

NCBI Resources How To shamim_cst My NCBI Sign Out

Gene Search

Advanced Help



Gene

Gene integrates information from a wide range of species. A record may include nomenclature, Reference Sequences (RefSeqs), maps, pathways, variations, phenotypes, and links to genome-, phenotype-, and locus-specific resources worldwide.

Using Gene	Gene Tools	Other Resources
Gene Quick Start	Submit GeneRIFs	HomoloGene
FAQ	Submit Correction	OMIM
Download/FTP	Statistics	RefSeq
RefSeq Mailing List	BLAST	RefSeqGene
Gene News	Genome Workbench	UniGene
Fastshot	Salmon	Protein Clusters

Windows taskbar: 23.29 17-12-18

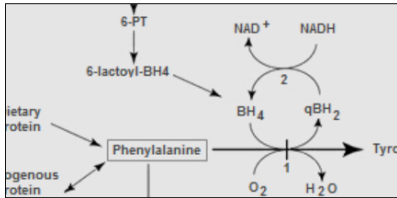
Search NCBI databases - NCBI | DNA & RNA - Site Guide - NCBI | Home - Gene - NCBI | Home - BioSystems - NCBI

https://www.ncbi.nlm.nih.gov/biosystems/

NCBI Resources How To shamim_cst My NCBI Sign Out

BioSystems Search

Limits Advanced Help



BioSystems

The NCBI BioSystems Database provides integrated access to biological systems and their component genes, proteins, and small molecules, as well as literature describing those biosystems and other related data throughout Entrez.

Using BioSystems	BioSystem Tools	Other Resources
About Biosystems	Tools Overview	Entrez Gene
How To (Quick Start) Guides	FLink Frequency-weighted Links	Entrez Protein
Help	E-Utilities (Entrez programming utilities)	PubChem
FTP		GEO Gene Expression

Windows taskbar: 23.30 17-12-18

Search NCBI data x DNA & RNA - Sit x Home - Nucleoti x RefSeq: NCBI Ref x Home - Gene - N x Home - BioSyste x

https://www.ncbi.nlm.nih.gov/guide/dna-rna/ 120%

Downloads

[BLAST \(Stand-alone\)](#)
 BLAST executables for local use are provided for Solaris, LINUX, Windows, and MacOSX systems. See the README file in the ftp directory for more information. Pre-formatted databases for BLAST nucleotide, protein, and translated searches are also available for downloading under the db subdirectory.

[FTP: BLAST Databases](#)
 Sequence databases for use with the stand-alone BLAST programs. The files in this directory are pre-formatted databases that are ready to use with BLAST.

[FTP: FASTA BLAST Databases](#)
 Sequence databases in FASTA format for use with the stand-alone BLAST programs. These databases must be formatted using formatdb before they can be used with BLAST.

[FTP: GenBank](#)
 This site contains files for all sequence records in GenBank in the default flat file format. The files are organized by GenBank division, and the full contents are described in the README.genbank file.

EN 23:31 17-12-18

Search NCBI data x DNA & RNA - Sit x Home - Nucleoti x RefSeq: NCBI Ref x Home - Gene - N x Home - BioSyste x

https://www.ncbi.nlm.nih.gov/nucleotide 110%

NCBI Resources How To shamim_cst My NCBI Sign Out

Nucleotide Nucleotide Search

Advanced Help

The Nucleotide database will include EST and GSS sequences in early 2019. [Read more.](#)

Nucleotide

The Nucleotide database is a collection of sequences from several sources, including GenBank, RefSeq, TPA and PDB. Genome, gene and transcript sequence data provide the foundation for biomedical research and discovery.

Using Nucleotide	Nucleotide Tools	Other Resources
Quick Start Guide	Submit to GenBank	GenBank Home
FAQ	LinkOut	RefSeq Home
Help	E-Utilities	Gene Home

EN 23:31 17-12-18

Search NCBI data x DNA & RNA - Sit x Home - Nucleoti x RefSeq: NCBI Ref x Home - Gene - N x Home - BioSystem x

https://www.ncbi.nlm.nih.gov/refseq/ 110%

NCBI Resources How To shamim_cst My NCBI Sign Out

RefSeq RefSeq Search

RefSeq: NCBI Reference Sequence Database

A comprehensive, integrated, non-redundant, well-annotated set of reference sequences including genomic, transcript, and protein.

Using RefSeq	RefSeq Access	RefSeq projects
About RefSeq	Human Genome Resources and Download	Consensus CDS (CCDS)
Human Reference Genome	RefSeq FTP	RefSeq Functional Elements
Prokaryotic RefSeq Genomes	RefSeq genomes FTP	RefSeqGene
FAQ	New RefSeq genomic (last 30 days)	Targeted Loci
NCBI Handbook	New RefSeq transcripts (last 30 days)	Virus Variation
Factsheet	New RefSeq proteins (last 30 days)	

EN 23:32 17-12-18

get protein from DNA sequenc... X ExPASy - Translate tool X Translate Tool - Results of tran... X

https://web.expasy.org/translate/

Home | Contact

Translate

Translate tool

New translate tool, please test!
Use the [ExPASy contact form](#) to submit feedback and bug reports

Translate is a tool which allows the translation of a nucleotide (DNA/RNA) sequence to a protein sequence.

Please enter a DNA or RNA sequence in the box below (numbers and blanks are ignored).

```

ATGCGGCAGAAAGCGGTATCGCTTTTCTTGTGCTACCTGGTGTCTTCACTTGCAGTGGGTGGAGGCAG
GTAAGAAAAGTGTCTCGGAGAGCTCGGACAGCGGCTCCGGGTTCTGGAAGCCCTGACCTTCATGGCCCT
CGGAGGAGGACTCGCAGTCCCGGGCTGCCCGGCTGGGCTTACCGGGCGCCGGCATCGCGCCCACTCG
GTGGTGCCTCGCTGATGAGCTGGTCTGCGATCCTGAATGGGGGGCGGCTGCCCGCGGGGGCTAGTGG
CCACGCTGCAGAGCCTCGGGGCTGGTGGCAGCAGCCTCGTCATAGGTAATATTGGTCCCTGATGGGCTA
CGCCACCCACAAGTATCTCGATAGTGAGGAGGATGAGGAGTTG
  
```

Output format: Verbose ("Met" "Stop" spaces between residues)

get protein from DNA sequenc... X Translate Tool - Results of tran... X Translate Tool - Results of tran... X

https://web.expasy.org/cgi-bin/translate/dna_aa

Home | Contact

Translate

Translate Tool - Results of translation

Open reading frames are highlighted in red. Please select one of the following frames - in the next page, you will be able to select your initiator and retrieve your amino acid sequence:

5'3' Frame 1
Met RQKAVSLFLCYLLLFTCSGVEAGKKKCESSESDSGSGFWKALTFMetAVGGGLAVAGLPALGFTGAGIAANSVAASL Met SWSAILNGGG VPAGGLVATLQSLGAGGSSVVIIGNIGAL Met GYATHKYLDSBEDEE

5'3' Frame 2
CGRRRYRFSCATCCSSLAVGWQRVRSARRARTAAPGSGRPSWPSEEDSQSPGCPRWASPAPASRPTRWLPR Stop Stop AGLRS Stop Met GAACPGG Stop WPCRASGLVAAASS Stop VILVP Stop WATPPTSISIVRR Met RS

5'3' Frame 3
AAEGGIAFLVLPAAHLQWGGGR Stop EKVLGELGQRLRVLEGPDLHGRRRRTRSRAARAGLHRRRHRGQLGGCLADELVCDPEWGRR ARRASGHAAEPRGWVQRRHR Stop YWCPDGLRHPQVSR Stop Stop GG Stop GV

3'5' Frame 1
QLLILLTIEILVGGVAHQGTNITYDDAAATSPEALQRGH Stop PPGGHAAPIQDRRPAHQRGSHRVGRDAGAGEAQRGQPGDCSSSDGHE GQGLPEPAAVRLRALFLTCLHPTASEEQVAQEKRRLPH

3'5' Frame 2
NSSSSLSRYLWVA Stop PIRAPILP Met TLLPPAPRLCSVATSPAGTPPPFRDIQLISEAATELAA Met PAPVKPSAGSPATASPPPTA Met K VRAFQNEPLSELSEHFFLPASTPLQVKSSR Stop HKKSDTAFCR

3'5' Frame 3
TPHPPHYRDTGWRSPSGHQYYL Stop RRCCHQPRGSAAWPLAPRRARRPHSGSQTSSSARQPPSWPCRPRR Stop SPARAARRLVLLRRP Stop RSGPSRTRSRCPSSPSTFSYLPHPCK Stop RAAGSTRKAIPPSAA

///

AFTER DELETING FIRST Nucleotide

Translate tool

New translate tool, please test!
Use the [ExPASy contact form](#) to submit feedback and bug reports

Translate is a tool which allows the translation of a nucleotide (DNA/RNA) sequence to a protein sequence.

Please enter a DNA or RNA sequence in the box below (numbers and blanks are ignored).

```
TGC GGCAGAAGGCGGTATCGCTTTCTTGTGCTACCTGCTGCTCTCACTGTCAGTGGGGTGGAGGCAGGTAAGAAAAGTGCCTCGGAGAGCTCGGACAGCGGCTCCGGGTTCTGGAAAGCCCTGACCTTCATGGCCGTCGGAGGAGGACTCGCAGTCGCCGGGCTGCCCGCGCTGGGCTTACCCGGCGCCGGCATCGCGGCCAACTCGTTGGCTGCCTCGCTGATGAGCTGGTCTCCGATCCTGAATGGGGCCGGCTGCCCGCCGGGGGGCTAGTGGCCACGCTGCAGAGCTCGGGGCTGGTGGCAGCAGCTCGTCATAGGTAATATTGGTGCCCTGATGGGCTACGCCACCACAAAGTATCTCGATAGTGAGGAGGATGAGGAGTTG
```

Translate Tool - Results of translation

Open reading frames are highlighted in red. Please select one of the following frames - in the next page, you will be able to select your initiator and retrieve your amino acid sequence:

5' Frame 1
CGRRRYRFSCATCCSSLA VGRVQRKSARRARTAAPGSRPStop P S W P S E E D S Q S P G C P R W A S P A P A S R P T R W L P R Stop Stop A G L R S Stop **Met GAACPPGG** Stop W P R C R A S G L V A A A S S Stop V I L V P Stop W A T P P T S I S I V R R **Met R S**

5' Frame 2
AAEGGIAFLVLPAAHLQWGGGRStop EKVLGELGQRLRVLEGPDLHGRRRRTRSRRAARAGLHRRRHRGQLGGCLADELVCDPEWGRRARRGASGHAAEPRGWQQRHRStop YWCPDGLRHPQVSRStop Stop GG Stop GV

5' Frame 3
RQKAVSLFLCYLLFTCSGVEAGKKKCESSDSGSFWKALTF **Met AVGGGLAVAGLPALGFTGAGIAANSVAASL** **Met SWSAILNGGGVP** **AGGLVATLQSLGAGGSSVVIGNIGAL** **Met GYATHKYLDSEDEEL**

3' Frame 1
QLLILLTIEILVGGVAHQGTNITYDDAAATSPEALQRGHStop P P G G H A A P I Q D R R P A H Q R G S H R V G R D A G A G E A Q R G Q P G D C E S S D G H E G Q L P E P G A A V R A L R A L F L T C L H P T A S E E Q Q V A Q E K R Y R L L P

3' Frame 2
N S S S S L S R Y L W V A Stop P I R A P I L P **Met TTLPPAPRLCSVATSPAGTPPPFRDIADQLISEAATELAA** **Met PAPVKPSAGSPATASPPPTA** **Met K VRAFQNPPELSESEHFFLPASTPLQVKSSR** Stop H K K S D T A F C R

3' Frame 3
T P H P P H Y R D T C G W R S P S G H Q Y Y L Stop R R C C H Q P R G S A A W P L A P R R A R R P H S G S Q T S S A R Q P P S W P R C R R R Stop S P A R A A R R L R V L L R R P Stop R S G P S R T R S R C P S S P T F S Y L P P P H C K Stop R A A G S T R K A I P P S A A

After deleting second Nucleotide

Translate tool

New translate tool, please test!
Use the [ExPASy contact form](#) to submit feedback and bug reports

Translate is a tool which allows the translation of a nucleotide (DNA/RNA) sequence to a protein sequence.

Please enter a DNA or RNA sequence in the box below (numbers and blanks are ignored).

```
GCGGCAGAGGCGGTATCGCTTTTCTGTGCTACCTGCTGCTCTTCACTTGCAGTGGGTGGAGGCAG
GTAGAAAAAGTCTCGGAGAGCTCGGACAGCGGCTCCGGGTTCTGGAAGGCCCTGACCTTCATGGCCGT
CGGAGGAGGACTCGCATGTCGCCGGGCTGCCCGGCTGGGCTTCACCGGCGCCGCATCGCGGCCAACTCG
GTGGCTGCTCGTATGAGCTGGTCTGCATCCTGAATGGGGCGGCGCTGCCCGCGGGGGCTAGTGG
CCACGCTCAGAGGCTCGGGGCTGGTGGCAGCAGCTGCTCATAGGTAATATTGGTCCCTGATGGGCTA
CGCCACCCACAGTATCTCGATAGTGGAGGATGAGGAGTGG
```

Output format: Verbose ("Met", "Stop", spaces between residues) ▾
Genetic code: Standard ▾

Reset or **TRANSLATE SEQUENCE**

Translate Tool - Results of translation

Open reading frames are highlighted in red. Please select one of the following frames - in the next page, you will be able to select your initiator and retrieve your amino acid sequence:

53' Frame 1
AAEGGIAFLVLPAAHLQWGGGR Stop EKVLGELGQRLRVLEGPDLHGRRRTRSRRAARAGLHRRRRHRGQLGGCLADE
LVCDPEWGRRARRGASGHAAEPRGWWQQRHR Stop YWCPDGLRHPQVSR Stop Stop GG Stop GV

53' Frame 2
RQKAVSLFLCYLLFTCSGVEAGKKKCESSESDSGSFWKALTF **Met AVGGGLAVAGLPALGFTGAGIAANSVAASL Met S**
WSAILNGGGVPAGGLVATLQSLGAGGSSVVIGNIGAL Met GYATHKYLDSEED E E L

53' Frame 3
GRRRYRFSCATCCSSLAVGWRQVRKSARRARTAAPGSGRP Stop PSWPSEEDSQSPGCPRWASPAPASRPTRWLPR Stop
Stop AGLRS Stop **Met GAACP PG G** Stop WPCRASGLVAAASS Stop VILVP Stop WATPPTSISIVR **Met R S**

3'5' Frame 1
QLLILLTIEILVGGVAHQGTNITYDDAAATSPEALQRGH Stop PPGHAAPIQDRRPAHQRGSHRVGRDAGAGEAQRGQP
GDCESSDGHGQGLPEPGA AVRALRALFLTCLHPTASEEQQVAQEKRYLLP

3'5' Frame 2
NSSSSLSRYLWVA Stop PIRAPILP **Met TLLLPPAPRLCSVATSPAGTPPPFRIADQLISEAATELAA Met PAPVKPSAGSPA**
TASPPPTA Met K VRAFQNP E L S E H F F L P A S T P L Q V K S S R Stop H K K S D T A F C R

3'5' Frame 3
TPHPPHYRDTCGWRSPSGHQYYL Stop RRCCHQPRGSAAWPLAPRRARRPHSGSQTSSARQPPSWPCRRCRRR Stop SPARAA
PRLRVLRRDQVPSGQRTDPSGQSGSTFXYDRRUCKS...DAAGSTRKALRDA