

ΒΑΡΒΑΚΕΙΟ ΠΡΟΤΥΠΟ ΛΥΚΕΙΟ

ΟΜΙΛΟΣ ΒΙΟΛΟΓΙΑΣ
«Βιολογία *in vitro* & *in silico*»

Εισαγωγή στη Βιοπληροφορική

Μαρία Καπασά

Βιολόγος MSc, PhD

BLAST ...

Basic Local Alignment Search Tool

Εργαλείο του NCBI για αναζήτηση ομοιότητας ακολουθιών
Ανάλυση σε βάσεις δεδομένων για DNA & πρωτεΐνες
80,000 περίπου αναζητήσεις καθημερινά

The screenshot shows the NCBI BLAST website. At the top, there is a navigation bar with the NIH logo, "U.S. National Library of Medicine", "NCBI National Center for Biotechnology Information", and a "Sign in to NCBI" link. Below the navigation bar, the "BLAST" logo is on the left, and navigation links for "Home", "Recent Results", "Saved Strategies", and "Help" are on the right. The main content area features a "Basic Local Alignment Search Tool" section with a description: "BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance." A "Learn more" link is provided. To the right of this section is a "NEWS" box with the headline "End of updates for BLAST+ version 4 databases (dbV4)", the subtext "Start moving to the new version 5 databases!", the date "Fri, 27 Sep 2019 16:00:00 EST", and a "More BLAST news..." link. Below the "Basic Local Alignment Search Tool" section is a "Web BLAST" section with three main options: "Nucleotide BLAST" (nucleotide to nucleotide), "blastx" (translated nucleotide to protein), and "tblastn" (protein to translated nucleotide). To the right of these options is a "Protein BLAST" section (protein to protein). At the bottom of the page, there is a "BLAST Genomes" link.

NIH U.S. National Library of Medicine NCBI National Center for Biotechnology Information Sign in to NCBI

BLAST Home Recent Results Saved Strategies Help

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)

NEWS

End of updates for BLAST+ version 4 databases (dbV4)
Start moving to the new version 5 databases!
Fri, 27 Sep 2019 16:00:00 EST [More BLAST news...](#)

Web BLAST

Nucleotide BLAST
nucleotide ► nucleotide

blastx
translated nucleotide ► protein

tblastn
protein ► translated nucleotide

Protein BLAST
protein ► protein

BLAST Genomes

Βασικές έννοιες

Ο Αλγόριθμος BLAST (Basic Local Alignment Search Tool)

Σύγκριση μιας αλληλουχίας έναντι των αλληλουχιών μιας ολόκληρης βάσης δεδομένων.

Ταχύτητα, ακρίβεια και ελεύθερη πρόσβαση διαδικτυακά.

Εύρεση ομοιότητας μια νουκλεοτιδικής ή αμινοξικής αλληλουχίας με κάποια/ες άλλες.

Αναζήτηση ομολόγων, ορθολόγων και παραλόγων.

Ανεύρεση νέων, μη χαρακτηρισμένων αλληλουχιών.

Προσδιορισμός πιθανής λειτουργίας μιας αλληλουχίας.

Εύρεση των δομικών λειτουργικών περιοχών των πρωτεϊνών.

Αναζήτηση μικρών εκφρασμένων αλληλουχιών (ESTs).

Αναζήτηση πολυμορφισμών του ενός νουκλεοτιδίου (SNPs).

Τέσσερα βήματα για μια BLAST αναζήτηση

- (1) Εύρεση αλληλουχίας- αίτημα (query)
 - (2) Επιλογή του κατάλληλου τύπου BLAST
 - (3) Επιλογή της κατάλληλης βάσης δεδομένων
 - (4) Επιλογή άλλων προαιρετικών παραμέτρων
- Και... πατάμε “BLAST”

Βήμα 1: Επιλογή του κατάλληλου τύπου BLAST

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)

Search Betacoronavirus Database

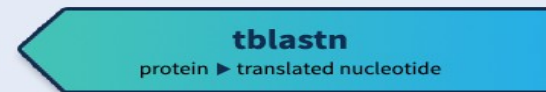
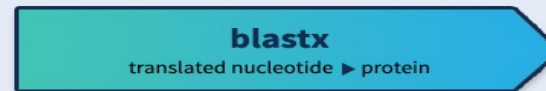
We have created a new BLAST database focused on the SARS-CoV-2 (Severe acute respiratory syndrome coronavirus 2) Sequences. For further detail please visit

[NCBI GenBank.](#)

Mon, 03 Feb 2020 10:00:00 EST

[More BLAST news...](#)

Web BLAST



Είσοδος προγράμματος

blastn

DNA



blastp

protein



blastx

DNA



tblastn

protein



Βάση Δεδομένων

DNA

protein

protein

DNA

Μορφές αλληλουχιών: Παραδείγματα

fasta format:

```
>sp|P01588|EPO_HUMAN ERYTHROPOIETIN PRECURSOR - Homo sapiens
MGVHECPAWLWLLLSLLSLPLGLPVLGAPPRLICDSRVLERYLLEAKEAE
NITTGCAEHCSLNENITVPDTKVNIFYAWKRMEVGQQAVEVWQGLALLSEA
VLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAISPPD
AASAAPLRTITADTFRKLFVYSNFLRGKCLKLYTGEACRTGDR
```

RAW format:

```
MGVHECPAWLWLLLSLLSLPLGLPVLGAPPRLICDSRVLERYLLEAKEAE
NITTGCAEHCSLNENITVPDTKVNIFYAWKRMEVGQQAVEVWQGLALLSEA
VLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAISPPD
AASAAPLRTITADTFRKLFVYSNFLRGKCLKLYTGEACRTGDR
```

Βήμα 3: Επιλογή της Βάσης Δεδομένων

NIH U.S. National Library of Medicine NCBI National Center for Biotechnology Information Sign in to NCBI

BLAST® » blastn suite Home Recent Results Saved Strategies Help

Standard Nucleotide BLAST

Search nucleotide databases using a nucleotide query. [more...](#) [Reset page](#) [Bookmark](#)

Enter Query Sequence
Enter accession number

Or, upload file
Job Title

Align two or more

Choose Search Strategy

Database
Organism
Exclude
Limit to
Entrez Query

- Nucleotide collection (nr/nt)
- Reference RNA sequences (refseq_rna)
- RefSeq Representative genomes (refseq_representative_genomes)
- RefSeq Genome Database (refseq_genomes)
- Whole-genome shotgun contigs (wgs)
- Expressed sequence tags (est)
- Sequence Read Archive (SRA)
- Transcriptome Shotgun Assembly (TSA)
- High throughput genomic sequences (HTGS)
- Patent sequences(pat)
- PDB nucleotide database (pdb)
- Human RefSeqGene sequences(RefSeq_Gene)
- Genomic survey sequences (gss)
- Sequence tagged sites (dbsts)
- Nucleotide collection (nr/nt)

query subrange

transcript databases Betacoronavirus

exclude +

Enter organism name or id—completions will be suggested
Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown


Models (XM/XP) Uncultured/environmental sample sequences

Sequences from type material

[YouTube](#) [Create custom database](#)

Enter an Entrez query to limit search

BLAST results will be displayed in a new format by default
You can always switch back to the Traditional Results page.



Βήμα 4: Επιλογή προαιρετικών παραμέτρων

NIH U.S. National Library of Medicine NCBI National Center for Biotechnology Information Sign in to NCBI

BLAST® » blastn suite Home Recent Results Saved Strategies Help

Standard Nucleotide BLAST

blastn blastp blastx tblastn tblastx

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

Enter Query Sequence

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

Or, upload file Δεν επιλέχθηκε αρχείο.

Job Title 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.):

Organism exclude Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

Exclude Models (XM/XP) Uncultured/environmental sample sequences

Limit to Sequences from type material

Entrez Query [YouTube](#) [Create custom database](#) Enter an Entrez query to limit search

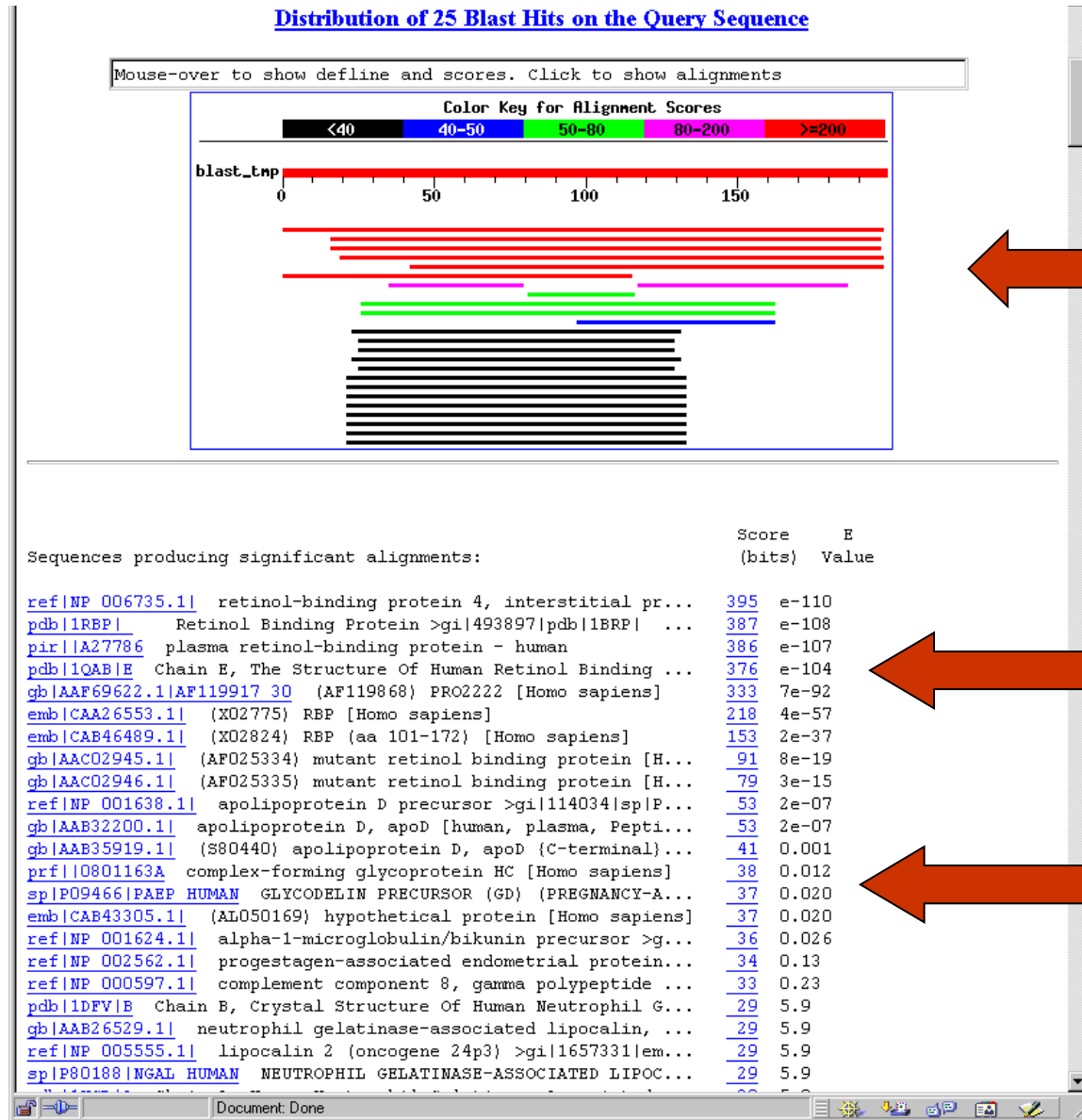
Program Selection

Optimize for Highly similar sequences (megablast) More dissimilar sequences (discontiguous megablast) Somewhat similar sequences (blastn) Choose a BLAST algorithm

The database **Organism** **Filter** **Expect**

BLAST Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)

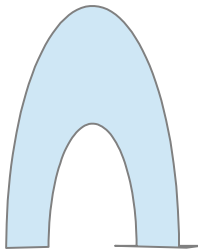
Μορφή παρουσίασης των αποτελεσμάτων BLAST



Graphical Overview
Similarity
Length

High scores
Low e values

Cut-off: 0.05?



$$e = m * n / 2^{\text{bit-score}}$$

m - query sequence length

n - total database length (sum of all sequences)

Bit-score- the required size of a sequence database in which the current match could be found just by chance

Μορφή παρουσίασης των αποτελεσμάτων BLAST

Στοιχισή αλληλουχιών κατά ζεύγη

>[gi|5803139|ref|NP_006735.1](#) retinol-binding protein 4, interstitial precursor [Homo sapiens]
[gi|132404|sp|P02753|RETB_HUMAN](#) PLASMA RETINOL-BINDING PROTEIN PRECURSOR (PRBP) (RBP)
[gi|72085|pir||VAHU](#) plasma retinol-binding protein precursor - human
[gi|35897|emb|CAA24959.1](#) (X00129) precursor RBP [Homo sapiens]
Length = 199

Score = 378 bits (971), Expect = e-104
Identities = 187/199 (93%), Positives = 187/199 (93%)

Query: 1 MKWVXXXXXXXXXXXXXXXXXERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAE 60
MKWV ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAE
Sbjct: 1 MKWVWALLLLAAWAAAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAE 60

Query: 61 FSVDETGQMSATAKGRVRLNNDVDCADMVGTFTDTEPAKFKMKYWGVASFLQKGNDDH 120
FSVDETGQMSATAKGRVRLNNDVDCADMVGTFTDTEPAKFKMKYWGVASFLQKGNDDH
Sbjct: 61 FSVDETGQMSATAKGRVRLNNDVDCADMVGTFTDTEPAKFKMKYWGVASFLQKGNDDH 120

Query: 121 WIVD TDYD TYAVQYSCRLNLDGTCADSYFVFSRDPNGLPPEAQKIVRQRQEELCLARQ 180
WIVD TDYD TYAVQYSCRLNLDGTCADSYFVFSRDPNGLPPEAQKIVRQRQEELCLARQ
Sbjct: 121 WIVD TDYD TYAVQYSCRLNLDGTCADSYFVFSRDPNGLPPEAQKIVRQRQEELCLARQ 180

Query: 181 YRLIVHNGYCDGRSERNLL 199
YRLIVHNGYCDGRSERNLL
Sbjct: 181 YRLIVHNGYCDGRSERNLL 199

Πολλαπλή στοιχισή αλληλουχιών

1_2146	3	WVXXXXXXXXXXXXXXXXXERDCRVSSFRVKENFDKARFSGTWYAMA-----KKDPE	49
132407	5	WALVLLAALGGGSAERDCRVSSFRVKENFDKARFSGLWYAIA-----KKDPE	51
6978523	33	VQENFDVKKYLGRWYEI-----EKIPV	54
6978497	29	QVQENFNEARIYGKWFNLA VGSTCPWLRRIKNKMSVS	65
266619	35	SVPLQPGFWTERFQGRWFVVGLAANAV-----QKERQ	66
6981430	30	VQPNFQQDKFLGRWYSAGLASNSSWF-----REKKE	60
204063	20	VVKDFDISKFLGFWYEIAFAS-----KMGTP	45
13162312	24	VVKDFDISKFLGFWYEIAFAS-----KMGTP	49
576102	2	VVKDFDISKFLGFWYEIAFAS-----KMGTP	27

Βήμα 3: Επιλογή της Βάσης Δεδομένων

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Enter Query Sequence
Enter accession number

Or, upload file
Job Title

Align two or more

Choose Search Strategy

Database
Organism
Optional

Exclude
Optional

Limit to
Optional

Entrez Query
Optional

- Nucleotide collection (nr/nt)
- Reference RNA sequences (refseq_rna)
- RefSeq Representative genomes (refseq_representative_genomes)
- RefSeq Genome Database (refseq_genomes)
- Whole-genome shotgun contigs (wgs)
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query subrange

transcript databases Betacoronavirus

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[YouTube](#) [Create custom database](#)

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- NCBI Home
- Resource List (A-Z)
- All Resources
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- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature
- Proteins
- Sequence Analysis
- Taxonomy
- Training & Tutorials
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[SNP](#)

[Gene](#)

[Protein](#)

[PubChem](#)

Nucleotide

Nucleotide

BRCA2 HUMAN

[Create alert](#) [Advanced](#)

[Help](#)

Species

- Animals (1,776)
- Plants (80)
- Fungi (155)
- Protists (65)
- Bacteria (176)
- Viruses (2)
- Customize ...

Molecule types

- genomic DNA/RNA (2,028)
- mRNA (563)
- Customize ...

Source databases

- INSDC (GenBank) (1,994)
- RefSeq (648)
- Customize ...

Sequence Type

- Nucleotide (2,624)
- EST (35)
- GSS (1)

Genetic

- compartments
- Mitochondrion (1)

Sequence length

Custom range...

Release date

Custom range...

Revision date

Custom range...

[Clear all](#)

[Show additional filters](#)

Summary 20 per page Sort by Default order

Send to:

Filters: [Manage Filters](#)

GENE

Was this helpful?



BRCA2 – BRCA2 DNA repair associated

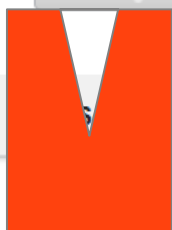
[Homo sapiens \(human\)](#)

Also known as: BRCC2, BROVCA2, FACD, FAD, FAD1, FANCD, FANCD1, GLM3, PNCA2, XRCC11

GeneID: 675

[RefSeq transcripts \(1\)](#) [RefSeq proteins \(1\)](#) [RefSeqGene \(1\)](#) [PubMed \(1,766\)](#)

-
-
-
-



Sequences



Items: 1 to 20 of 2660

<< First < Prev Page of 133 Next > Last >>

[Human breast cancer susceptibility \(BRCA2\) mRNA, complete cds](#)

1. 10,987 bp linear mRNA
Accession: U43746.1 GI: 1161383
[Protein](#) [PubMed](#) [Taxonomy](#)

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

[H.sapiens brca2 gene exon 2 \(and joined coding region\)](#)

2. 1,106 bp linear DNA
Accession: X95152.1 GI: 1171546
[Protein](#) [PubMed](#) [Taxonomy](#)

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

Results by taxon

Top Organisms [Tree](#)

- Homo sapiens (1110)
- unidentified (384)
- Escherichia coli (163)
- Mus musculus (83)
- Rattus norvegicus (29)
- All other taxa (891)

[More...](#)

Find related data

Database:

Search details

```
BRCA2[All Fields] AND ("Homo sapiens"[Organism] OR HUMAN[All Fields])
```

[See more...](#)

Recent activity

[Turn Off](#) [Clear](#)

BRCA2 HUMAN (2660)

Nucleotide

BRCA2 (11289)

Nucleotide

[See more...](#)

NCBI Orthologs [How was this calculated?](#)

0 items

Genes Literature

SEARCH THE TAXONOMY TREE

Enter taxonomic name

- ▾ jawed vertebrates
 - birds
 - alligators and others
 - turtles
 - lizards
 - mammals
 - amphibians
 - coelacanth
 - bony fishes
 - cartilaginous fishes

268 genes for: jawed vertebrates (*Gnathostomata*)

Add to cart **Protein alignment** **Download**

2 selected.

	Species	Gene	Architecture	aa	
<input checked="" type="checkbox"/>	<i>Homo sapiens</i> human	BRCA2 BRCA2 DNA repair associated		3,418	▼
<input checked="" type="checkbox"/>	<i>Mus musculus</i> house mouse	Brca2 breast cancer 2, early onset		3,329	▼
<input type="checkbox"/>	<i>Rattus norvegicus</i> Norway rat	Brca2 BRCA2, DNA repair associated		3,343	▼
<input type="checkbox"/>	<i>Canis lupus familiaris</i> dog	BRCA2 BRCA2 DNA repair associated		3,446	▼
<input type="checkbox"/>	<i>Danio rerio</i> zebrafish	brca2 BRCA2 DNA repair associated		2,874	▼

0 items

Genes

Literature

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268 genes for: jawed vertebrates (*Gnathostomata*)

Add to cart

Protein alignment

Download

2 selected.

Species

Homo sapiens
human

Mus musculus
house mouse

Protein alignment ✕

one sequence per gene (2)

all sequences per gene (6)

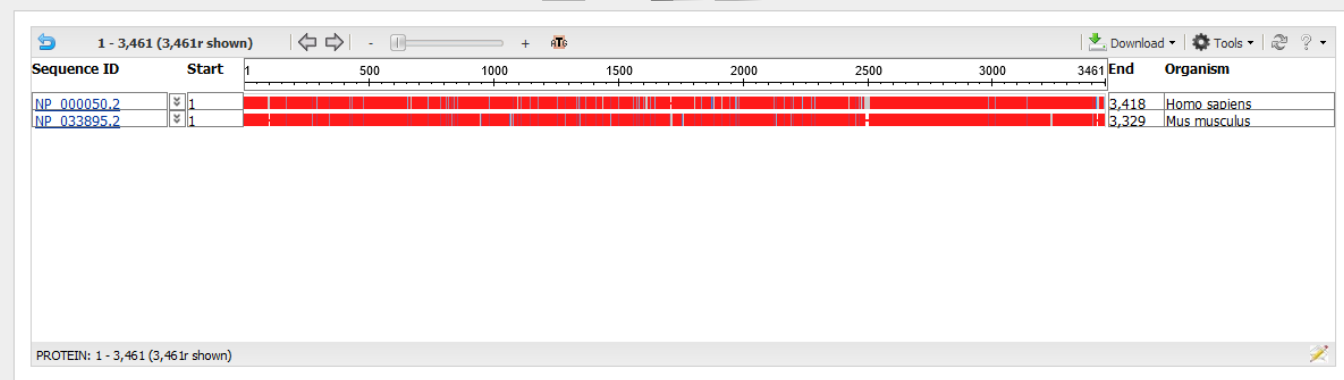
Align

aa

3,418

3,329

BRCA2
breast cancer
early onset



Descriptions Select All [Re-align](#) [Alignment parameters](#)

Accession	Description	Links
<input checked="" type="checkbox"/> NP_000050.2	breast cancer type 2 susceptibility protein [Homo sapiens]	Related Information
<input checked="" type="checkbox"/> NP_033895.2	breast cancer type 2 susceptibility protein homolog [Mus musculus]	Related Information

Alignments Select All [Re-align](#) [Mouse over the sequence identifier for sequence title](#)

View Format: [Compact](#) Conservation Setting: [2 Bits](#)

<input checked="" type="checkbox"/> NP_000050.2	1	MPIGSKERPTFFEIFKTRCNKADLGPISLWNFEELSSEAPPYNSEPAEESKHNNVYENLTKTPQRKPSYNQLASTPII	80
<input checked="" type="checkbox"/> NP_033895.2	1	MPVEYKRRPTFWEIFKARCSTADLGPISLWNFEELSSEAPPYNSEPPPESEYKPHGYEPQLFKTPQRNPPYHQFASTPIM	80
<input checked="" type="checkbox"/> NP_000050.2	81	FKEQGLILPLYSFVKELDKFKLDLGRNVFNSRHKSLRIVTKMDQADDVSCPLLNSCLSESPVVLQCHVTIQRDKSVV	160
<input checked="" type="checkbox"/> NP_033895.2	81	FKERSQILPLDQSPFREL-----GKVVASSKHKTHSKKTKVDFVVDVASPFLKSCLSSEPLTLRCTQAVLQREKPVV	153
<input checked="" type="checkbox"/> NP_000050.2	161	CGSLFHTPKFVGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSTVLIVRNEEASETVFPHDTTANVKSYSFNHDESL	240
<input checked="" type="checkbox"/> NP_033895.2	154	SGSLFYTPKLEGG-QTPKPISESLGVEVDPDMSWSSSLATPPTLSSTVLIVRNEEARSVTPADSPATLKSFCFSNHNESE	232

Nucleotide

Nucleotide

BRCA2 HUMAN

X

Search

Create alert Advanced

Help

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- Orthologs
- Genome Browser
- BLAST
- Download

References

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More...

Find related data

Database:

Find items

Search details

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Search

See more...

Recent activity

Turn Off Clear

BRCA2 HUMAN (2660)

Nucleotide

BRCA2 (11289)

Nucleotide

See more...

Genome Data Viewer

Homo sapiens: GRCh38.p13 (GCF_000001405.39) Chr 13 (NC_000013.11): 32,306,363 - 32,408,349

Reset All Share this page FAQ Help Browser Agreement Version 4.8.2

Genome Data Viewer now supports Haplotype Tag sorting for alignment tracks! Click on track name to access track display options.

Pick Assembly

Switch organism

GCF_000001405.39 (GRCh38.p13)

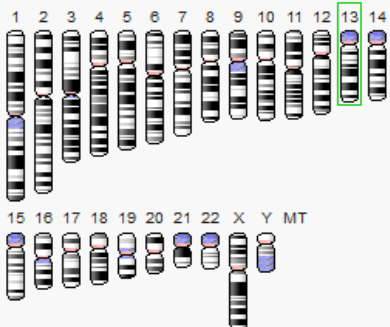
Locations for Gene BRCA2

Sequence	Location
NC_000013.11	32,314,862 - 32,399,850

Select an assembly to change view

Ideogram View

Unplaced/unlocalized scaffolds: 168
Alt loci/patches: 446



Search

Location, gene or phenotype
Enter a location, gene name or phenotype
Search examples:

User Data and Track Hubs

BLAST

Add Tracks



Nucleotide

Nucleotide

BRCA2 HUMAN



Search

Create alert Advanced

Help

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Homo sapiens (human)

Also known as: BRCC2, BROVCA2, FACD, FAD, FAD1, FANCD, FANCD1, GLM3, PNCA2, XRCC11

GeneID: 675

RefSeq transcripts (1) RefSeq proteins (1) RefSeqGene (1) PubMed (1,766)

- Orthologs
- Genome Browser
- BLAST
- Download

RefSeq Sequences



Items: 1 to 20 of 2660

<< First < Prev Page 1 of 133 Next > Last >>

Human breast cancer susceptibility (BRCA2) mRNA, complete cds

1. 10,987 bp linear mRNA
 Accession: U43746.1 GI: 1161383
[Protein](#) [PubMed](#) [Taxonomy](#)

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

H.sapiens brca2 gene exon 2 (and joined coding region)

2. 1,106 bp linear DNA
 Accession: X95152.1 GI: 1171546
[Protein](#) [PubMed](#) [Taxonomy](#)

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

Results by taxon

Top Organisms [Tree]

- Homo sapiens (1110)
- unidentified (384)
- Escherichia coli (163)
- Mus musculus (83)
- Rattus norvegicus (29)
- All other taxa (891)

More...

Find related data

Database: Select

Find items

Search details

BRCA2[All Fields] AND ("Homo sapiens"[Organism] OR HUMAN[All Fields])

Search

See more...

Recent activity

Turn Off Clear

BRCA2 HUMAN (2660)

Nucleotide

BRCA2 (11289)

Nucleotide

See more...

BLAST

NIH

Descriptions

Graphic Summary

Alignments

Taxonomy

Descriptions


Graphic Summary

Alignments

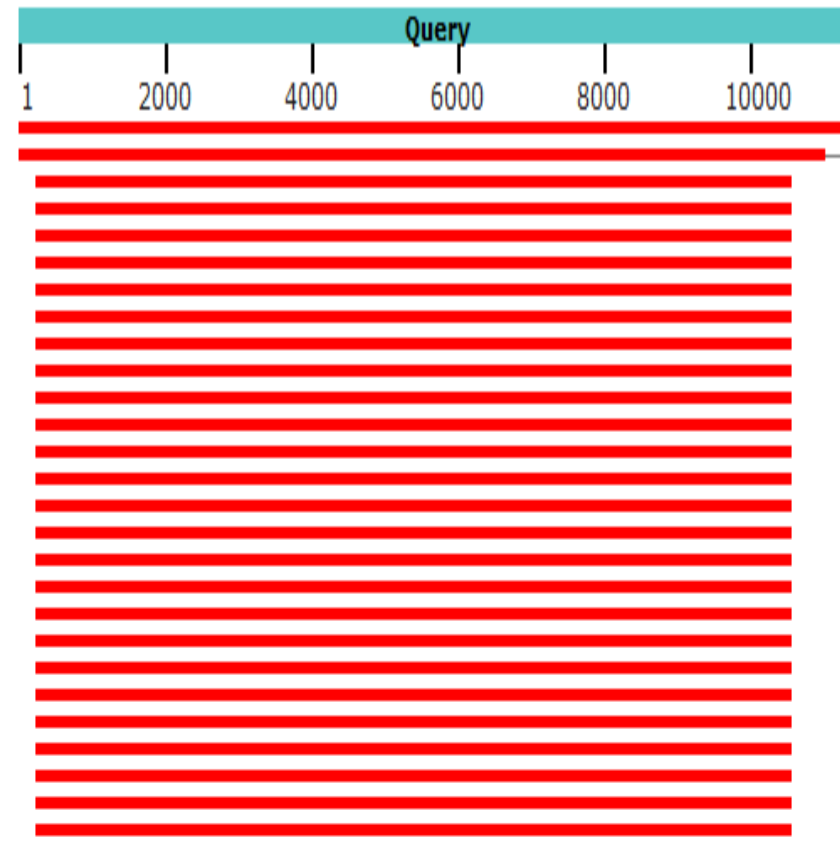
Taxonomy

 *hover to see the title*  *click to show alignments*

Alignment Scores  < 40  40 - 50  50 - 80  80 - 200  ≥ 200 

100 sequences selected 

Distribution of the top 200 Blast Hits on 100 subject sequences



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All Databases [Search]

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Resource List (A-Z)

- All Resources
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- Domains & Structures
- Genes & Expression
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- Proteins
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- Taxonomy
- Training & Tutorials
- Variation

ORGANELLE

Was this helpful?

Human mitochondrial reference genome

[Homo sapiens](#)

Included in the human reference assembly ([GRCh38_p13](#))

RefSeq: NC_012920.1 Length: 16,569 bp circular

TRNF [RefSeq protein \(13\)](#) [PopSet \(1,010\)](#) [PubMed \(2\)](#)

Genome Browser Primer-BLAST Download

[See all archival Homo sapiens complete mitochondrial genomes \(48,476\)](#)

Search details

```
("Homo sapiens"[Organism] OR Homo sapiens[All Fields]) AND mitochondrion[All Fields]
```

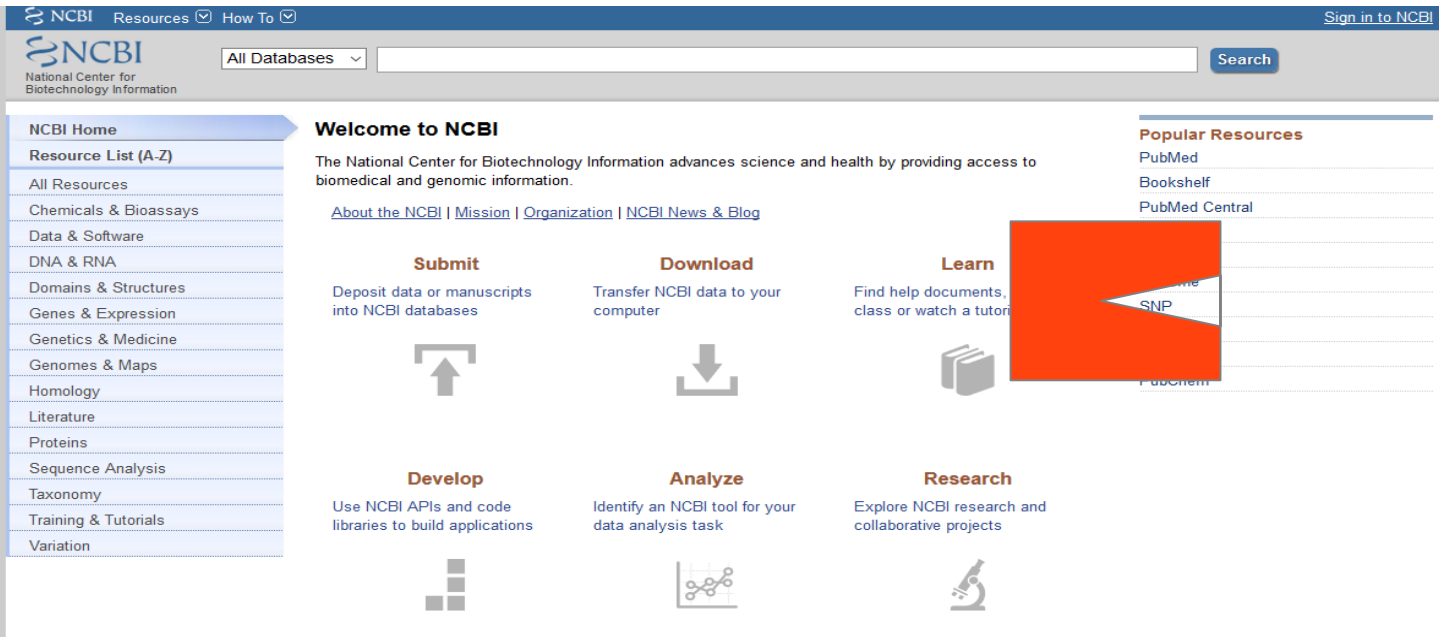
Search [See more...](#)

Recent activity

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- Homo sapiens mitochondrion (0) Genome
- Homo sapiens Genome
- homo sapiens[orgn] (1) Genome

NCBI: Μεταλλάξεις/ Πολυμορφισμοί



Ορισμοί

SNPs: Πολυμορφισμοί του ενός νουκλεοτιδίου

c-SNPs: coding single nucleotide polymorphisms (Πολυμορφισμοί του ενός νουκλεοτιδίου σε cDNA ακολουθίες, δηλαδή σε αλληλουχίες που κωδικοποιούν αμινοξέα)

SAPs: Πολυμορφισμοί του ενός αμινοξέος

Μετάλλαξη με άλλο νόημα: -> SAP

Μετάλλαξη χωρίς νόημα: -> STOP

Προσθήκη / Έλλειψη νουκλεοτιδίων -> Μεταλλάξεις αλλαγής του αναγνωστικού πλαισίου (frameshift)...

NCBI: Επιπλέον...

The image shows a screenshot of the NCBI website with several Greek annotations overlaid. The website header includes the NCBI logo, navigation links for 'Resources' and 'How To', and a search bar. A left sidebar lists various resource categories. The main content area features a 'Welcome to NCBI' message and six primary service icons: Submit, Download, Learn, Develop, Analyze, and Research. A 'Popular Resources' list is on the right. Three large Greek text annotations with arrows point to specific parts of the page: 'Κατάθεση δεδομένων' (Data Submission) points to the 'Submit' icon, 'Απόκτηση δεδομένων' (Data Acquisition) points to the 'Download' icon, and 'Αναζήτηση Βιβλίων Σεμιναρίων κλπ..' (Search for Books, Seminars, etc.) points to the 'Learn' icon.

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BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem

Κατάθεση δεδομένων

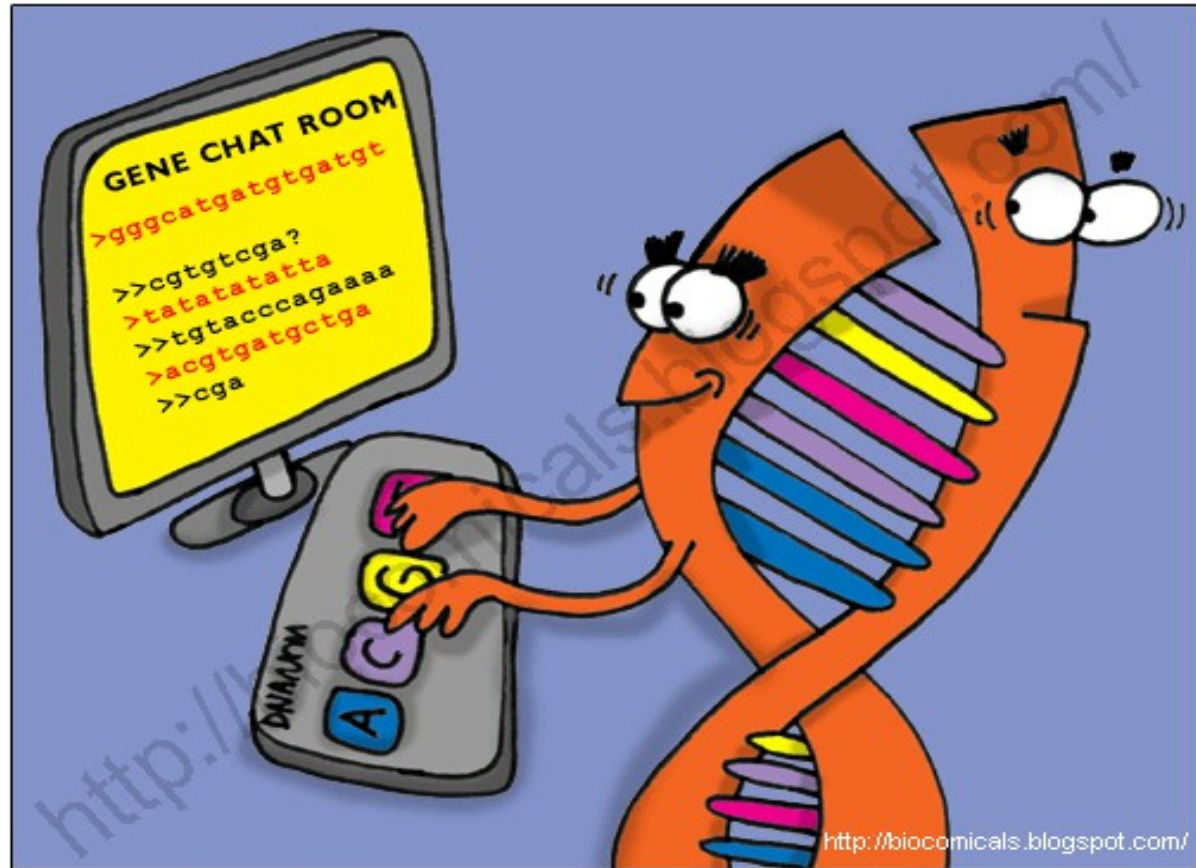
Απόκτηση δεδομένων

Αναζήτηση Βιβλίων Σεμιναρίων κλπ..

Πρακτική Άσκηση

- Επισκεφθείτε την σελίδα του NCBI και με «query» την πρωτεΐνη «hsp1» από το φυτό *Cistus creticus* αναζητήστε με τον αλγόριθμο BLAST αλληλουχίες που μοιάζουν σε άνθρωπο (επιλογή-organism).
- Περιοριστείτε στα πρώτα 5 αποτελέσματα.
- Εξάγατε τις ακολουθίες των 5 πρωτεϊνών αυτών σε «fasta format» ή σημειώστε τα accession numbers τους.
- Με «query» αυτές τις αλληλουχίες ή τα accession numbers τους επαναλλάβατε την αναζήτηση (μία μία εννοείται) ανάποδα δηλ. εναντίον των πρωτεϊνών των φυτών του γένους *Cistus*.
- Σε περίπτωση που δεν έχετε αποτελέσματα επεκτείνετε την αναζήτηση σε όλα τα θηλαστικά και σε όλα τα φυτά.
- **Σχολιάστε τα αποτελέσματά σας.**
- **Τι σχέση έχουν μεταξύ τους οι πρωτεΐνες που “χτυπούν” ή μια πάνω στην άλλη και αντίστροφα με το BLAST?**

Ευχαριστώ



mkapasa@gmail.com