

Question: Use BLAST (<https://www.ncbi.nlm.nih.gov/blast/>) to reproduce this experiment. Submit the "dinosaur DNA" sequence provided by the file dino1.fasta to a nucleotide-nucleotide BLAST (blastn) search. Identify and shortly describe any actual organisms in the top ten.

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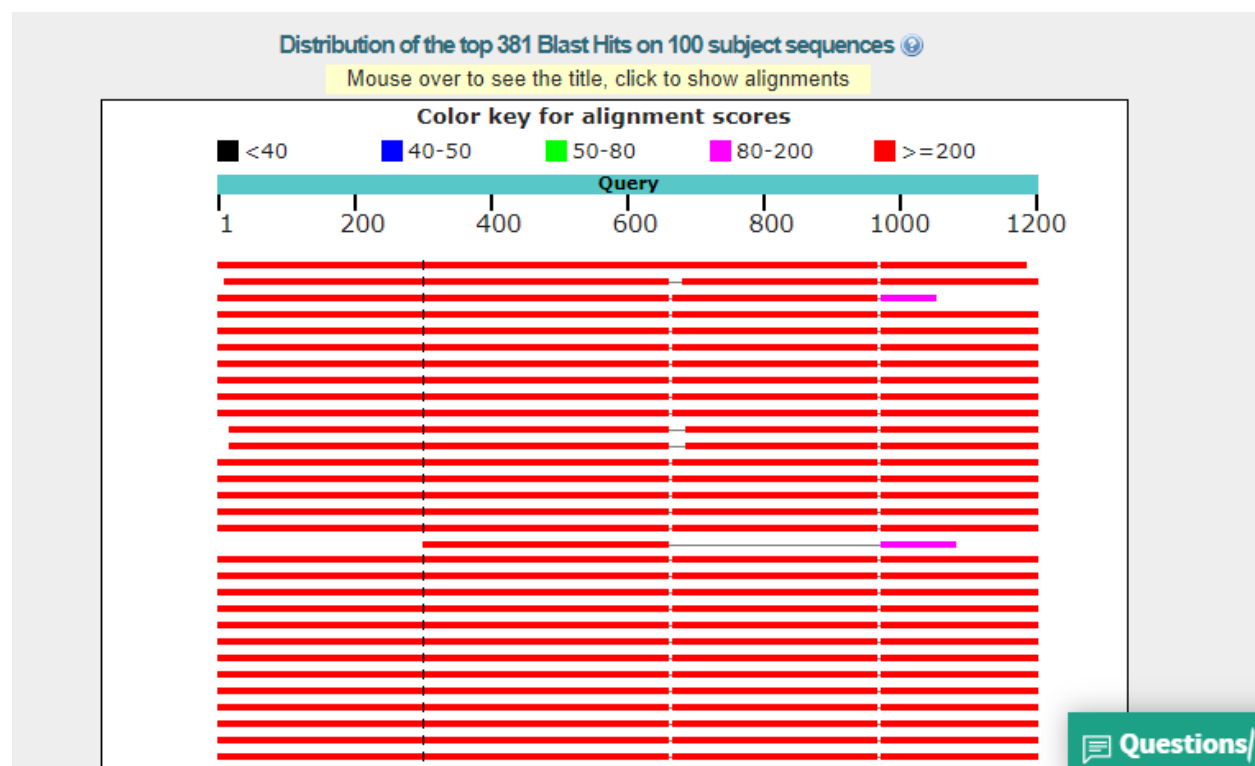
Job title: **DinoDNA** [You Tube](#) [How to read this page](#) [Blast report description](#) **NEW** [Click here to use the new BLAST results page](#)

**"Dinosaur DNA" from Crichton JURASSIC**

<b>RID</b>	<a href="#">1W1T9Z6N016</a> (Expires on 01-16 01:23 am)	<b>Database Name</b>	nt
<b>Query ID</b>	lcl Query_40331	<b>Description</b>	Nucleotide collection (nt)
<b>Description</b>	DinoDNA "Dinosaur DNA" from Crichton JURASSIC	<b>Program</b>	BLASTN 2.10.0+ <a href="#">Citation</a>
<b>Molecule type</b>	dna		
<b>Query Length</b>	1200		

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

[Graphic Summary](#)



To answer the above question, we need to take a look at the “Taxonomy reports” of this BLAST result. Based on the acquired result from BLAST, the number of hits and organisms for artificial sequences are 74 and 73, respectively. (see figure 1)

Taxonomy Report			
Taxonomy	Number of hits	Number of Organisms	Description
[-] <a href="#">root</a>	<a href="#">76</a>	75	
. [-] <a href="#">artificial sequences</a>	<a href="#">74</a>	73	
. [-] <a href="#">Gammaproteobacteria</a>	<a href="#">2</a>	2	
. . <a href="#">Escherichia coli</a>	<a href="#">1</a>	1	<a href="#">Escherichia coli hits</a>
. . <a href="#">Francisella tularensis</a>	<a href="#">1</a>	1	<a href="#">Francisella tularensis hits</a>

Figure 1 (Taxonomy Report)

The number of identified actual organisms from this BLAST result is two. To be more specified that, one is “*Escherichia coli*” and another is “*Francisella tularensis*”. Both are belonging to the domain of “Bacteria” and the phylum of “Proteobacteria”. As well, they are in the same “Gammaproteobacteria”.

For “*Escherichia coli*”, its heterotypic synonym is “*Bacterium coli commune*” and common name is “*E. coli*”. It is under the order of “Enterobacterales” and the family of “Enterobacteriaceae”. *E. coli* are a large and having various group of bacteria. Majority species are harmless, some of them will be responsible for causing some sickness such as diarrhea. *E. coli* normally lives in the intestines of humans and animals, as well as, could be found in the environment, and foods.

Another one is “*Francisella tularensis*” which has the order of “Thiotrichales” and the family of “Franchisellaceae”. It is known as one of the most infectious pathogens and causing lethal disease, tularemia or “rabbit fever” that is transmissible to humans. There are several ways humans could be infected with the disease – tick and deer fly bites, skin contact with infected animals, contaminated water drinking, contaminated aerosols/dust, laboratory accident. Also, it uses a way of bioterrorism.

Question: Once again, invoke nucleotide-nucleotide BLAST (blastn) with the second "dinosaur DNA" sequence provided by the file dino2.fasta. Identify all organisms of the top ten matches. Are either of these organisms related to dinosaurs?

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**Job title: DinoDNA**

**"Dinosaur DNA" from Crichton THE**

**RID** [1WD5MMXN01R](#) (Expires on 01-16 04:37 am)

**Query ID** [Id|Query\\_35867](#)

**Description** DinoDNA "Dinosaur DNA" from Crichton THE LOST WORLD p. 135

**Molecule type** dna

**Query Length** 1435

**Database Name** nt

**Description** Nucleotide collection (nt)

**Program** BLASTN 2.10.0+ [Citation](#)

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

Search Parameters	
Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Database	
Posted date	Dec 10, 2019 10:53 PM
Number of letters	253,561,826,700
Number of sequences	55,411,115
Entrez query	None

Karlin-Altschul statistics		
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

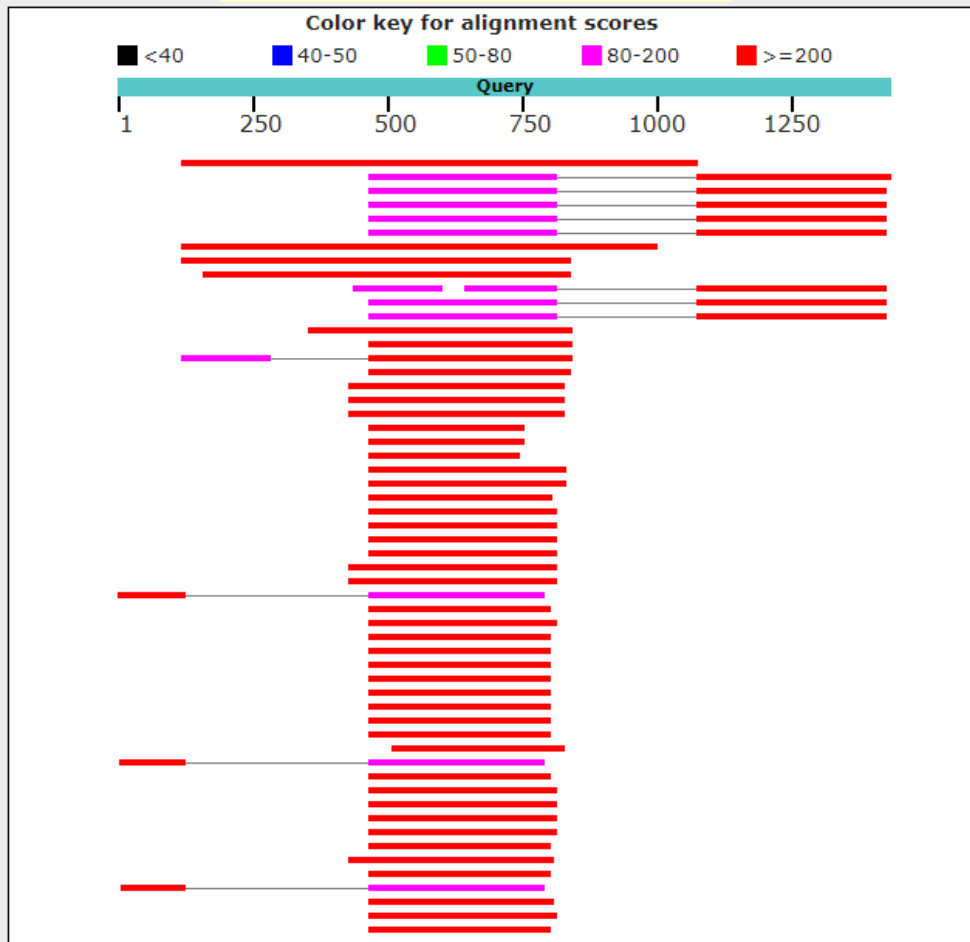
Results Statistics	
Length adjustment	39
Effective length of query	1396
Effective length of database	251400793215
Effective search space	350955507328140
Effective search space used	350955507328140

[Questions/comment](#)

## Graphic Summary

Distribution of the top 113 Blast Hits on 100 subject sequences

Mouse over to see the title, click to show alignments



To identify all organisms of the top ten matches, in the “Organisms Report”, the list of identified organisms can be determined including all the title list of “Description” except “sus scrofa (pig) and synthetic construct. For instance, the first three titles of the list, *Xenopus laevis* (African clawed frog), *Strigops habroptila* (Kakapo), and *Parus major* (Great Tit) are identified organisms. Again, in the last three titles; synthetic construct, *Bubalus bubalis* (water buffalo), and *Nomascus leucogenys* (northern white-cheeked gibbon), the one with the title of “synthetic construct” is not the one of the actual organisms. Otherwise, *Bubalus bubalis* and *Nomascus leucogenys* are actual organisms.

From various resources including Wikipedia, many researchers agree birds are treated as the only animal species that have descended from the dinosaurs. In addition, researchers state that there may be a possibility of relating to some species such as turtles, crocodiles, lizards, and snakes. The reason is that the dinosaurs are in the reptile group. As well, after searched on the internet, more current existing species such as shark, bony fish, are related to the dinosaurs.

<https://www.cbc.ca/kidscbc2/the-feed/5-animals-with-prehistoric-ancestors>

<https://www.newsweek.com/400-million-year-old-ancestor-dinosaurs-humans-and-bony-fish-discovered-954474>

Based on the information (figure 2, Organisms Report), it may be confirmed that the following organisms, *Strigops habroptila* (Kakapo), *Parus major* (Great Tits), *Pseudopodoces humilis* (Tibetan ground-tit), *Lonchura striata domestica* (Bengalese finch), *Taeniopygia guttata* (zebra finch), *Camarhynchus parvulus*, *Chrysemys picta belli* (western painted turtle), *Columba livia* (rock pigeon), *Ficedula albicollis* (collared flycatcher), *Cyanistes caeruleus* (blue tit), *Alligator mississippiensis* (American alligator), *Alligator sinensis* (Chinese alligator), *Callorhynchus milii* (elephant shark), *Xiphophorus couchianus* (Monterrey platyfish), *Globicephala melas* (long-finned pilot whale), *Delphinapterus leucas* (beluga whale), *Physeter catodon* (sperm whale), *Orcinus orca* (killer whale), *Chelonia mydas* (Green sea turtle), *Lipotes vexillifer* (Yangtze River dolphin), *Poecilia Formosa* (Amazon molly), *Poecilia latipinna* (sailfin molly), *Betta splendens* (Siamese fighting fish), *Salarias fasciatus* (jeweled blenny), *Lepisosteus oculatus* (spotted gar), *Numida Meleagris* (helmeted guineafowl).

root			78	
. <a href="#">Gnathostomata</a>	<a href="#">vertebrates</a>		75	
. . <a href="#">Euteleostomi</a>	<a href="#">vertebrates</a>		74	
. . . <a href="#">Tetrapoda</a>	<a href="#">vertebrates</a>		63	
. . . . <a href="#">Xenopus</a>	<a href="#">frogs &amp; toads</a>		14	
. . . . . <a href="#">Xenopus laevis</a>	<a href="#">frogs &amp; toads</a>	626	12	<a href="#">Xenopus laevis hits</a>
. . . . . <a href="#">Xenopus tropicalis</a>	<a href="#">frogs &amp; toads</a>	383	2	<a href="#">Xenopus tropicalis hits</a>
. . . . <a href="#">Strigops habroptila</a>	<a href="#">birds</a>	560	1	<a href="#">Strigops habroptila hits</a>
. . . . <a href="#">Parus major</a>	<a href="#">birds</a>	483	2	<a href="#">Parus major hits</a>
. . . . <a href="#">Pseudopodoces humilis</a>	<a href="#">birds</a>	451	2	<a href="#">Pseudopodoces humilis hits</a>
. . . . <a href="#">Lonchura striata domestica</a>	<a href="#">birds</a>	368	1	<a href="#">Lonchura striata domestica hits</a>
. . . . <a href="#">Taeniopygia guttata</a>	<a href="#">birds</a>	363	1	<a href="#">Taeniopygia guttata hits</a>
. . . . <a href="#">Camarhynchus parvulus</a>	<a href="#">birds</a>	343	1	<a href="#">Camarhynchus parvulus hits</a>
. . . . <a href="#">Chrysemys picta bellii</a>	<a href="#">turtles</a>	293	3	<a href="#">Chrysemys picta bellii hits</a>
. . . . <a href="#">Columba livia</a>	<a href="#">birds</a>	285	1	<a href="#">Columba livia hits</a>
. . . . <a href="#">Ficedula albicollis</a>	<a href="#">birds</a>	267	1	<a href="#">Ficedula albicollis hits</a>
. . . . <a href="#">Cyanistes caeruleus</a>	<a href="#">birds</a>	254	1	<a href="#">Cyanistes caeruleus hits</a>
. . . . <a href="#">Alligator mississippiensis</a>	<a href="#">vertebrates</a>	248	1	<a href="#">Alligator mississippiensis hits</a>
. . . . <a href="#">Alligator sinensis</a>	<a href="#">vertebrates</a>	239	1	<a href="#">Alligator sinensis hits</a>
. . . . <a href="#">Ornithorhynchus anatinus</a>	<a href="#">monotremes</a>	227	2	<a href="#">Ornithorhynchus anatinus hits</a>
. . . . <a href="#">Globicephala melas</a>	<a href="#">whales &amp; dolphins</a>	220	1	<a href="#">Globicephala melas hits</a>
. . . . <a href="#">Delphinapterus leucas</a>	<a href="#">whales &amp; dolphins</a>	220	2	<a href="#">Delphinapterus leucas hits</a>
. . . . <a href="#">Physeter catodon</a>	<a href="#">whales &amp; dolphins</a>	220	2	<a href="#">Physeter catodon hits</a>
. . . . <a href="#">Orcinus orca</a>	<a href="#">whales &amp; dolphins</a>	220	1	<a href="#">Orcinus orca hits</a>
. . . . <a href="#">Chelonia mydas</a>	<a href="#">turtles</a>	218	1	<a href="#">Chelonia mydas hits</a>
. . . . <a href="#">Lipotes vexillifer</a>	<a href="#">whales &amp; dolphins</a>	215	1	<a href="#">Lipotes vexillifer hits</a>
. . . . <a href="#">Sus scrofa</a>	<a href="#">even-toed ungulates</a>	210	3	<a href="#">Sus scrofa hits</a>
. . . . <a href="#">Camelus dromedarius</a>	<a href="#">even-toed ungulates</a>	206	1	<a href="#">Camelus dromedarius hits</a>
. . . . <a href="#">Camelus bactrianus</a>	<a href="#">even-toed ungulates</a>	206	1	<a href="#">Camelus bactrianus hits</a>
. . . . <a href="#">Ochotona princeps</a>	<a href="#">rabbits &amp; hares</a>	202	1	<a href="#">Ochotona princeps hits</a>
. . . . <a href="#">Bos indicus</a>	<a href="#">even-toed ungulates</a>	199	1	<a href="#">Bos indicus hits</a>
. . . . <a href="#">Numida meleagris</a>	<a href="#">birds</a>	196	1	<a href="#">Numida meleagris hits</a>
. . . . <a href="#">Monodelphis domestica</a>	<a href="#">marsupials</a>	196	4	<a href="#">Monodelphis domestica hits</a>
. . . . <a href="#">Bos taurus</a>	<a href="#">even-toed ungulates</a>	195	2	<a href="#">Bos taurus hits</a>
. . . . <a href="#">Bison bison bison</a>	<a href="#">even-toed ungulates</a>	195	1	<a href="#">Bison bison bison hits</a>
. . . . <a href="#">Capra hircus</a>	<a href="#">even-toed ungulates</a>	193	1	<a href="#">Capra hircus hits</a>
. . . . <a href="#">Pan troglodytes</a>	<a href="#">primates</a>	193	1	<a href="#">Pan troglodytes hits</a>
. . . . <a href="#">Ceratotherium simum simum</a>	<a href="#">odd-toed ungulates</a>	193	2	<a href="#">Ceratotherium simum simum hits</a>
. . . . <a href="#">Gorilla gorilla gorilla</a>	<a href="#">primates</a>	193	1	<a href="#">Gorilla gorilla gorilla hits</a>
. . . . <a href="#">Pan paniscus</a>	<a href="#">primates</a>	193	1	<a href="#">Pan paniscus hits</a>
. . . . <a href="#">Bubalus bubalis</a>	<a href="#">even-toed ungulates</a>	190	1	<a href="#">Bubalus bubalis hits</a>
. . . . <a href="#">Nomascus leucogenys</a>	<a href="#">primates</a>	188	1	<a href="#">Nomascus leucogenys hits</a>
. . . <a href="#">Xiphophorus couchianus</a>	<a href="#">bony fishes</a>	230	2	<a href="#">Xiphophorus couchianus hits</a>
. . . <a href="#">Poecilia formosa</a>	<a href="#">bony fishes</a>	214	2	<a href="#">Poecilia formosa hits</a>
. . . <a href="#">Poecilia latipinna</a>	<a href="#">bony fishes</a>	214	2	<a href="#">Poecilia latipinna hits</a>
. . . <a href="#">Betta splendens</a>	<a href="#">bony fishes</a>	207	1	<a href="#">Betta splendens hits</a>
. . . <a href="#">Salarias fasciatus</a>	<a href="#">bony fishes</a>	204	2	<a href="#">Salarias fasciatus hits</a>
. . . <a href="#">Lepisosteus oculatus</a>	<a href="#">bony fishes</a>	203	2	<a href="#">Lepisosteus oculatus hits</a>
. . <a href="#">Callorhynchus milii</a>	<a href="#">chimaeras</a>	239	1	<a href="#">Callorhynchus milii hits</a>
. <a href="#">synthetic construct</a>	<a href="#">other sequences</a>	193	3	<a href="#">synthetic construct hits</a>

Figure 2 (Organisms Report)

Question: Afterwards, apply translated nucleotide vs. protein database BLAST (blastx) with the same sequence and the Swiss-Prot data base. Look at the amino acid sequence of the query sequence aligned to the best hit. What is the hidden message Dr. Boguski included in this sequence?

Job title: DinoDNA "Dinosaur DNA" [YouTube](#) [How to read this page](#) [Blast report description](#) **NEW** [Click here to use the new BLAST results page](#)  
from Crichton THE

RID [1WXCX4C501R](#) (Expires on 01-16 09:14 am)

**Query ID** |cl|Query\_82640  
**Description** DinoDNA "Dinosaur DNA" from Crichton THE LOST WORLD p.  
135  
**Molecule type** dna  
**Query Length** 1435

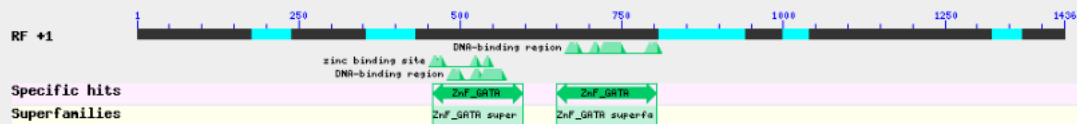
**Database Name** nr  
**Description** All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF excluding  
environmental samples from WGS projects  
**Program** BLASTX 2.10.0+ [Citation](#)

Other reports: [Search Summary](#) [Taxonomy reports](#)

### Graphic Summary

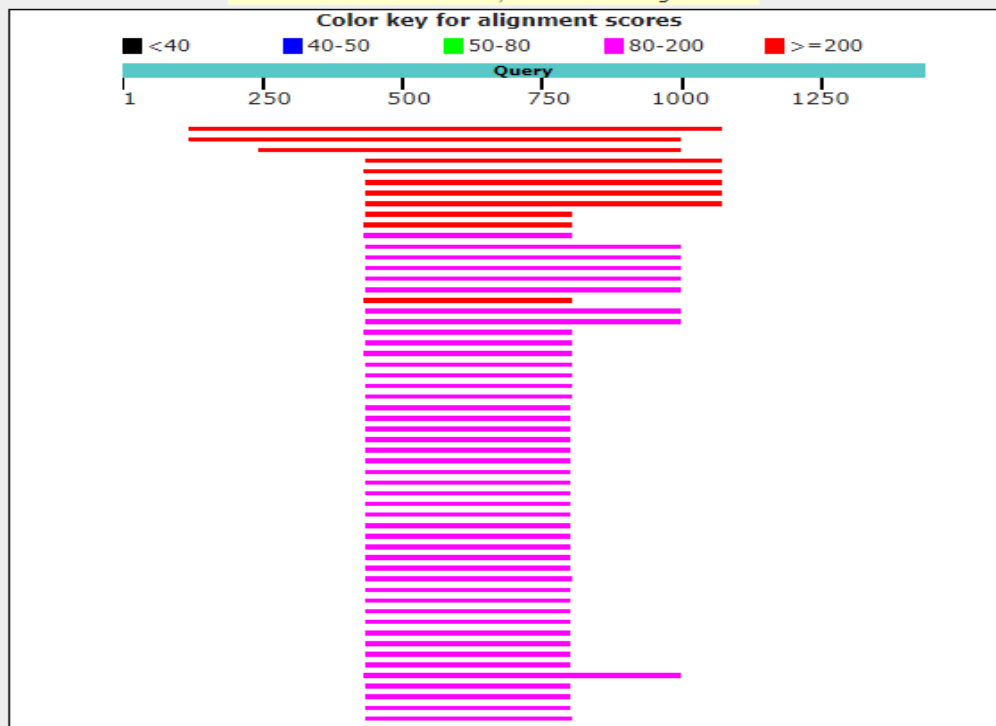
#### Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



#### Distribution of the top 100 Blast Hits on 100 subject sequences

Mouse over to see the title, click to show alignments



Descriptions							
Sequences producing significant alignments:							
Select: <a href="#">All</a> <a href="#">None</a> Selected: 0							
<a href="#">Alignments</a> <a href="#">Download</a> <a href="#">GenPept</a> <a href="#">Graphics</a>							
	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/>	<a href="#">erythroid transcription factor [Gallus gallus]</a>	348	348	66%	3e-114	95.60%	<a href="#">NP_990795.1</a>
<input type="checkbox"/>	<a href="#">erythroid transcription factor [Strigops habroptila]</a>	228	228	61%	8e-67	64.16%	<a href="#">XP_030330160.1</a>
<input type="checkbox"/>	<a href="#">hypothetical protein HGM15179_017468 [Zosterops borbonicus]</a>	224	224	52%	4e-66	62.70%	<a href="#">TRZ09635.1</a>
<input type="checkbox"/>	<a href="#">erythroid transcription factor [Taeniopygia guttata]</a>	220	220	44%	6e-65	64.32%	<a href="#">XP_030116285.1</a>
<input type="checkbox"/>	<a href="#">erythroid transcription factor-like [Lonchura striata domestica]</a>	217	217	44%	3e-64	62.73%	<a href="#">XP_021410409.1</a>
<input type="checkbox"/>	<a href="#">PREDICTED: erythroid transcription factor isoform X1 [Pseudopodoces humilis]</a>	214	214	44%	3e-62	65.00%	<a href="#">XP_014117351.1</a>
<input type="checkbox"/>	<a href="#">PREDICTED: erythroid transcription factor isoform X2 [Parus major]</a>	213	213	44%	4e-62	65.00%	<a href="#">XP_018860987.1</a>
<input type="checkbox"/>	<a href="#">PREDICTED: erythroid transcription factor isoform X1 [Parus major]</a>	213	213	44%	1e-61	65.00%	<a href="#">XP_018860986.1</a>
<input type="checkbox"/>	<a href="#">erythroid transcription factor [Camarhynchus parvulus]</a>	200	200	25%	5e-56	84.68%	<a href="#">XP_030826123.1</a>
<input type="checkbox"/>	<a href="#">PREDICTED: erythroid transcription factor [Alligator mississippiensis]</a>	200	200	26%	6e-56	81.60%	<a href="#">XP_019352182.1</a>
<input type="checkbox"/>	<a href="#">LOW QUALITY PROTEIN: erythroid transcription factor [Alligator sinensis]</a>	199	199	26%	7e-56	81.60%	<a href="#">XP_025069504.1</a>
<input type="checkbox"/>	<a href="#">erythroid transcription factor [Python bivittatus]</a>	199	199	39%	3e-55	59.57%	<a href="#">XP_007422274.1</a>
<input type="checkbox"/>	<a href="#">erythroid transcription factor [Protobothrops mucrosquamatus]</a>	198	198	39%	5e-55	59.57%	<a href="#">XP_015670436.1</a>
<input type="checkbox"/>	<a href="#">PREDICTED: erythroid transcription factor [Thamnophis sirtalis]</a>	198	198	39%	6e-55	59.04%	<a href="#">XP_013931011.1</a>

To look at the amino acid sequence to the best hits, we need to take the highest value of “Max Score” of the BLASTX result. The result represents that the query sequence written as a protein, which is using the 20 matched letters of amino acids. In figure 3, we can see the result of the matching sequence of amino acids from the database. To find the hidden message, dashes, where represent gaps, have to match their corresponding amino acid letter. Therefore, the result of a hidden message found is that “MARK WAS HERE NIH”. “MARK” can be found in the second-row subject when you try to match its corresponding query sequence. Others are the same method as described for finding the “MARK”.



► [See 2 more title\(s\)](#)

to NP\_990795.1

Figure 3