



BLAST home page

BLAST Assembled RefSeq Genomes

Choose a species genome to search, or [list all genomic BLAST databases](#).

- [Human](#)
- [Mouse](#)
- [Rat](#)
- [Arabidopsis thaliana](#)
- [Oryza sativa](#)
- [Bos taurus](#)
- [Danio rerio](#)
- [Drosophila melanogaster](#)
- [Gallus gallus](#)
- [Pan troglodytes](#)
- [Microbes](#)
- [Apis mellifera](#)

Step 1. Click here if you have a DNA sequence.

(Click here if you have a protein sequence)

Basic BLAST

Choose a BLAST program to run.

- [nucleotide_blast](#) Search a nucleotide database using a nucleotide query
Algorithms: blastn, megablast, discontinuous megablast
- [protein_blast](#) Search protein database using a protein query
Algorithms: blastp, psi-blast, phi-blast
- [blastx](#) Search protein database using a translated nucleotide query
- [tblastn](#) Search translated nucleotide database using a protein query
- [tblastx](#) Search translated nucleotide database using a translated nucleotide query

Nucleotide BLAST: Search nucleotide databases using a nucleotide query

http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&BLAST_PROGRAMS=megaBlast

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Nucleotide BLAST: Search nucleoti... +

BLAST Basic Local Alignment Search Tool

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NCBI BLAST/ blastn suite

blastn blastp blastx tblastn tblastx

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

Enter Query Sequence

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

```
ATTTTCAGCCGACCCCTGACTACTSCTACAAAGCCACAAAGATATGGACACATACCTACTACTTCCGGT
GGATGAGCCTGGAGTCTCCTGGGACAGCCCTTAGGCTCCTCTATCTGAGCTAGCCACCCAGCCAA
CTCCCTAGGTAAATGACAGACTACAAAGCCATGCTGACAGCCATGCTGCTAAATATCTCTCTCATA
CTAATG
```

From

To

Or, upload file Browse...

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 Optional Exclude

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

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

Entrez Query Optional

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

Searching for Matches to your Mystery DNA

Step 2. Paste your sequence in the big box.

Step 3. Make sure to click this radio button (if not already selected)

Step 4. Click the BLAST button to start the search.

NCBI Blast:Nucleotide Sequence (180 letters)

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

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Gmail - Inbox (91) - drscottk... Google Image Result for http:... http://www.ebi...display=fasta NCBI BI

BLAST Basic Local Alignment Search Tool

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▶ NCBI/ BLAST/ blastn suite/ Formatting Results - VEG4XRBW01S [\[Formatting options\]](#)

Job Title: Nucleotide Sequence (180 letters)

Request ID	VEG4XRBW01S
Status	Searching
Submitted at	Tue Apr 26 18:01:01 2011
Current time	Tue Apr 26 18:01:04 2011
Time since submission	00:00:02

This page will be automatically updated in 9 seconds

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This means that your Job is running and you have to wait.

It will keep updating until (next slide)

NCBI Blast:Nucleotide Sequence (180 letters)

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

BLAST Basic Local Alignment Search Tool

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NCBI BLAST/blastn suite/ Formatting Results - VEG4XRBW015

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Nucleotide Sequence (180 letters)

Query ID	id 991	Database Name	nr
Description	None	Description	All GenBank+EMBL+DBJ+POB sequences (but no GSS, environmental samples or phase 0, 1 or 2 HTG sequences)
Molecule type	nucleic acid	Program	BLASTN 2.2.25+ Citation
Query Length	180		

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#)

▼ [Graphic Summary](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments

Color key for alignment scores

<40	40-50	50-60	60-100	>=200
-----	-------	-------	--------	-------

Query 1 30 60 90 120 150 180

Results Page

Once you get a page that looks like this:

Step 5. SCROLL DOWN to the interesting stuff...



Results Table

You'll see a big table of "hits" or matches to your sequence. The top ones in the table are the best matches.

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

Alignments Download GenBank Graphics Distance tree of results

	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/>	Xenopus borealis voucher MHNG Herp:2644.64 cytochrome oxidase subunit 1 (COI) gene, partial	647	647	100%	0.0	100%	EU566842.1
<input type="checkbox"/>	Xenopus borealis voucher xen225 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitoch	641	641	100%	0.0	99%	EU599025.1
<input type="checkbox"/>	Xenopus borealis mitochondrion, complete genome	625	625	100%	1e-175	99%	JX155859.1
<input type="checkbox"/>	Xenopus muelleri voucher xen225 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitoch	422	422	99%	1e-114	89%	EU599031.1
<input type="checkbox"/>	Hoplitis producta voucher MHNG Herp:2644.60 cytochrome oxidase subunit 1 (COI) gene, partia	418	418	98%	2e-113	88%	EU566847.1
<input type="checkbox"/>	Xenopus muelleri voucher MHNG Herp:2644.63 cytochrome oxidase subunit 1 (COI) gene, partia	409	409	98%	1e-110	88%	EU566833.1
<input type="checkbox"/>	Xenopus sp. new tetraploid BJE-2004 cytochrome oxidase subunit 1 gene, partial cds; mitochon	374	374	89%	4e-100	88%	EU588990.1
<input type="checkbox"/>	Onychodactylus zhangyapingi voucher LC0704027 cytochrome oxidase subunit 1 (COI) gene, p	339	339	96%	1e-89	85%	JX158108.1
<input type="checkbox"/>	Onychodactylus zhangyapingi voucher LC0704028 cytochrome oxidase subunit 1 (COI) gene, p	339	339	96%	1e-89	85%	JX158107.1
<input type="checkbox"/>	Onychodactylus zhangyapingi voucher LC0704029 cytochrome oxidase subunit 1 (COI) gene, p	339	339	96%	1e-89	85%	JX158106.1

Description: This line gives some information about the match. The link takes you to the alignment.

Genbank Accession Number: This link takes you to the full genbank file with all the details.

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#)

E value: Expected Value
Probability of a match like this by chance. (Note: 0.0 = so unlikely we won't even calculate the prob.)

Ident: Identity
Percentage of nucleotides that are a perfect match.

Description	Length	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Xenopus borealis voucher MHNG:Herp:2644.64 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrion, complete genome	647	647	100%	0.0	100%	EU566842.1
<input type="checkbox"/> Xenopus borealis voucher xen226 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrion, complete genome	641	641	100%	0.0	99%	EU599025.1
<input type="checkbox"/> Xenopus borealis mitochondrion, complete genome	625	625	100%	1e-175	99%	JX155859.1
<input type="checkbox"/> Xenopus muelleri voucher xen225 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrion, complete genome	422	422	99%	1e-114	89%	EU599031.1
<input type="checkbox"/> Hoplistis producta voucher MHNG:Herp:2644.60 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrion, complete genome	418	418	98%	2e-113	88%	EU566847.1
<input type="checkbox"/> Xenopus muelleri voucher MHNG:Herp:2644.63 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrion, complete genome	339	339	96%	1e-89	85%	JX158108.1
<input type="checkbox"/> Xenopus muelleri voucher MHNG:Herp:2644.62 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrion, complete genome	339	339	96%	1e-89	85%	JX158107.1
<input type="checkbox"/> Xenopus muelleri voucher MHNG:Herp:2644.61 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrion, complete genome	339	339	96%	1e-89	85%	JX158106.1

The Accession link takes you to the Genbank file and much more information about the sequence matched.

Xenopus borealis voucher MHNG:Herp:2644.64 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial

GenBank: [EU566842.1](#)

[FASTA](#) [Graphics](#) [PopSet](#)

Go to:

LOCUS EU566842 648 bp DNA linear VRT 27-SEP-2013
 DEFINITION *Xenopus borealis* voucher MHNG:Herp:2644.64 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial.
 ACCESSION EU566842
 VERSION EU566842.1 GI:193504230
 KEYWORDS BARCODE.
 SOURCE mitochondrion *Xenopus borealis* (Kenyan clawed frog)
 ORGANISM *Xenopus borealis*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Pipidoidea; Pipidae; Xenopodinae; Xenopus; *Xenopus*.
 REFERENCE 1 (bases 1 to 648)
 AUTHORS Evans,B.J., Carter,T.F., Tobias,M.L., Kelley,D.B., Hanner,R. and Tinsley,R.C.
 TITLE A new species of clawed frog (genus *Xenopus*), from the Itombwe Plateau, Democratic Republic of the Congo: implications for DNA barcodes and biodiversity conservation

Step 6. Click on the description link:



And this will take you to the BLAST alignment between your input sequence (Query) and the best match sequence (Sbjct).

Download v GenBank Graphics

Xenopus borealis voucher MHNH:Herp:2644.64 cytochrome oxidase subunit I (COI) gene,
Sequence ID: [gb|EU566842.1](#) Length: 648 Number of Matches: 1

Range 1: 1 to 350 GenBank Graphics

Next Match Previous Mat

Score	Expect	Identities	Gaps	Strand
647 bits(350)	0.0	350/350(100%)	0/350(0%)	Plus/Plus

Query	1	CCTCTATCTAATTTTGGTGCATGAGCAGGCATAGTAGGAACAGCATTGAGTCTGTTGAT	60
Sbjct	1	CCTCTATCTAATTTTGGTGCATGAGCAGGCATAGTAGGAACAGCATTGAGTCTGTTGAT	60
Query	61	TCGAGCTGAATTAAGCCAACCAGGTACACTACTTGG	
Sbjct	61	TCGAGCTGAATTAAGCCAACCAGGTACACTACTTGG	
Query	121	CGTTACGGCACATGCCTTTATTATGATTTTCTTCAT	
Sbjct	121	CGTTACGGCACATGCCTTTATTATGATTTTCTTCAT	
Query	181	TTTTGGAAATTGATTAGTCCCATTAATAATTGGAGC	
Sbjct	181	TTTTGGAAATTGATTAGTCCCATTAATAATTGGAGC	
Query	241	AAACAATATAAGTTTTTGACTCTTACCTCCATCAT	
Sbjct	241	AAACAATATAAGTTTTTGACTCTTACCTCCATCAT	

Query = Your sequence

Sbjct = The sequence that matches

The vertical lines between the sequences mean they both have the same nucleotide at that position.

More information about your top BLAST "hit":

Scientific name of organism

Name of the gene

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

Xenopus borealis voucher MHNG:Herp:2644.64 cytochrome oxidase subunit I (COI) gene,
Sequence ID: [gb|EU566842.1](#) Length: 648 Number of Matches: 1

Range 1: 1 to 350 [GenBank](#) [Graphics](#)

[Next Match](#) [Previous Mat](#)

Score	Expect	Identities	Gaps	Strand
647 bits(350)	0.0	350/350(100%)	0/350(0%)	Plus/Plus
Query 1	CCTCTATCTAATTTTGGTG	ATGAGCAGGCATAGTAGGAACAGCATTGAGTCTGTTGAT	60	
Sbjct 1	CCTCTATCTAATTTTGGTG	ATGAGCAGGCATAGTAGGAACAGCATTGAGTCTGTTGAT	60	
Query 61	TCGAGCTGAATTTTGGAGACGATCAGATTTATAACGTTAT	120		
Sbjct 61	TCGAGCTGAATTTTGGAGACGATCAGATTTATAACGTTAT	120		
Query 121	CGTTACGGCACATGCCTTTATTATGATTTTCTTCATGGTAATGCCAATTATAATTGGCGG	180		
Sbjct 121	CGTTACGGCACATGCCTTTATTATGATTTTCTTCATGGTAATGCCAATTATAATTGGCGG	180		
Query 181	TTTTGGAAATTGATTAGTCCCATTAATAATTGGAGCACCTGATATAGCCTTCCCACGAAT	240		
Sbjct 181	TTTTGGAAATTGATTAGTCCCATTAATAATTGGAGCACCTGATATAGCCTTCCCACGAAT	240		
Query 241	AAACAATATAAGTTTTGACTCTTACCTCCATCATTCCTTCTTTTATTAGCCTCATCTGG	300		
Sbjct 241	AAACAATATAAGTTTTGACTCTTACCTCCATCATTCCTTCTTTTATTAGCCTCATCTGG	300		

How many nucleotides area perfect match. In this case all 350!

What is the organisms common name? What does this gene do?

Let's Ask Dr. Wiki!

