

Metodología análisis bioinformático elemental

Desde acceso al GenBank y tener la información para análisis genético

Pasos

1. Ingresar a la base de datos <https://www.ncbi.nlm.nih.gov/>

2. Selecciona qué tipo de información registrada se desea acceder (ej. genes, genoma completo, proteínas ..)

The screenshot shows the NCBI website homepage. The browser address bar displays 'ncbi.nlm.nih.gov'. The page header includes the NIH logo and 'National Library of Medicine' text. A notice banner is visible, with the phrase 'government operating status' circled in red. Below the notice is a search bar with a dropdown menu set to 'All Databases'. The main content area includes a 'Welcome to NCBI' message and a 'Popular Resources' list on the right. The Windows taskbar is visible at the bottom.

Nota: Cuando es un fragmento de un gen, dejar “All Databases”.

3. Colocar la búsqueda del gen o proteína requerido "Search"

The screenshot shows the NCBI search interface. The search bar contains the text "ITS-1 Toxocara" and is highlighted with a red circle. Below the search bar, the results are categorized into four databases: Literature, Genes, Proteins, and Genomes. The Literature category shows 108 results in PubMed Central and 13 in PubMed. The Genes category shows 0 results. The Proteins category shows 0 results. The Genomes category shows 55 results in Nucleotide, which is highlighted with a red circle. The search bar also has a "Search" button.

Database	Count
Literature	
Bookshelf	0
MeSH	0
NLM Catalog	0
PubMed	13
PubMed Central	108
Genes	
Gene	0
GEO DataSets	0
GEO Profiles	0
Proteins	
Conserved Domains	0
Identical Protein Groups	0
Protein	0
Protein Family Models	0
Structure	0
Genomes	
Assembly / Genome	0
BioCollections	0
BioProject	0
BioSample	0
Nucleotide	55
SRA	0
Taxonomy	0

Nota: Para este caso fue un fragmento del DNA ribosomal del nematodo *Toxocara* (ITS-1)

4. Buscando secuencias depositadas (o nucleóticos, o péptidos, o documentos publicados con ese fragmento de DNA en *Toxocara* ...)

The screenshot shows the NCBI search interface. The search bar contains the text "ITS-1 Toxocara" and is highlighted with a red circle. Below the search bar, the results are categorized into four databases: Literature, Genes, Proteins, and Genomes. The Literature category shows 108 results in PubMed Central and 13 in PubMed. The Genes category shows 0 results. The Proteins category shows 0 results. The Genomes category shows 55 results in Nucleotide, which is highlighted with a red circle. The search bar also has a "Search" button.

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Structure	0
Genomes	
Assembly / Genome	0
BioCollections	0
BioProject	0
BioSample	0
Nucleotide	55
SRA	0
Taxonomy	0

Nota: para este caso fue nucleótidos.

5. Identificar la parte amplificada versus lo depositado en NCBI + Secuencia FASTA

The screenshot shows the NCBI GenBank record for the sequence OM822767.1. The title "Toxocara cati isolate 20-728 internal transcribed spacer 1, partial sequence" is circled in red. The FASTA format is also circled in red. The record details include:

- LOCUS: OM822767 490 bp DNA linear INV 02-MAR-2022
- DEFINITION: Toxocara cati isolate 20-728 internal transcribed spacer 1, partial sequence.
- ACCESSION: OM822767
- VERSION: OM822767.1
- KEYWORDS: .
- SOURCE: Toxocara cati (cat roundworm)
- ORGANISM: Toxocara cati
- REFERENCE 1 (bases 1 to 490): Toce, M., Romano, A.C., Pietragalla, I., Marucci, G. and Palazzo, L. Detection of Toxocara cati larvae in a common buzzard (Buteo buteo) and in a red kite (Milvus milvus) in Basilicata Region, Italy
- REFERENCE 2 (bases 1 to 490): Unpublished

6. Copiar secuencia e ir a BLAST

The screenshot shows the same NCBI GenBank record, but with the FASTA sequence displayed. The "Run BLAST" button in the "Analyze this sequence" section is circled in red. The FASTA sequence is as follows:

```
>OM822767.1 Toxocara cati isolate 20-728 internal transcribed spacer 1, partial sequence
ATCGAGCCAAGAAAAAGCTCCGAACTGACATAGCACCATTTGCAGTATGCGTGAGCCGCGCAGC
AAGCTGCACACATGTGGTCCGGTGTAGCGCTCAGCCGTCTTTATTGGCGGCAATGGCCTGTGGCTTG
GTGCTGTTGAGGGAAATGGGTGACGTGCTGGGCAAGTTAGAAAGCGCGCGAATAGGCCCATTTTCT
CGCTATTCTCAACAACGGTATCCAGTTTGGCGTCTCCGCTCACCAGCTATCGCTGGCCGTCGGTAG
CTATGAAAGGTGGGAGAAAGCTCCGTTTCAGAGTTGAGTAGACTTAATGAACATTAGCCAGAATGTC
GCCAAAAACCAAAAACACAACATCAGTTACGTTTCTGTTTCAACTGTCGAGGATGAGCGGATGTC
TCGTGACGCGCAGCTTTTGTGTTGTTGCAACTGAACATGCTCCAGCGCACACACATACAAAATACATA
```

7. o desde la página inicial de BLAST acceder (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) a BLASTn

The screenshot shows the BLAST homepage. At the top, there's a navigation bar with 'Home', 'Recent Results', 'Saved Strategies', and 'Help'. Below that, an 'Important update' banner states that the 'ClusteredNR' database is now the default for Protein BLAST. The main section is titled 'Basic Local Alignment Search Tool' and describes BLAST's function. A 'Web BLAST' section contains three buttons: 'blastx' (translated nucleotide to protein), 'tblastn' (protein to translated nucleotide), and 'Protein BLAST' (protein to protein). The 'Nucleotide BLAST' button is circled in red. A 'NEWS' box on the right mentions a new BLAST+ release.

8. A. Pegar secuencia FAST + B. Procurar el organismo + C. clic “BLAST”

The screenshot shows the BLAST search interface. The 'Enter Query Sequence' section has a text input field containing a FASTA sequence: 'CGCTATTCTCAACAACGGTATCCAGTTTGGCGTCTCCGCCTCACCTAGCTA...'. A red arrow points to this input field. Below it, the 'Choose Search Set' section has a 'Database' dropdown set to 'ClusteredNR (nr_cluster_seq)'. The 'Organism' dropdown is open, showing a list of organisms including 'Toxocara' (taxid 6264), 'Toxocara canis' (taxid 6265), 'Toxocara cati' (taxid 6266), 'Toxocara mystax' (taxid 6266), 'Toxocara vitulorum' (taxid 62080), and 'Toxocara malaysiensis' (taxid 321169). A red arrow points to the 'Toxocara' entry. At the bottom left, a blue 'BLAST' button is highlighted with a red arrow. The 'Algorithm parameters' section is partially visible at the bottom.

9. Esperar cargue de información en página nueva e ir a las secuencias depositadas en la parte inferior de la página

BLAST® » blastx » results for RID-FZ547MYD014

Important update
The **ClusteredNR** database is now the **default** Protein BLAST database. [Learn more about ClusteredNR](#)

[Edit Search](#) [Save Search](#) [Search Summary](#) [How to read this report?](#) [BLAST Help Videos](#) [Back to Traditional Results Page](#)

Your search is limited to records include: **Toxocara (taxid:6264)**

Job Title: **Nucleotide Sequence**

RID: **FZ547MYD014** Search expires on 10-28 23:49 pm [Download All](#)

Program: **BLASTX** [Citation](#)

Database: **ClusteredNR** [See details](#)

Query ID: **lcl|Query_7859978**

Description: **None**

Molecule type: **dna**

Query Length: **490**

Other reports: [?](#)

Filter Results

Organism *only top 20 will appear* **NEW**

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity: to

E value: to

Query Coverage: to

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

Navigation: [Clusters](#) [Graphic Summary](#) [Alignments](#) [Taxonomy](#)

10. Seleccionar las secuencias para el estudio genético (ej. a través de árboles filogenéticos)

Other reports: [Distance tree of results](#) [MSA viewer](#)

Navigation: [Descriptions](#) [Graphic Summary](#) [Alignments](#) [Taxonomy](#)

Sequences producing significant alignments

Download Select columns Show 100

select all 100 sequences selected

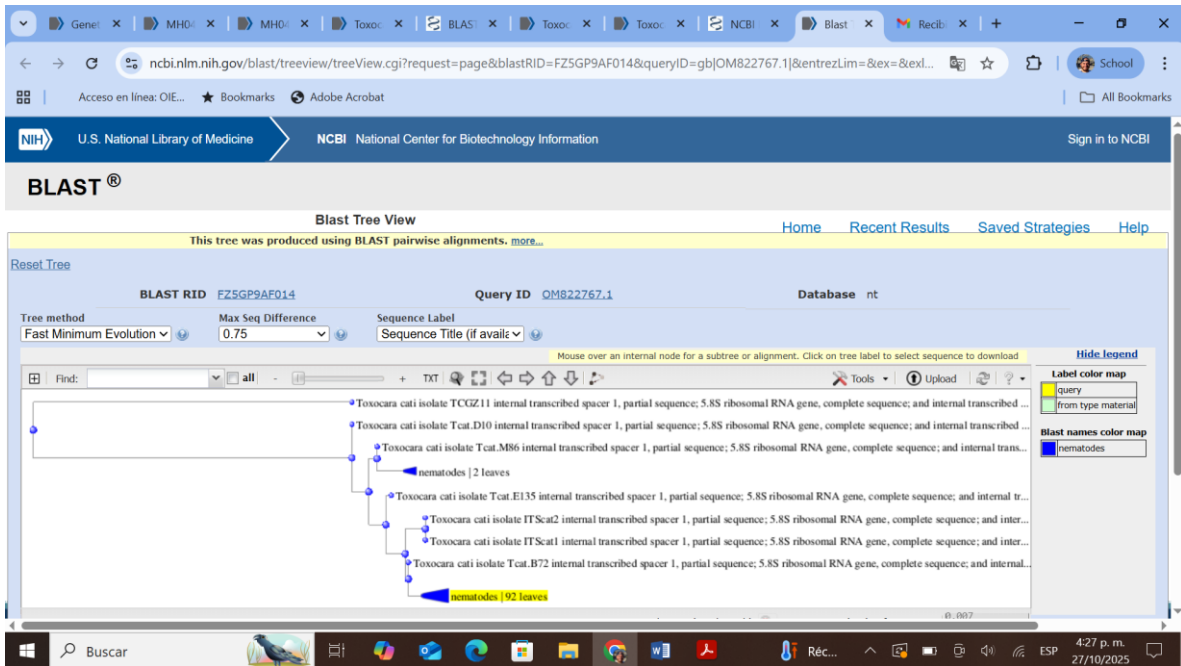
[GenBank](#) [Graphics](#) [Distance tree of results](#) [MSA Viewer](#)

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Toxocara cati isolate No. 768 small subunit ribosomal RNA gene, partial sequence: internal transcribed spacer...	Toxocara cati	905	905	100%	0.0	100.00%	554	PV329859.1
<input checked="" type="checkbox"/> Toxocara cati isolate TCF515 internal transcribed spacer_1, partial sequence: 5.8S ribosomal RNA gene and i...	Toxocara cati	905	905	100%	0.0	100.00%	1053	KY003079.1
<input checked="" type="checkbox"/> Toxocara cati isolate 20-728 internal transcribed spacer_1, partial sequence	Toxocara cati	905	905	100%	0.0	100.00%	490	OM822767.1
<input checked="" type="checkbox"/> Toxocara cati isolate 21-116 internal transcribed spacer_1, partial sequence	Toxocara cati	905	905	100%	0.0	100.00%	490	OM822766.1
<input checked="" type="checkbox"/> Toxocara cati genes for ITS1, 5.8S rRNA, ITS2, complete and partial sequence, isolate: Tc1	Toxocara cati	905	905	100%	0.0	100.00%	979	AB571303.1
<input checked="" type="checkbox"/> Toxocara cati genes for internal transcribed spacer 1, 5.8S ribosomal RNA, partial sequence, isolate: Tc1	Toxocara cati	902	902	100%	0.0	99.80%	509	AB110025.1
<input checked="" type="checkbox"/> Toxocara cati isolate TCJM-19 internal transcribed spacer_1, partial sequence, 5.8S ribosomal RNA gene and...	Toxocara cati	896	896	100%	0.0	99.59%	1064	KY003083.1
<input checked="" type="checkbox"/> Toxocara cati (Australia) first internal transcribed spacer ribosomal DNA	Toxocara cati	894	894	100%	0.0	99.59%	490	AJ002436.1
<input checked="" type="checkbox"/> Toxocara cati isolate 1 clone 25 internal transcribed spacer_1, partial sequence: 5.8S ribosomal RNA gene, co...	Toxocara cati	881	881	100%	0.0	99.18%	978	KJ777179.1
<input checked="" type="checkbox"/> Toxocara cati isolate Wk072 internal transcribed spacer_1, partial sequence: 5.8S ribosomal RNA gene and in...	Toxocara cati	876	876	97%	0.0	99.79%	996	PP812131.1
<input checked="" type="checkbox"/> Toxocara cati isolate Tc7 internal transcribed spacer_1, partial sequence: 5.8S ribosomal RNA gene and inter...	Toxocara cati	874	874	97%	0.0	99.79%	1043	PV366861.1

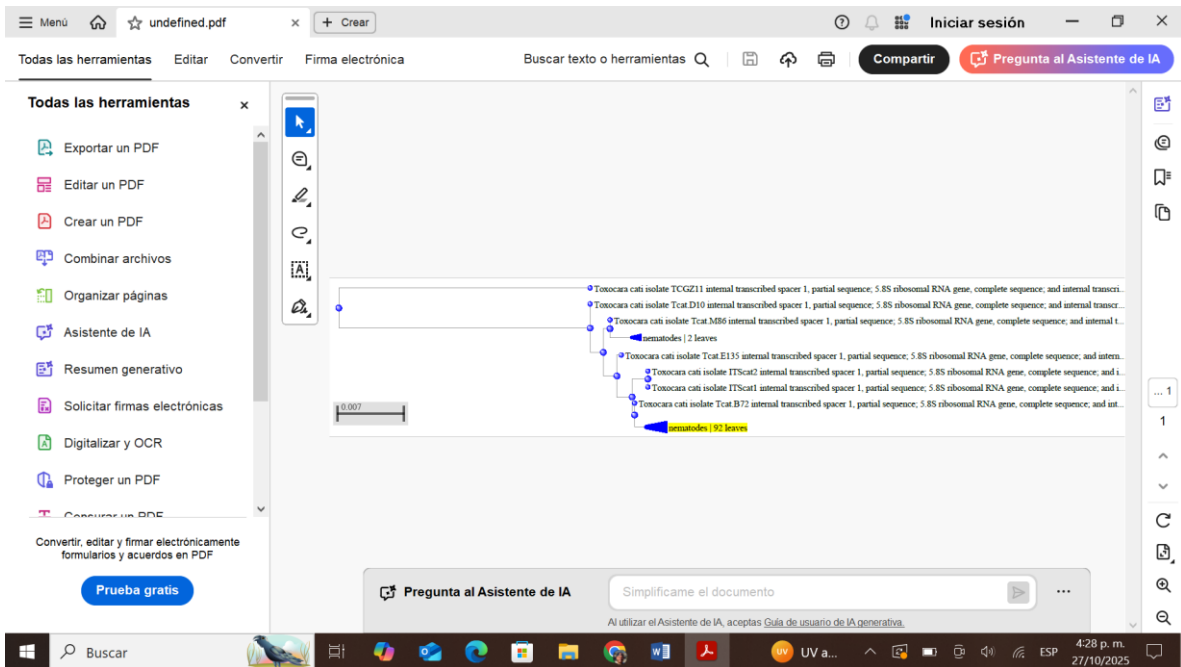
Navigation: [Home](#) [Recent Results](#) [Saved Strategies](#) [Help](#)

Windows taskbar: [Buscar](#) [Lluvia por la tarde](#) [10:52 a. m.](#) [27/10/2025](#)

11. BLAST permite generar estudios filogenéticos a través de distanciamiento génico por arboles, esta salida del software permite descargarse en varios tipos de archivos, hasta en PDF.

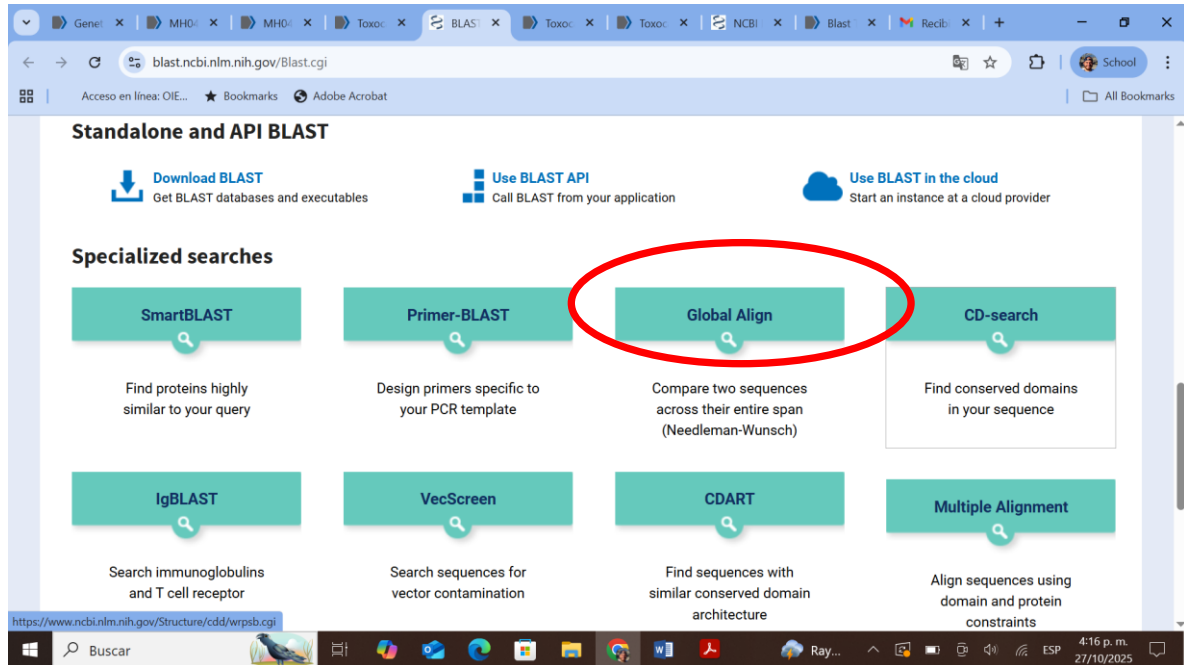


Anexo. PDF - salida del BLAST del árbol Filogenético de ITS-1 de *Toxocara*



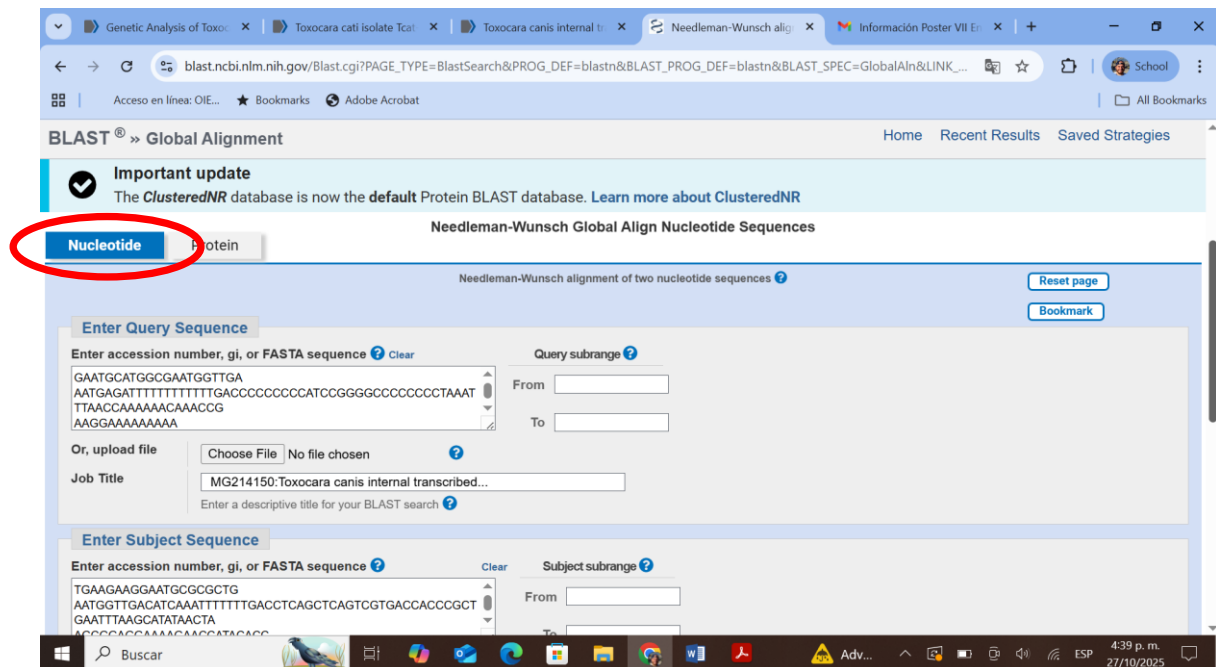
Por otro lado ...

12. En la página inicial de BLAST (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) acceder al “Global Align”



The screenshot shows the BLAST homepage with several navigation options. Under the 'Specialized searches' section, the 'Global Align' button is circled in red. The other options include SmartBLAST, Primer-BLAST, CD-search, IgBLAST, VecScreen, CDART, and Multiple Alignment. The 'Global Align' description reads: 'Compare two sequences across their entire span (Needleman-Wunsch)'.

13. Permite comparar depósitos de secuencias de nucleótidos (Para este caso ITS-2 de *T. canis* versus *T. cati*) + Click “BLAST”



The screenshot shows the BLAST Global Alignment interface. The 'Nucleotide' radio button is selected and circled in red. The interface includes fields for 'Enter Query Sequence' and 'Enter Subject Sequence', both containing nucleotide sequences. The 'Job Title' field is filled with 'MG214150:Toxocara canis internal transcribed...'. The 'Needleman-Wunsch alignment of two nucleotide sequences' section is visible at the bottom.

14. Análisis específicos de distanciamiento genético entre dos fragmentos de gen o genes.

Descriptions | Graphic Summary | **Alignments** | Dot Plot

Alignment view: Pairwise | CDS feature: | Restore defaults | Download

1 sequences selected

Download | Graphics | Next | Previous | Descriptions

Sequence ID: Query_779403 | Length: 374 | Number of Matches: 1

Range 1: 1 to 374 | Graphics | Next Match | Previous Match

NW Score	Identities	Gaps	Strand
-88	290/549(53%)	184/549(33%)	Plus/Plus

Query 1: MGTCAACACINSITRNATRANSCRBSACKARTASTTRCCTAGCTGCGATAATAGTGGCAA 60
Sbjct 1: -----GA--AT-GTGC--- 8

Query 61: TTGCAGACACATTGAGCACTAAAATTCGAACGCACATTGCGCCATCGGGTTCATCCCG 120
Sbjct 9: TT-----AACGGCTAA-GCT---TCTGGTGATTC--- 34

Query 121: TTGGCACGCTGGCTGAGGGTCAGTATATTAAGGAGTATGATGGCGGCCAAATTTATGG 180
Sbjct 35: -----T--- 37

Query 181: AATGTGATTAACGCGCAAGGTTGGTGCATTGCTGAGCTATGCTGGTGGTAATGGA 240
Sbjct 28: ----- 73

Se puede graficar el análisis:

NCBI Sequence Viewer 3.51.1 | Help | Release Notes

lcl|Query_779403 | Link To This View | Feedback

Query_779403 | Find: | Tools | Tracks | Download

(U) BLAST Results for: M9214150:Toxocara canis internal transcribed...

Query_779403: 1..374 (374 nt)

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