

An Introduction to NCBI



**CENTURION
UNIVERSITY**
*Shaping Lives...
Empowering Communities!*

What is NCBI?

NCBI stands for National Center for Biotechnological Information.

Coordinating efforts to gather biotechnology information

House of Database act as bioinformatics tool

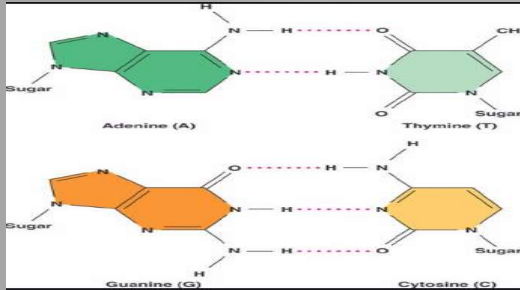
Supports a student, as it is easy to access

Allows researchers analyze desired data.

Allows researchers interpret the desired data



What can we get from here?



Nitrogenous base pairs



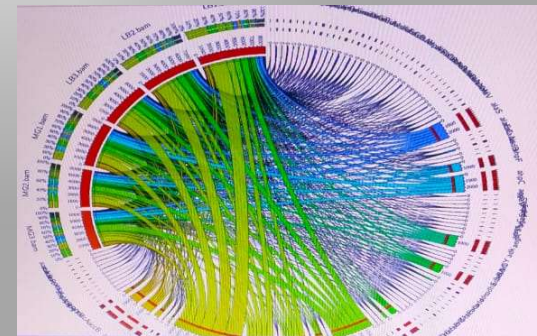
Gene and Genomics

NCBI

Proteins

Databases and tools

Amino Acids



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Applications

1

Research and biological work is done in silico then after in physical laboratory.

2

Initiates analysis and comparison among various crops and animal models.

3

Genomic data are accessible like base pairs, size, proteins, genes liable for a particular disease.

4

Reduces the understanding gap and make easier for enzyme targeting



THE PROCEDURE IS SHOWN BELOW.

The screenshot shows a Google search for 'ncbi'. The search bar contains 'ncbi' and the search button is visible. Below the search bar, there are navigation options: All, Books, News, Images, Shopping, More, Settings, and Tools. The search results show 'About 10,40,00,000 results (0.56 seconds)'. The first result is 'www.ncbi.nlm.nih.gov' with the title 'National Center for Biotechnology Information'. Below the title, there is a description: 'Welcome to NCBI. The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information. You've visited this page many times. Last visit: 14/10/20'. There are several related links: PubMed, Nucleotide, Gene, All Resources, and BLAST. A 'People also ask' section is visible at the bottom left. On the right side, there is a knowledge panel for 'National Center for Biotechnology Information' with a share icon and the NCBI logo. The panel includes the website 'ncbi.nlm.nih.gov', a description of the center as part of the United States National Library of Medicine, and details about its founder (Claude Pepper), founding date (4 November 1988), headquarters location (Bethesda, Maryland, United States), and parent organization (National Library of Medicine).

Search for NCBI in Google page.



ncbi

All Books News Images Shopping More Settings Tools

About 10,40,00,000 results (0.56 seconds)

www.ncbi.nlm.nih.gov

National Center for Biotechnology Information

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

You've visited this page many times. Last visit: 14/10/20

PubMed

PubMed® comprises more than 30 million citations for biomedical ...

Gene

RefSeqGene - Genome Workbench - Statistics - ...

BLAST

The Basic Local Alignment Search Tool (BLAST) finds regions of ...

More results from nih.gov »

Nucleotide

The Nucleotide database is a collection of sequences from ...

All Resources

The NIH genetic sequence database, an annotated ...

National Center for ...

The National Center for Biotechnology Information ...

People also ask

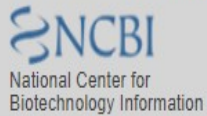


The screenshot shows the NCBI home page with a search bar at the top. Below the search bar is a red banner with COVID-19 information. The main content area is divided into several sections: 'Welcome to NCBI' with a brief description, 'Submit' (Deposit data or manuscripts), 'Download' (Transfer NCBI data to your computer), 'Learn' (Find help documents), 'Develop' (Use NCBI APIs and code libraries), 'Analyze' (Identify an NCBI tool for your data analysis task), and 'Research' (Explore NCBI research and collaborative projects). On the right side, there are 'Popular Resources' (PubMed, Bookshelf, PubMed Central, BLAST, Nucleotide, Genome, SNP, Gene, Protein, PubChem) and 'NCBI News & Blog' (BLAST now offers RefSeq Select databases, RefSeq Select offers a human ortholog set, Announcing the RefSeq annotation of mouse GRCm39, NCBI RefSeq has finished its initial annotation of the new mouse reference genome, NCBI Datasets now provides downloads of gene data for more than 30 thousand organisms, NTR1 Database now offers Gene to Gene).

Enter into the website.

NCBI home page.





Nucleotide Oryza sativa

Search



COVID-19 is an emerging, rapidly evolving situation. Get the latest public health information from CDC: https://www.coronavirus.gov. Get the latest research from NIH: https://www.nih.gov/coronavirus. Find NCBI SARS-CoV-2 literature, sequence, and clinical content: https://www.ncbi.nlm.nih.gov/sars-cov-2/.

- 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

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

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Submit

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Use NCBI APIs and code

Download

Transfer NCBI data to your computer



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Learn

Find help documents, attend a class or watch a tutorial



Research

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Popular Resources

- PubMed
Bookshelf
PubMed Central
BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem

NCBI News & Blog

BLAST now offers RefSeq Select databases for faster searches and better results

Enter nucleotide in the pop up box and search for a organism. Here I've taken Rice.



- EST (1,277,677)
- GSS (822,690)
- Genetic compartments
 - Chloroplast (3,011)
 - Mitochondrion (272)
 - Plasmid (152)
 - Plastid (3,045)
- Sequence length
 - Custom range...
- Release date
 - Custom range...
- Revision date
 - Custom range...

Clear all
Show additional filters

Items: 1 to 20 of 2909523

<< First < Prev Page 1 of 145477 Next > Last >>

[Triticum aestivum chromosome 3B, genomic scaffold, cultivar Chinese Spring](#)

1. 774,434,471 bp linear DNA
Accession: HG670306.1 GI: 669026884
[BioProject](#) [Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Digitaria exilis annotation](#)

2. 48,169,323 bp linear DNA
Accession: LR792837.1 GI: 1833616914
[BioProject](#) [Protein](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Oryza sativa Japonica Group genomic DNA, chromosome 1, complete sequence](#)

3. 43,342,410 bp linear DNA
Accession: BA000010.8 GI: 55417890
[Assembly](#) [BioProject](#) [Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Digitaria exilis annotation](#)

4. 52,445,811 bp linear DNA
Accession: LR792836.1 GI: 1833611964
[BioProject](#) [Protein](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Digitaria exilis annotation](#)

5. 38,778,756 bp linear DNA
Accession: LR792829.1 GI: 1833595496
[BioProject](#) [Protein](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

"Oryza sativa"[Organism] OR Oryza sativa[All Fields]

Search

See more...

Recent activity

Turn Off Clear

Oryza sativa (2909523) Nucleotide

rice (5477782) Nucleotide

Oryza sativa cultivar 9311 chromosome 1, whole genome shotgun sequence Nucleotide

ASM1463603v1 - Genome - Assembly - NCBI Assembly

Oryza sativa cultivar 9311 chromosome 12, whole genome shotgun sequence Nucleotide

See more...

Enter on the FASTA sequence of Oryza sativa japonica group.



Nucleotide Nucleotide Search

Advanced

Help

COVID-19 is an emerging, rapidly evolving situation. Get the latest public health information from CDC: https://www.coronavirus.gov. Get the latest research from NIH: https://www.nih.gov/coronavirus. Find NCBI SARS-CoV-2 literature, sequence, and clinical content: https://www.ncbi.nlm.nih.gov/sars-cov-2/.

FASTA

Send to

Change region shown

Customize view

Oryza sativa Japonica Group genomic DNA, chromosome 1, complete sequence

GenBank: BA000010.8

GenBank Graphics

>BA000010.8 Oryza sativa Japonica Group genomic DNA, chromosome 1, complete sequence

ACGACGCAGCTATGCCCTCCCCGCCACCGCCGCCAGCCAGCCACAACAGCTGACTAGGTAGGCTTCTAG
GTAGGGATCCCATCCCTCGATTCCCTACTCCCTCCCCGATTGATTGATTGATTGATTAAATTCGA
TTGCCCTGCTTTTCAGGTGCATGCATCATCAGATTCAATCTCCCTTCGTTCCCTGTCCTAATCCAATA
CCAATAGGGAGCAATCAGCTGCTCCTCGACGGCGAGGGAGATGTCGTGGCCGCGGGCCAAGACAACGGA
GATACCGCTGGGGACTACATCAAGTGATGTGCAGCCGTTGGCCGTTGCGGGCGGCGCCATGGCCAACC
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TCGCTACTCCTACTCTAGCTCCATATGGATATGGATTGATTAGCTGTCTACATTCTATGCCATCAATT
TGTTTTCCATCAGTTCTCATTATACATCTCCATTGCTCTCTAAATTAAGGCTTCTCTAGCTATCCCTAT
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ATAAGTCCGTTATTGTCATTGGCATATGTTGATAGATAACACTTCAGCCAGGGACTTCTATTG
CCACTTTTATACATATACAATCAACATTAGCATATGTATATCCTGTACCGCTCAGTTGACTGCTGCTT
TGAAGATAATGTTGCAAAACATATGAGCTCACACACGAGGCTAGATGCTGCATAGGCTGCACAATGGGG
TAGCCATTTGATACTTCTTAATGCTATTTATGCTGGTCCAAATGTTCAATGGTAGCCTCAGGCAGAGAA
TTTTAGGGAGATAATTATGTCMAACTCCCTGGATTCACTATGATTATACMAATTAACCAATCAATCCATT
CAAATAAATTTCCAGGTCAACTCACATATTGACTGAAAGAAGACTAATTTGCACTAATCATATCCCTTT
ATCCACAGAGTATATGAGATTGCTTCTATATGCAATTTACTTCATATCGACATTTTCTGCAGAAATG
CAAACTGACGCCCTGTTTCCATCTGGAATTGTGACGGGGAGCAAAATGCTCAAACCGGAAAAATGGCA

Analyze this sequence

Run BLAST

Pick Primers

Related information

Assembly

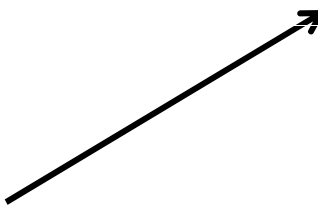
BioProject

Protein

PubMed

Taxonomy

Components (Core)



Large Sequence: 1.47MB

Pause

Sequences are copied and entered for BLAST.



COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: <https://www.coronavirus.gov>.
Get the latest research from NIH: <https://www.nih.gov/coronavirus>.
Find NCBI SARS-CoV-2 literature, sequence, and clinical content: <https://www.ncbi.nlm.nih.gov/sars-cov-2/>.

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)

```
TAGCCATTTGACTTCTTAATGCTATTTATGCTGGTCCAAATGTTTCATTGGTAGCCTCAGGCAGAGAA  
TTTTAGGGAGATATTATGCAAACTCCCTGGATTACATATGATTACAATATACCCATTCAATCCATT  
CAATAAAATTCAGGTCACTCACATATGTACTGAAAGAAGACTAATTCACATAATCATATCCCTTT  
ATCCACAGAGTATAGAGATTGCTTCTATATGCAATTTACTTCATATCGACATTTTCTGCGAAGATTG  
CAAAACTGACGCCTTGTTCATCTGGAATTGTGCAAGGGAGCAAAATGCTCAAACCGGAAAAATGGC
```

Clear Query subrange

From

To

Or, upload file Choose File No file chosen

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

BLAST has New Default Parameters and Search Limits.
Click [here](#) for more info.

Program Selection

Optimize for

Highly similar sequences (megablast)

More dissimilar sequences (discontiguous megablast)

Somewhat similar sequences (blastn)

Choose a BLAST algorithm

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

Show results in a new window

[Algorithm parameters](#)

Nucleotide sequences are pasted and then run for BLAST.

blast.ncbi.nlm.nih.gov/Blast.cgi

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

BLAST » **blastn suite** » **RID-SUFXEUDS016** Home Recent Results Saved Strategies Help

Format Request Status

[Formatting options]

Job Title: Nucleotide Sequence

Request ID	SUFXEUDS016
Status	Searching
Submitted at	Mon Oct 19 03:26:38 2020
Current time	Mon Oct 19 03:26:41 2020
Time since submission	00:00:02

This page will be automatically updated in 2 seconds

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NCBI
National Center for Biotechnology Information, U.S. National Library of Medicine
8600 Rockville Pike, Bethesda MD, 20894 USA

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https://www.nlm.nih.gov

Running status.





COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: <https://www.cdc.gov/coronavirus/>.
Get the latest research from NIH: <https://www.nih.gov/coronavirus>.
Find NCBI SARS-CoV-2 literature, sequence, and clinical content: <https://www.ncbi.nlm.nih.gov/sars-cov-2/>.

BLAST® » blastn suite » results for RID-SUFXEUDS016

Home Recent Results Saved Strategies Help

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Job Title	Nucleotide Sequence		
RID	SUFXEUDS016	Search expires on 10-20 15:26 pm	Download All ▾
Program	BLASTN	Citation ▾	
Database	nt	See details ▾	
Query ID	Ic Query_23925		
Description	None		
Molecule type	dna		
Query Length	1190		
Other reports	Distance tree of results	MSA viewer	?

Filter Results

Organism only top 20 will appear exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity to E value to Query Coverage to

[Filter](#) [Reset](#)

Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments

Download ▾ Manage Columns ▾ Show 100 ▾

select all 39 sequences selected

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
↶	Oryza sativa Japonica Group DNA, chromosome 1, cultivar Nipponbare, complete sequence	2198	2198	100%	0.0	100.00%	AF014967.1
↶	Oryza sativa Indica Group cultivar RP Bio-225 chromosome 1 sequence	2198	2198	100%	0.0	100.00%	CP012609.1
↶	Oryza sativa Japonica Group genomic DNA, chromosome 1, fosmid clone OSJNCa264G09	2198	2198	100%	0.0	100.00%	AF068218.1
↶	Oryza sativa Japonica Group genomic DNA, chromosome 1, PNC clone P0672D08	2198	2198	100%	0.0	100.00%	AF003727.3
↶	Oryza sativa Indica Group cultivar Shuhua458 chromosome 1 sequence	2187	2187	100%	0.0	99.83%	CP018157.1
↶	PREDICTED: Oryza sativa Japonica Group small G protein signaling modulator 1 (LOC4326813), mRNA	482	690	31%	2e-134	100.00%	XM_015766519.2
↶	Oryza sativa Japonica Group cDNA, clone: J175199P03, full insert sequence	482	690	31%	2e-134	100.00%	AK242338.1
↶	PREDICTED: Oryza brachyantha small G protein signaling modulator 1-like (LOC102699346), transcript variant X3, mRNA	254	254	15%	1e-62	91.05%	XM_019832638.1
↶	PREDICTED: Oryza brachyantha small G protein signaling modulator 1-like (LOC102699346), transcript variant X2, mRNA	254	254	15%	1e-62	91.05%	XM_006643556.2
↶	PREDICTED: Oryza brachyantha small G protein signaling modulator 1-like (LOC102699346), transcript variant X1, mRNA	254	254	15%	1e-62	91.05%	XM_019832636.1
↶	Setaria viridis cultivar MED34v chromosome E	202	202	11%	4e-47	92.86%	CP000799.1
↶	PREDICTED: Setaria viridis small G protein signaling modulator 1-like (LOC117855408), transcript variant X4, mRNA	200	200	11%	2e-46	93.33%	XM_034737792.1
↶	PREDICTED: Setaria viridis small G protein signaling modulator 1-like (LOC117855408), transcript variant X3, mRNA	200	200	11%	2e-46	93.33%	XM_034737791.1
↶	PREDICTED: Setaria viridis small G protein signaling modulator 1-like (LOC117855408), transcript variant X2, mRNA	200	200	11%	2e-46	93.33%	XM_034737790.1
↶	PREDICTED: Setaria viridis small G protein signaling modulator 1-like (LOC117855408), transcript variant X1, mRNA	200	200	11%	2e-46	93.33%	XM_034737789.1
↶	PREDICTED: Setaria italica small G protein signaling modulator 1 (LOC101786736), transcript variant X4, mRNA	200	200	11%	2e-46	93.33%	XM_022826827.1
↶	PREDICTED: Setaria italica small G protein signaling modulator 1 (LOC101786736), transcript variant X3, mRNA	200	200	11%	2e-46	93.33%	XM_022826826.1
↶	PREDICTED: Setaria italica small G protein signaling modulator 1 (LOC101786736), transcript variant X2, mRNA	200	200	11%	2e-46	93.33%	XM_022826825.1
↶	PREDICTED: Setaria italica small G protein signaling modulator 1 (LOC101786736), transcript variant X1, mRNA	200	200	11%	2e-46	93.33%	XM_022826824.1

Result shows the similar sequences



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source      1..43270923
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            /mol_type="genomic DNA"
            /cultivar="Nipponbare"
            /db_xref="taxon:39947"
            /chromosome="1"
gene        3449..10297
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            /locus_tag="OSNPB_010100100"
CDS         join(3449..3616,4357..4455,5457..5560,7136..7944,
            8028..8150,8232..8320,8408..8608,9210..9615,10102..10187,
            10274..10297)
            /gene="Os01g0100100"
            /locus_tag="OSNPB_010100100"
            /note="Os01t0100100-01: RabGAP/TBC domain containing
            protein."
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            /protein_id="BAS69908.1"
            /translation="MSSAAGQDNGDTAGDYIKWMCAGGGRAGGAMANLQRGVGSLVRD
            IGDPLNPSPVKGSKMLKPEKWHTCFDNDGKVIQFRKALKFIVLGGVDPTIRAEVWF
            LLGCYALSSSEYRRKLRVRRREKYQILVRQCQSMHPSIGTGELAYAVGSKLMDVRTM
            SKETHIAEEVSTSQQTQNTAGSLVEDSDYGGGAQQSQKRESCSKSAELVGFVIMHND
            TSLYDSSNFIVSSTEVMNCSKDSQDYNDMGEPRYDTETFDYVPSLPVTNFFSTDGVS
            NGVDKNHCSFVPEDLRLRHRDRMHSFQINNIDLIIESNSCSSDVFASNSDSAIHF
            SDAYKQDRHLLDDNGYNREVIDSLRISDAPEADFVDTGKSNVAVASKDRVSEWLWTLHR
            IVVDVVRTDSHLDFYGESRNMARMSDILAVYAVVDPSTGYCQGMISDLLSPFVLYEDD
            ADAFWCFEHLRRMRENFMHEGPTGVMKQLQALMKIMEITDVELFEHLSTIGAESLHF
            AFRMLLVLFRRRELSFEESLSMWMEMMAADFMEVDVTLHLFEENCLEPLVDMRNDLSCEV
            KEEHRVINSYTRRKSRSRKPPIRNGEMIRVACHLGMKPNTRNPLCGLSGATIMARHQQMP
            HSTINVLAKNGDDLPITFCVAAILVIRHKIITRETRSIDDAIKMFNDMLKINVKRCV
            RMAIKLRKYIYKLLKGSSE"
gene        complement(11372..>12284)
            /gene="Os01g0100300"
            /locus_tag="CSNPB_010100300"
CDS         complement(join(11372..12042,12146..>12284))
            /gene="Os01g0100300"
            /locus_tag="CSNPB_010100300"
            /note="Os01t0100300-00: Cytochrome P450 domain containing
            protein;"
```

Identical RefSeq

PubMed (Weighted)

LinkOut to external resources

reagents [ExactAntigen/Labome]

reagents [ExactAntigen/Labome]

reagents [ExactAntigen/Labome]

Recent activity

Turn Off Clear

Oryza sativa Japonica Group DNA, chromosome 1, cultivar: Nipponbare Nucleotide

Oryza sativa (2909523) Nucleotide

rice (5477782) Nucleotide

Oryza sativa cultivar 9311 chromosome 1, whole genome shotgun sequence Nucleotide

ASM1463603v1 - Genome - Assembly - NCBI Assembly

See more...

Downloading Large Sequence: 2.35MB

Pause Cancel

Translated sequence are shown on entering the accession.

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise CDS feature [Restore defaults](#) Download

39 sequences selected

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Oryza sativa Japonica Group DNA, chromosome 1, cultivar: Nipponbare, complete sequence

Sequence ID: [AP014957.1](#) Length: 43270923 Number of Matches: 1

Range 1: 3199 to 4388 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
2198 bits(1190)	0.0	1190/1190(100%)	0/1190(0%)	Plus/Plus

```

Query 1  ACGACGCAGCTATGGCCTCCCCGCCACCAGGCCGCCAGCCACAACCAGCTGACTAGGTA 60
          |||
Sbjct 3199 ACGACGCAGCTATGGCCTCCCCGCCACCAGGCCGCCAGCCACAACCAGCTGACTAGGTA 3258

Query 61  GGCTTCCTAGGTAGGGATCCCATCCCTTCGATTCCCTACTCCCTCCCCGATTGATTGA 120
          |||
Sbjct 3259 GGCTTCCTAGGTAGGGATCCCATCCCTTCGATTCCCTACTCCCTCCCCGATTGATTGA 3318

Query 121 TTTGATTTGATTTAATTCGATTGCCTGCTTTTCAGGTCGCATGCATCAGATTTCAAT 180
          |||
Sbjct 3319 TTTGATTTGATTTAATTCGATTGCCTGCTTTTCAGGTCGCATGCATCAGATTTCAAT 3378

Query 181  CTCCCTTCGTTCCCTGTCCCTAATCCAATACCAATAGGGAGCAATCAGCTGCTCCTCGAC 240
          |||
Sbjct 3379 CTCCCTTCGTTCCCTGTCCCTAATCCAATACCAATAGGGAGCAATCAGCTGCTCCTCGAC 3438

Query 241  GGCAGGGGAGATGTCGTCGGCCGCGGGCCAAGACAACGGAGATACCGCTGGGGACTACAT 300
          |||
Sbjct 3439 GGCAGGGGAGATGTCGTCGGCCGCGGGCCAAGACAACGGAGATACCGCTGGGGACTACAT 3498
    
```

Related Information

[Genome Data Viewer](#) - aligned genomic context

[Feedback](#)

Alignment shows the score, identities and gaps for every respective similar species.



blast.ncbi.nlm.nih.gov/Blast.cgi

Descriptions **Graphic Summary** Alignments Taxonomy

hover to see the title click to show alignments

Alignment Scores ■ < 40 ■ 40 - 50 ■ 50 - 80 ■ 80 - 200 ■ >= 200

39 sequences selected

Distribution of the top 44 Blast Hits on 39 subject sequences

The chart displays the distribution of the top 44 Blast Hits on 39 subject sequences. The x-axis represents the query sequence length from 1 to 1000. The y-axis represents the subject sequences. The bars are color-coded by alignment score: red (>= 200), magenta (80-200), green (50-80), and blue (40-50). The chart shows that most subject sequences have high alignment scores (red and magenta) across the entire query length, with some sequences showing lower scores (green and blue) at specific positions.

Query

1 200 400 600 800 1000

Blog Support Feedback

Graphic summary

Descriptions Graphic Summary Alignments **Taxonomy**

Reports **Lineage** Organism Taxonomy

39 sequences selected ?

Organism	Blast Name	Score	Number of Hits	Description
Eukaryota	eukaryotes		39	
. Mesangiospermae	flowering plants		30	
. Poaceae	monocots		29	
. BOP clade	monocots		11	
. Oryza	monocots		10	
. Oryza sativa	monocots		7	
. Oryza sativa Japonica Group	monocots	2198	5	Oryza sativa Japonica Group hits
. Oryza sativa Indica Group	monocots	2198	2	Oryza sativa Indica Group hits
. Oryza brachyantha	monocots	254	3	Oryza brachyantha hits
. Phyllostachys edulis	monocots	185	1	Phyllostachys edulis hits
. Setaria viridis	monocots	202	6	Setaria viridis hits
. Setaria italica	monocots	200	5	Setaria italica hits
. Panicum hallii	monocots	189	3	Panicum hallii hits
. Digitaria exilis	monocots	100	4	Digitaria exilis hits
. Gossypium raimondii	eudicots	58.4	1	Gossypium raimondii hits
. Asterias rubens	starfish	56.5	1	Asterias rubens hits
. Danio kyathit	bony fishes	56.5	2	Danio kyathit hits
. Larimichthys crocea	bony fishes	54.7	1	Larimichthys crocea hits
. Sclerotinia sclerotiorum 1980 UF-70	ascomycetes	54.7	1	Sclerotinia sclerotiorum 1980 UF-70 hits



Taxonomy

Blast Tree View

This tree was produced using BLAST pairwise alignments. [more...](#)

[Reset Tree](#)

BLAST RID SUFXEUDS016

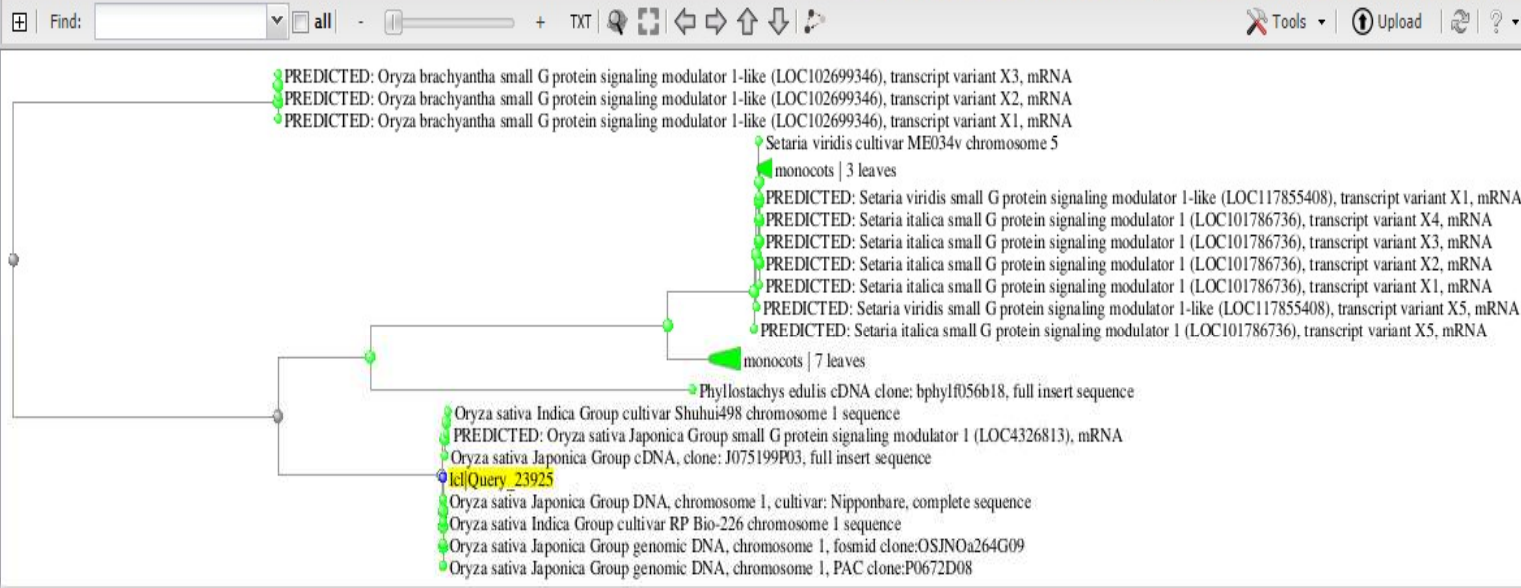
Query ID Ic|Query_23925

Database nt

Tree method: Fast Minimum Evolution
Max Seq Difference: 0.75
Sequence Label: Sequence Title (if avail:)

Mouse over an internal node for a subtree or alignment. Click on tree label to select sequence to download

[Hide legend](#)



Label color map

- query
- from type material

[Show removed seqs](#)

Blast names color map

- monocots
- unknown

Success Nodes 59(0 selected) View port at (0,0) of 1178x316

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NCBI

National Center for Biotechnology Information, U.S. National Library of Medicine



Distance tree result.



Thank you



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