



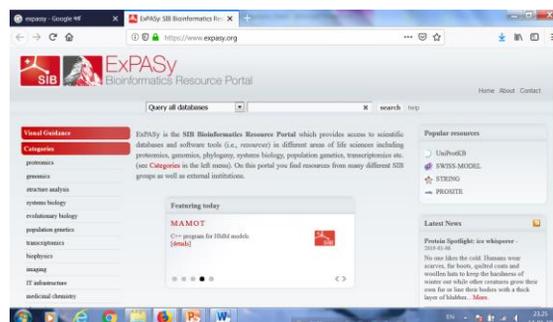
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# ExpASY

GIP3-Interferon

GIP3-Interferon  
339 bp long mRNA

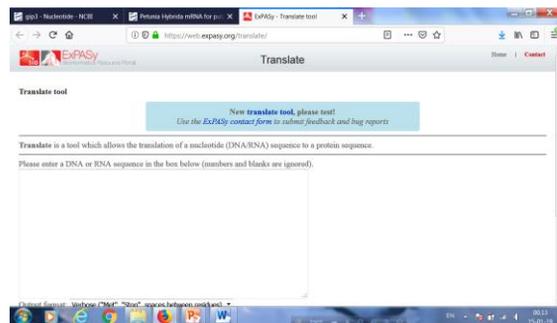
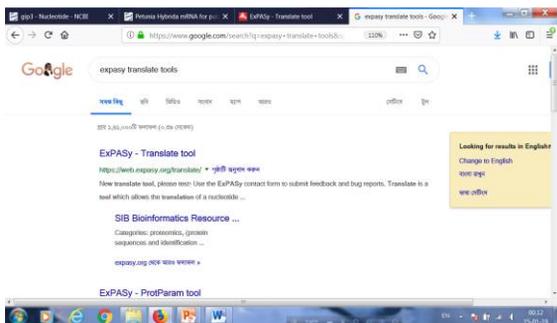


The screenshot shows the NCBI Nucleotide database page for the sequence **Saccharomyces cerevisiae strain GLBRCY22-3 chromosome XVI, whole genome shotgun sequence**. The accession number is **CM004309.1**. The FASTA format sequence is displayed, starting with `>CM004309.1 Saccharomyces cerevisiae strain GLBRCY22-3 chromosome XVI, whole genome shotgun sequence`. The right-hand sidebar contains various tools and options such as "Change region shown", "Customize view", "Analyze this sequence", "Run BLAST", "Pick Primers", "Find in the Sequence", "Related information", "Assembly", "BioProject", "BioSample", "Protein", and "PubMed".

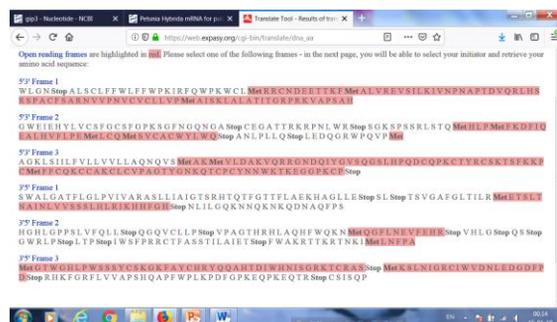
The screenshot shows search results for the query **gip3**. The top result is **Saccharomyces cerevisiae clone FLH202796.01X, GIP3 gene, complete sequence** with accession number **GU351829.1**. Other results include **Petunia hybrida mRNA for putative gibberellin induced protein 3 (gip3 gene)** (accession **AJ417390.1**) and **Saccharomyces cerevisiae S288C chromosome XVI, complete sequence** (accession **NC\_001084.4**). The interface includes search filters, a list of results with accession numbers and dates, and links to view details for each entry.

This screenshot shows the search results page for the query **gip3**. The search criteria are set to "Nucleotide" and "Advanced". The results list includes **Saccharomyces cerevisiae strain GLBRCY22-3 chromosome XVI, whole genome shotgun sequence** (accession **CM004309.1**) and **910.614 bp linear DNA** (accession **GU351829.1**). The page also displays filters for species (Fungi), molecule types (genomic DNA), and source databases (GenBank). A summary indicates 209 items found.

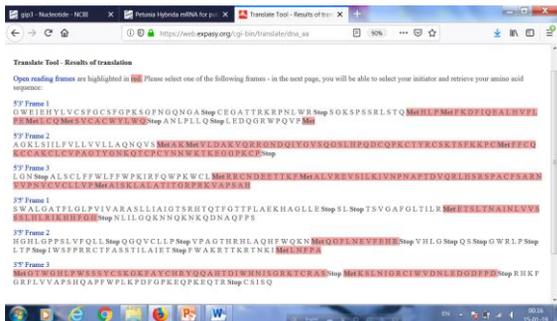
The screenshot displays the detailed view of the **Petunia hybrida mRNA for putative gibberellin induced protein 3 (gip3 gene)**. The accession number is **AJ417390.1**. The FASTA format sequence is shown, starting with `>AJ417390.1 Petunia hybrida mRNA for putative gibberellin induced protein 3 (gip3 gene)`. The right sidebar offers options for "Change region shown", "Customize view", "Analyze this sequence", "Run BLAST", "Pick Primers", "Highlight Sequence Features", "Find in the Sequence", and "Related information".



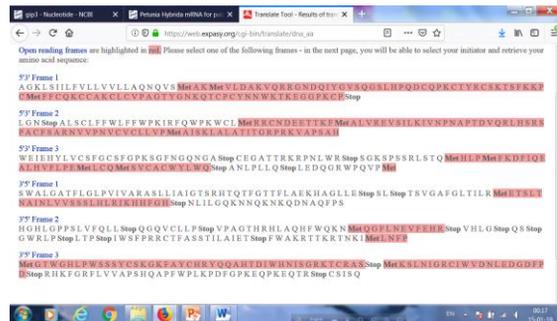
After Deleting First Nucleotide



After Deleting Second Nucleotide



After Deleting Third Nucleotide



## Using BLASTx



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

BLAST+ 2.8.1 is released  
New databases, better performance  
Wed, 19 Dec 2018 17:00:00 EST

More BLAST news...

Web BLAST

Nucleotide BLAST  
nucleotide  $\rightarrow$  nucleotide

blastx  
translated nucleotide  $\rightarrow$  protein

tblastn  
protein  $\rightarrow$  translated nucleotide

Protein BLAST  
protein  $\rightarrow$  protein

BLAST search protein database

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

BLAST® - blastx

Home Recent Results Saved Strategies Help

Translated BLAST: blastx

BLASTx search protein databases using a translated nucleotide query. [blast page](#) [bookmarks](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

Clear Query subrange

From

To

Or, upload file  No file selected

Genetic code Standard (1)

Job Title

Align two or more sequences

Choose Search Set

Database Non-redundant protein sequences (nr)

Organism

Exclude  Models (DMMX)  Non-redundant RefSeq proteins (WPs)  Uncultured/environmental sample sequences

Entire Query

BLAST search protein database

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

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Enter Query Sequence

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Or, upload file  No file selected

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Align two or more sequences

Choose Search Set

Database Non-redundant protein sequences (nr)

Organism

Exclude  Models (DMMX)  Non-redundant RefSeq proteins (WPs)  Uncultured/environmental sample sequences

Entire Query

Sending query to blast.ncbi.nlm.nih.gov...

NCBI Blast Nucleotide Sequences

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

BLAST® - blastx - RID-3TMMWJHK014

Home Recent Results Saved Strategies Help

Format Request Status

Formatting options

Job Title: Nucleotide Sequence (339 letters)

Request ID	3TMMWJHK014
Status	Searching
Submitted at	Mon, Jan 14 13:23:18 2019
Current time	Mon, Jan 14 13:23:32 2019
Time since submission	00:00:15

This page will be automatically updated in 7 seconds.

BLAST is a registered trademark of the National Library of Medicine

Support center Making list

NCBI  
National Center for Biotechnology Information, U.S. National Library of Medicine  
blast.ncbi.nlm.nih.gov



After Deleting upto Third Nucleotide

The screenshot displays a BLAST search interface with the following details:

- Search Term:** gibberellin induced protein 3 [Petunia x hybrida]
- Sequence ID:** CAD10104.1
- Length:** 112
- Number of Matches:** 1
- Score:** 209 bits(531)
- Expect:** 6e-68
- Method:** Compositional matrix adjust
- Identifiers:** 112/112(100%)
- Positives:** 112/112(100%)
- Gaps:** 0/112(0%)
- Frame:** +1

The alignment shows a perfect match between the query and subject sequences:

```

Query 1  MARGLSIIIIVLVVLLAGNQVZMANKYLDKAVRGRNDQTYVDSGSLRFPQDQFRCTY 180
Subject 1 MARGLSIIIIVLVVLLAGNQVZMANKYLDKAVRGRNDQTYVDSGSLRFPQDQFRCTY 60
Query 181 RCNRTSFRKPFQKCCAKCLVFAVTVGRNKZTCFCYNMNRKGGSPKCF 336
Subject 61 RCNRTSFRKPFQKCCAKCLVFAVTVGRNKZTCFCYNMNRKGGSPKCF 112
  
```

Below the alignment, the search results for **gip1 [Petunia x hybrida]** are shown, with Sequence ID **CAA60677.1** and Length **112**. A "Questions/comments" button is visible.