

**Title:** Using DNA data to generate phylogenetic trees

**Author(s):**

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**Abstract:**

*This activity can be a stand-alone activity to demonstrate how DNA sequence is used to generate a phylogenetic tree. The intended use of the lesson is as a final activity of a Comparative Proteomics unit that explores alternative methods for analyzing evolutionary relationships between various species of fish. Students will first analyze potential evolutionary relationships based on environmental niche and morphology. Generating protein profiles using extraction and SDS-PAGE becomes a second method for considering species differences that students can utilize to develop their own cladograms. As a final activity, DNA and a web based bioinformatics tool will be used to generate a final version of a phylogenetic tree. DNA can be isolated and used for sequencing, the DNA sequence used in the online tool DNA Subway. Alternatively, DNA sequence obtained from NCBI can be loaded. Students can generate DNA sequence to be analyzed using NCBI-BLAST. DNA sequence for mitochondrial [cytochrome c oxidase 1 gene](#) for six common fish is provided. [Cytochrome c oxidase](#) was chosen because of its use in DNA barcoding.*

**Subject, Grade, Level:**

Biotechnology II (10<sup>th</sup> and 11<sup>th</sup> grade)  
Biology/AP Biology

**Learning objectives:**

*Students will access internet based websites to study evolution and biodiversity.  
Students will consider DNA sequence differences between six common fish to reinforce the concept of evolution  
Students will learn to access DNA sequence to look at evolutionary relationships  
Students will generate a phylogenetic tree showing the evolutionary relationship between selected organisms.*

**Timeframe:**

*If using supplied DNA sequence, this activity will take one class period.  
Additional time would be needed if students obtain their own DNA sequences. To generate authentic DNA sequence, (see DNA Barcoding- [www.dnabarcoding101.org](http://www.dnabarcoding101.org)) several additional class periods would be necessary.*

**List of materials:**

*Students will need a computer*

**Procedure and general instructions (for instructor). REQUIRED.**

Students should be familiar with phylogenetic trees. Molecular data provides an alternative method for creating the tree. Provide the following information to students. Access the blue line of DNA Subway from the DNALC website (can enter as a guest). Copy DNA sequence provided below by highlighting all sequence in every cell. (or generate your own sequence). Paste into the [Enter sequences in FASTA format](#) box. Select project type (Mitochondrial DNA) and name the project. Continue. In the next

window you will focus on analyze the sequence by 1)Selecting data 2)Running Muscle. When Muscle is completed, you then have the option of running either of the two phylogenetic tree generating programs. When completed a V will appear for viewing. Note that there is an option for looking at alternative trees.

**Procedure and general instructions (for students).**

*Students will need instruction on using DNA subway. If using the provided DNA sequence it will need to be available electronically.*

**Comparative Proteomics Kit I: Protein Profiler Module**



It is recommended to purchase the kit for first time use. If SDS-PAGE is a routine technique in your course, all you really need is the sample buffer for subsequent use

**Overview**

-  Curriculum Fit
-  Theory of Evolution
-  PowerPoint Presentation for Educational Use

This activity uses the BioRad Proteomic kit to help study cladistics and phylogenetic relationships. Students first collect morphological and behavioral information on common fish from the website, [Fish Base](http://FishBase.org) and then use the information to construct cladograms. These traditional classification methods are then complemented by molecular methods of classification using SDS-gel electrophoresis to analyze the protein profiles of muscle extracted from each fish. Cladograms can be constructed by analyzing differences in the profiles.

- Description
- Specifications
- Ordering
- Refills
- Documents



**Comparative Proteomics Kit I: Protein Profiler Module**  
**1662700EDU**  
 Protein profiling classroom study kit, includes buffers, standards, stains, DTT, test tubes/holders, disposable pipets/tips, trays, curriculum, and more, for 32 students; education use only

List Price: \$222.50  
 EDU Price: \$178.00 [What is this?](#)  
 Quantity:  [Add to Cart](#)  
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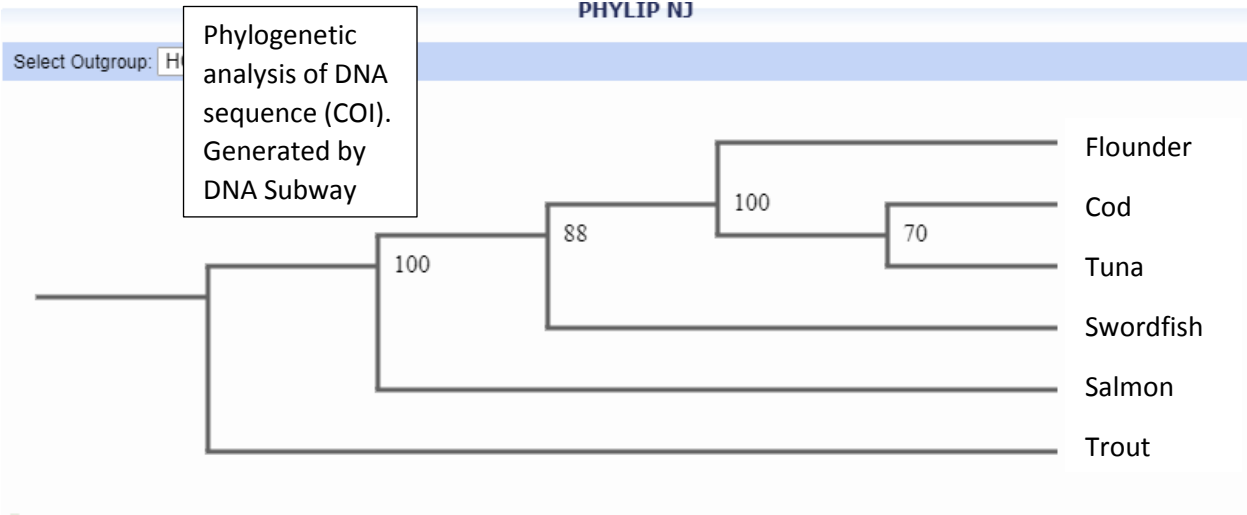
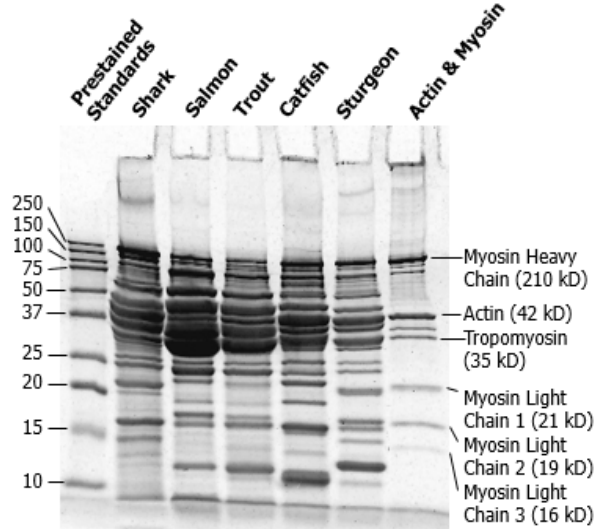
The lesson provided here will compare DNA from each fish to generate a cladogram using the web based DNA Subway.  
<https://dnasubway.cyverse.org/>

DNA can be extracted from the fish. The DNA would be amplified via PCR and then sequenced. Analyzing DNA sequence from the mitochondrial gene *COI* (cytochrome c oxidase subunit I) in animals is typically used in Bar Coding—a technique that exploits differences in DNA. See the website: [www.dnabarcoding101.org](http://www.dnabarcoding101.org)

In lieu of actual DNA sequence, data can also be obtained from an NCBI BLAST search and used in the DNA Subway program. See the attached table of DNA sequences that can easily be cut/pasted into DNA Subway.

# Polyacrylamide Gel Analysis

Example of an SDS-PAGE gel students will analyze for differences in protein profiles





DNA Subway ties together key bioinformatics tools and databases to assemble gene models, investigate genomes, work with phylogenetic trees and analyze DNA barcodes. Roll over the "stations" on the subway map to find out more about the analysis steps. Analyze your own data or sample data provided. To start a project, select one of the "lines" (red, yellow, blue, green). Register and login to be able to save and share your results.

This "line" will create phylogenetic trees with DNA data

LOG OUT *Guest Fny49y*
FAST TRACK TO GENOME ANALYSIS

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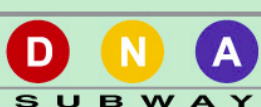
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[Align Sequences](#)

[Generate Tree](#)

**Select Project Type\***

<p>Phylogenetics:</p> <p><input type="radio"/> DNA</p> <p><input type="radio"/> Protein</p> <p><input checked="" type="radio"/> mtDNA</p>	<p>Check the source of DNA</p>	<p>Barcoding:</p> <p><input type="radio"/> rbcL</p> <p><input type="radio"/> COI</p> <p><input type="radio"/> 16S</p> <p><input type="radio"/> ITS</p>
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**Select Sequence Source\***

Upload AB1 trace files or sequences in [FASTA format](#): (max 150kb)

No file chosen

Enter sequences in [FASTA format](#) (max 150kb):

Input data here

Import trace files from DNALC

Select a set of sample sequences:

**Name Your Project\***

Project title:

**Description**





Total characters (max. 140): 0





**Continue**

\* Required information

Fish	Scientific Name	Accession #	FASTA Nucleotide sequence coding for CO1
Tuna	Thunnus thynnus	<a href="#">AB097669.1</a>	<pre> &gt;AB097669.1 Thunnus thynnus thynnus mitochondrial DNA, complete genome TTCCACCGTGCGCGCATATTTCAATATGTCTGCGC ATGTACATATATGTAATTACACCATATTCATATAT AGACCATATATAATAATGTTTTAGGACATATATGT ATTAAAACCATTACTAGTATTTAAACCATTCATATG TCAATAAATGATGAAGATTTACATAAACCATACAA ATAAACCTCAACATTCATCTTGAATTCAGGCGATT AAACGAGATTTAAGACCTAACATAAATCTAAATCG TCTAAGCCATACCAAGTCTCCTCATCTCTGACATC TCGTAAACTTAAGCGCAGTAAGAGCCTACCATCCA GTCCATTTCTTAATGCATACGGTTATTGAAGGTGA </pre>

LOG OUT *Guest Fny49y*

- Home
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- Annotate a Genomic Sequence 
- Prospect Genomes Using TARGET 
- Determine Sequence Relationships 
- Next Generation Sequencing 

Navigation icons:    

			GGGACAATAATTGTGGGGGTAACACTTAGTGAATT ATTCCTGGCATTGGTTCCTACTTCAGGGCCATAG CTTGGTAACACTCCCCATTCTTTCATTGACGCTTG CATAAGTTGTTGGTGGAGTACATGAGATTCATTAA GCCACATGCCGGGCGTCTCTCTAGGGGGTCAGGT TATTTTTTCTCTCCTTCCTTTTCATTTGACATCTC ACAGTGCAAATGCAACAATGATCAACAAGGTAGAA CATTTTCTTGCTTGCAAGGTAAATAGCCTGCATGG CTTAATTCCTATTACCTAAATAACCACATAAGAGG ATATCATGAGCATAATGATAATATTACCCGTA TATCTAAGACACCCCTCTCGGCTTTTGCGCGTTA AACCCCTTACCCCTTAAACTCGTGATATCATTAA ACACTCCTGTAAACCCCGTAAACAGGAAAATCT CGAGTGGGGTATTTTATGGCCAAAACGTATCTAT TTACATTATTGTAATATTACGCACGCTAGCGTAG CTTAACTAAAGCATAACACTGAAGATGTTAAGATG GGCCCTAGAAAAGCCCCGAGGCACAAAGGCTTGGT CCTGACTTTACTGTCAACTCTAGCTAACTTACAC ATGCAAGTATCCGCGACCCTGTGAGAATGCCCCAC AGTTTTCCGCCCCAAAACAAGGAGCTGGTATCAGG CACACCAACGAAAGCCCATGACGCCTTGCTTAGC CACACCTCAAGGGAACTCAGCAGTGATAAACCTT AAGCTATAAGTGAAAACCTGACTTAGTTAAAGCTA AGAGGCCGGTAAAACCTCGTGCCAGCCACCGCGGTT ATACGAGAGGCCCAAGTTGACAGACACCGGCGTAA AGCGTGGTTAAGGTACACGAAAACCTAAAGCCGAAC ACCTTCAGGGCAGTTATACGCATCCGAAGGCACGA AGCCCCACCACGAAAGTGGCTTTATAAACCCCTGAC TCCACGAAAGCTATGACACAAAACCTGGGATTAGATA CCCCACTATGCCCTAGCCGTAAACATTGATAGAATT TTACACCTCTATCCGCTGGGTACTACGAGCATT AGCTTGAAACCCAAAGGACTTGGCGGTACTTTAGA TCCCCCTAGAGGAGCCTGTTCTATAACCGATGACC CCCGTTCAACCTCACCTCCCTTGTTCCTCCCGCC TATATACCGCCGTCGTCAGCTTACCCTGTGAAGGT CTAATAGTAAGCAAAATTTGGCACCGCCAGAAGCT CAGGTCGAGGTGTAGCGCATGAGAGGGGAAGAAAT GGGCTACATTCGCTAACATAGCGAATACGAACGAT GCACTGAAAACGTTTCATCTGAAGGAGGATTTAGCA GTAAGTGGAAAATAGAGTGTTCCTGAAATCGGC TCTGAAGTGCCTACACACCGCCCGTCACTCTCCCC AAGCTTACCAATTTATATATCTAAAACGCTTTAAC TGCGAAGGGGAGGCAAGTCGTAACATGGTAAGTGT ACCGGAAGGTGCACTTGGAAAAATCAGAGTATAGC TAAGATAGAATAGCATTTCCTTACACTGAAAAGT CATCCGTGCAAACCGGATTACCCTGATGCTGACCA GCTAGCCCACCTAACAAAAACAACAACCCAAATAT AAATAACCCCAAACACACTACTCCTCTATAAAACA AACCATTTTACCCCTTAGTATGGGCGACAGAAAA GGAACATTGGAGCGATAGAGAAAGTACCGCAAGG GAACGCTGAAAGAGAAATGAAATAACCCAGTAAAG CCTAAAAAGCAGAGATTTTACCTCGTACCTTTTG CATCATGATTTAGCTAGTACTACCCAAGCAAAGAG AACTTTAGTTTGGACCCCGAACTAGGTGAGCTA CTCCAAGACAGCCTATCAATAGGGCAAACCCGTCT CTGTGGCAAAAGAGTGGGAAGAGCTTTGAGTAGAG GTGACAGACCTACCGAACCTAGTTATAGCTGGTTG
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			<p>CCTGAGAATTGGATAGGAGTTCAGCCTCCAGGCTT  CTCTATTCACCGCGGTCTTACCCCTACCGATGCAC  TAAAGAAGCCTAGAGAGTTAATCAAAGGGGTACA  GCCCTTTGAGACAAGATACAACCTTTTCCAGGAGG  GTAAAGATCATATTTACCCAAGGTAACAATGCCCA  GGTGGGCCATAAAGCAGCCATCCTTACAGAAAGCG  TTAAAGCTCAAGCATTACACCTTCCCACATATTC  GATAACCATATCCCAACCCCTAATATTATCAGGC  CATCTCATGCATACATGAGAGTGCACATGCTAATA  TGAGTAACAAGAGAGCCTCCGCCTCTCTCCTTGCA  CACGTGTAATCGGAACGAACCCCAACCGAACTT  AACGGCCCCAAACAAAGAGGGCAATGAACAACAAG  TAAGCAACCAGAAAACCATCCAAAAACAACCGTT  AACCCACACTGGTGTGCCATTAAGGAAAGACTAA  AAGAAAAAGAAGGAACCTCGGCAAACATACCAAGCC  TCGCCTGTTTACCAAAAACATCGCCTCTTGCAAAA  CAAAGAATAAGAGGTCCAGCCTGCCCTGTGACTAT</p>
Salmon	Salmo salar	<a href="#">HQ167685.1</a>	<p>&gt;HQ167685.1 Salmo salar voucher  Ss004 cytochrome oxidase subunit I  (COI) gene, complete cds;  mitochondrial</p> <p>GTGGCAATCACACGATGATTTTTCTCAACCAACCA  CAAAGACATTGGCACCCTCTATTTAGTATTTGGTGT  CCTGAGCCGGAATAGTCGGCACCAGCCCTAAGTCTC  TTGATTCGAGCAGAACTCAGCCAGCCTGGCGCCCT  TCTGGGAGATGACCAAATTTATAACGTAATTGTTA  CAGCCCATGCCTTCGTCATAATTTCTTTATAGTC  ATACCGATTATGATCGGCGGCTTTGGAAACTGATT  AATTCCTCTTATAATCGGGGCCCCGACATAGCAT  TCCCCGAATGAATAACATAAGTTTTTGACTTCTC  CCTCCCTCCTTTCTTCTCCTCCTGGCCTCATCTGG  AGTTGAAGCCGGCGCTGGCACCAGGATGAACAGTCT  ACCCCCCTCTAGCAGGTAATCTTGCCCACGCAGGA  GCTTCCGTTGACTTAACATTTTTTCCCTCCATTT  GGCTGGTATTTCTTCAATTCTTGGGGCCATTAATT  TTATCACAACCATTATTAATATAAAAACCCCAAGCT  ATCTCTCAGTATCAAACCCACTTTTTGTTTGAGC  TGTATTAGTCACTGCCGTCCTTTTATTACTCTCCC  TCCCTGTTCTAGCAGCAGGCATTACCATACTACTT  ACAGACCGAAATCTAAATACCACTTTCTTTGACCC  GGCAGGCGGAGGGGACCCAATCTTGTACCAACATC  TCTTTTGGTTCTTTGGCCATCCAGAAGTCTATATC  CTCATTCTCCCAGGCTTTGGTATAATTTACACAT  CGTTGCATACTACTCTGGCAAAAAAGAACCTTTCG  GGTATATAGGAATAGTCTGAGCTATGATAGCCATC  GGACTCTTAGGTTTTATCGTTTGAGCCCACCATAT  GTTTACTGTCGGGATAGATGTAGACACTCGTGCCT  ACTTTACATCTGCCACCATAATCATCGCCATCCCA  ACTGGAGTAAAAGTGTTTAGTTGACTAGCCACACT  GCACGGCGGCTCAATCAAATGAGAAACGCCACTTC  TTTGAGCCCTGGGGTTTTATTTTCTCTTTACAGTA  GGAGGACTTACGGGCATTGTCCTTGCTAATTCCTC  ACTAGACATCGTCCTCCACGATACTTACTATGTAG  TCGCCCCTTCCACTATGTTTTATCTATGGGAGCT  GTCTTTGCTATTATAGGCGCTTTTGTACACTGATT  CCCCTATTACGGGATATACCCTCCACAGTACAT</p>

			<p>GAACCAAAATCCATTTTCGGGATTATATTTATCGGC  GTAAATTTAACCTTTTTTCCCCAGCACTTCCTAGG  CCTTGCGGGGATACCTCGACGGTACTCCGACTACC  CAGACGCCTACACACTCTGAAACACTATCTCCTCA  ATCGGATCTCTTATCTCCTTAGTCGCTGTAATTAT  GTTCTGTTTATTCTTTGAGAAGCCTTTGCTGCTA  AACGAGAAGTAGCATCAATTGAAATAACTTCAACA  AACGTTGAGTGACTACACGGGTGCCCTCCACCTTA  CCACACATTTGAAGAACCAGCATTGTCCAAGTAC  AAGCAAGTTAA</p>
Swordfish	Xiphias gladius	GQ202122.2	<p>&gt;GQ202122.2 Xiphias gladius  cytochrome c oxidase subunit I  (COI) gene, complete cds;  mitochondrial</p> <p>GTGGCAATCACACGTTGATTTTTCTCGACCAATCA  CAAAGACATCGGCACCCCTCTATCTAGTATTCGGTG  CTTGAGCCGGTATAGTAGGCACAGCCCTAAGTCTA  CTAATCCGAGCAGAACTCAGCCAACCTGGCGCCCT  ACTAGGGGATGACCAGATTTACAACGTAATCGTTA  CAGCTCACGCCTTTGTAATGATTTTCTTTATAGTA  ATGCCAATCATGATTGGAGGGTTCGGAAATTGACT  AATTCCCCTAATGATCGGAGCCCCCGATATAGCAT  TCCCTCGAATGAATAACATAAGCTTCTGACTCCTC  CCTCCATCATTCCTCCTCCTCCTTGCTTCTTCTGG  AGTTGAAGCTGGCGCTGGAACCGGGTGAAGTGTCT  ACCCTCCTCTAGCAGGTAACCTAGCCCACGCAGGT  GCATCTGTTGACCTTACCATCTTCTCCCTTACCT  AGCTGGGATCTCCTCTATTCTGGGGGCAATCAACT  TCATCACAAC TATTATCAATATAAAAACCAGCTGCC  GTTTCTATGTACCAGATTCCTCTGTTCGTGTGAGC  CGTACTAATTACAGCTGTCCCTCCTCCTCCTCCTCC  TTCCCCTTAGCTGCCGGAATTACCATGCTCTTA  ACAGACCGTAATTTAAACACCGCCTTCTTTGACCC  TGCAGGAGGTGGGGATCCCATCCTCTACCAACACC  TGTTCTGATTCTTCGGCCACCCCGAAGTATATATT  CTGATCCTCCCCGGCTTCGGAATAATTTCCCATAT  TGTTGCCTACTACTCAGGCAAAAAGAGCCTTTCG  GCTATATGGGTATGGTATGGGCTATGATGGCCATC  GGCCTTCTAGGCTTCATTGTATGAGCTCACCACAT  GTTTACAGTCGGAATGGATGTAGACACCCGAGCCT  ACTTTACATCCGCCACAATAATTATCGCTATCCCG  ACTGGTGTAAGTCTTCAGCTGGCTCGCAACTCT  GCACGGAGGTGCTATTTAAATGGGAAACCCCTCTAC  TATGGGCCCTTGGCTTTATTTTCTCCTTTACGGTA  GGTGGACTAACTGGAATTGTCTGGCTAATTCCTC  TCTGGATATTGTGCTCCACGACACTTACTATGTAG  TTGCCCACTTCCACTACGACTTTCAATGGGTGCC  GTCTTCGCCATTGTTGCAGCCTTTGTACACTGATT  CCCCCTGTTTACGGGCTACACCCCTCACAGCACAT  GAACAAAAATCCACTTCGGAGTTATATTCGTCGGT  GTTAACCTTACCTTCTTCCCTCAACACTTCCTAGG  ACTGGCTGGCATGCCCTCGACGATATTCAGACTACC  CAGATGCTTACGCACTGTGAAACACAGTCTCCTCT  ATCGGATCCTTAGTTTTCTCTAGTAGCAGTTATTAT  GTTCTATTTATCATTTGAGAAGCATTACCGCCA</p>



			AGCGAGAGGTTCTCTCAGTAGAACTAACCGCCACA AACGTGGAATGACTACATGGCTGCCCTCCACCTTA CCACACATTTGAACAGCCTGCATTTCGTTCAAGTAC GATCACACTAA
Trout	Oncorhynchus mykiss	<a href="#">HQ167682.1</a>	>HQ167682.1 Oncorhynchus mykiss voucher Om004 cytochrome oxidase subunit I (COI) gene, complete cds; mitochondrial GTGGCAATCACACGATGATTTTTCTCAACCAACCA CAAAGACATTTGGCACCCTCTATTTAGTATTTGGTG CCTGAGCCGGGATAGTAGGCACCGCCCTGAGTCTA CTGATTCGGGGCGAACTAAGCCAGCCGGGGCGCTCT TCTGGGGGATGACCAAATCTATAACGTGATCGTCA CAGCCCATGCCTTCGTTATGATTTTTCTTTATAGTC ATGCCAATTATAATCGGGGGCTTTGGAACTGATT AATTTCCCCTAATAATCGGAGCCCCCTGATATGGCAT TCCCTCGAATAAATAACATAAGCTTCTGACTCCTT CCTCCATCCTTTCTCCTCCTCCTGTCTTCATCAGG AGTTGAAGCCGGCGCGGGTACTGGATGAACAGTAT ACCCCCCTCTAGCCGGCAACCTCGCCCACGCAGGA GCCTCTGTTGATTTAACTATCTTCTCCCTTCATTT AGCTGGAATCTCCTCAATTTTAGGAGCCATTAATT TTATTACGACCATTATTAACATAAAACCTCCAGCC ATCTCTCAGTACCAAACCCCCCTATTCGTTTGAGC CGTGCTAGTTACTGCTGTCTTCTGTTACTTTCCC TCCCCGTCTGGCAGCAGGCATTACTATGTTACTT ACAGACCGAAATCTAAACACCCTTTCTTTGACCC GGCAGGCGGGGGAGATCCAATTTTATACCAACACC TCTTTTGATTCTTCAGCCACCCAGAGGTCTATATT CTCATGCTCCAGGCTTTGGTATAAATTCACACAT CGTTGCGTACTACTCCGGCAAAAAGGAACCCCTCG GGTATATAGGAATGGTCTGAGCTATAATAGCCATC GGGTTGTTAGGATTTATCGTTTGAGCCCACCATAT GTTCACTGTAGGGATAGACGTGGACACTCGTGCTT ACTTTACATCTGCCACCATGATTATCGCTATCCCC ACAGGAGTAAAAGTATTTAGCTGACTAGCTACACT ACACGGAGGCTCAATCAAATGAGAAACACCCTTC TTTGAGCCTTAGGGTTTATTTTCTGTTTACAGTG GGTGGACTTACAGGTATTGTCTTGCTAACTCCTC ATTAGACATTGTTCTACATGACACTTATTACGTAG TTGCTCATTTCCACTACGTACTATCTATAGGAGCT GTATTTGCCATTATAGGCGCTTTCGTACACTGGTT CCCCTATTTACAGGGTACACCCTCCACAGCACAT GAACCAAAATCCATTTTGGAAATATATTTATCGGT GTAAATTTAACCTTTTCCCACAGCATTTCTTAGG CCTCGCAGGGATACCACGACGGTACTCTGATTACC CAGACGCTTATACACTGTGAAACACTGTATCCTCA ATCGGATCCCTTGTATCCCTAGTAGCTGTAATTAT GTTCCATTTTATTTCTTTGAGAAGCTTTTGTGCCA AACGAGAGGTAGCATCAATCGAACTAACTTCAACA AACGTAGAATGACTACACGGATGCCCCCCACCCTA CCACACATTTGAAGAACCAGCATTTGTCCAAGTAC AAGCAAATAA
Cod	Gadus	X99772.1	>X99772.1 Gadus morhua complete mitochondrial DNA sequence

	morhua		GCTATCGTAGCTTAATTAAAGTTTAAACTGAAGA TATTAGGATGGACCCTAGAAAGTCCCGAAAGCACA AAGGTTTGGTCCCTGACTTTACTATCAATTGTACCC TAATTTACACATGCAAGTCTCCGCCCTCCCGTGAG AATGCCCTTAATGTCTGCCCCGGAATTAAGGAGCA GGTATCAGGCACATCTAATAGTTTACTAGCCATA ACGCCCTTGCTCAGCCACACCCCTACGGGTATTCAG CAGTGATAAAATTTAAGCCATAAGTGAAAGCTTGA CTTAGTTAAGGGAAAGAGGGCCGGTAAAACCTCGTG CCAGCCACCGCGGTTATACGAGAGGCCCAAATTGA TGAAAAACGGCGTAAAGCGTGGTTAAGAAAAAGA GAAAAATATGGCCGAACAGCTTCAAAGCAGTTATA GCATCCGAAGTCACGAAGAACAATCACGAAAGTTG CCCTAAAACCTCCGATTCACGAAAGCCATAAAAC AAACTGGGATTAGATACCCACTATGTATGGTCGT TAACATTGATGGTTTTATACCCAAACCATCCGCCT GGGAACTACGAGCAATAGCTTAAAACCCAAAGGAC TTGGCGGTGCTTTAGACCCCTAGAGGAGCCTGT TCTAGAACTGATAACCCCGTTTAACTCACCATC CTTTGTTTTCCCGCCTATATACCACCGTCGTCAG CTTACCCTGTGAAGGAAAATAGTAAGCATAAATGC AAAGCCAAAACGTCAGGTCGAGGTGTAGCGTATG GGATGGGAAGAAATGGGCTACATTCCTGTTACAG AGAATACGAATTGTAATTTGAAAAAATTACCTGA AGGAGGATTTAGCAGTAAGTAGGGACTAGAGTGCC CTGCTGAAAACGGCCCTGAAGCGCGCACACCCGC CCGTCCTCTCTCCAAATAAACCCCTAGATATTACC TAAAATGCTTTTTATAATAAGGGGAGGCAAGTCGT AACATGGTAAGCGTACCGGAAGGTGCGCTTGGATG AACCAGAGCATAGCCAAGTTAGTAAAGCATCTCCC TTACACCGAGAAGTCGTCCGTGCAAATCGGACTGC CCTGATGCCCTAACAGCTAGCCTCAAAAATAAAAAT TTTACTATTATGGACCTAAAAACTCATAATAAACT TAAACAAATCATTTTACCCCTGAGTACGGGCGAC AGAAAAGGAGAAAAGAGCAACAGACAAAGTACCGC AAGGGAACGCTGAAAAGAAATGAAATAAACCAT TAAGCACCAAGCAGCAGAGTTTTCTACTCGTACCT TTTGCATCATGATTTAGCAAGAAAAC TACAAGCAA AGAGCCCTTTAGTTTGTAACCCCGAAACTGAGCGA GCTACTCCAAGACAGCCTATAAAGGGCAAACCCGT CTCTGTGGCAAAGAGTGGGAAGAGCTTTGAGTAG AGGTGACAAACCTACCGAGCCCAGTTATAGCTGGT TGCCCTGTGAAATGAATAGGAGTTCAGCCCTTTAAG TCTTTCCCCCTCACCCATGCTTACGCTAAAATTG ATTAAGGAACTAAAGGCGTTAATCAAAGGGGTA CAGCCCTTTTGATAGAAGAAACAAC TTTAACAGGT GACCCAAGATCATATTACCCAAGGATTTCAAATTA AGTGGGCC TAAAAGCAGCCATCTTATCAGAAAGCG TTAAAGCTCAAATTAGCCTATATCCTCATATACTG ATATTACATCTCCCTCCCTGCCCTTACCAGGCTG TCTTATGCCCCATAAGAACAATTATGCTAAAATG AGTAATAAGAAGAATTTAATTCCTCTCCTAGCACA
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<p>Flounder</p>	<p>Paralichthys lethostigma a</p>	<p>NC_029223.1</p>	<p>&gt;NC_029223.1 Paralichthys lethostigma mitochondrion, complete genome  GCTAACGTAGCTTAATTAAAGCATAAACACTGAAGA  TGTTAAGATGAGCCGTAGAAAGCCCCGTAAGCACA  AAGGCTTGGTCCCTGACTTTACTGTGACTCTAACT  AGACTTACACATGCAAGTATCCGCCCCCCTGTGAG  AATGCCCATAACTCCCTGCTTGGGAACAAGGAGCT  GGCATCAGGCACAGACCCCTCTAGCCCACGACGCC  TTGCTTTGCCACACCCCTCAAGGGAACCTCAGCAGTG  ATAAATATTAAGCTATAAGTGCAAACCTGACTTAG  TTAAAGTTAAGAGGGCCGGTAAAACCTCGTGCCAGC  CACCGCGGTTATACGAGAGGCCCAAGTTGACAGC  AGCGGCGTAAAGGGTGGTTAGGGGATTATCCAAAC  TAAAGCCGAACGCTCTCAGAAGTGTATAAGTACC  CGAGAGTATGAAACTCAATCACGAAAGTAGCTTTA  TTTACCCTGAACCCACGAAAGCTAAGGAACAAACT  GGGATTAGATACCCCACTATGCTTAGCCCTAAACA  TCGATTGTACAGTACATTCACATCCGCCTGGGGA  TTACGAACATTAGTTTAAAACCCAAAGGACTTGGC  GGTGCTTAACATCCACCTAGAGGAGCCTGTTCTAG  AACCGATAACCCCGTTAAACCTCACCTCTCTTG  CTTTTTTCCGCCTATATACCACCGTCGTCAGCTTA  CCCTGTGAAGGCTTAACAGTAAGCAAAGTTGGCAA  AGCCCAAACGTCAGGTCGAGGTGTAGTGAATGAG  AGGGGAAGAAATGGGCTACATTTGCTAAGACTAGC  AAATACGAACGATGCATTTGAAATATGCAACTGAAG  GAGGATTTAGCAGTAAGCAGGGAATAGAGTGCCCC  GCTGAAACTGGCCCTAAAGCGCGCACACACCGCCC  GTCACCTCCCCGAGCCCCAAGACTAAACTAACT  AAAAACAAC TACCCGGAAGGGGAGGAAAGTCGTA  ACATGGTAAGTGTACCGGAAGGTGTACTTGGAAAA  ATCAGGGCGTAGCTAAGCTAGACCCAGCACCTCAC  TTACACCGAGAAGACATCCGTGCAAGTCGGATCAC  CCTGACGCCCATTAGCTAGCCCAACCCCTTCACTC  ACAACCCCTATTAATAACCCCTAAAACACGTGA  CATCCACATAACCAAACCATTTTTCCCCCAAGTC  CAGGCGATGAAAAAGGAAATCCGGAGCAATAGAAA  AAGTACCGCAAGGGAAAGCTGAAAGAGAGATGAAA  CAGCCCAGTAAAGCTTAATGAAGCAGAGATTTAGA  CTCGTACCTTTTGCATCATGATTTAGCTAGCACTT  TCAAGCAAAGAGAAGTCTAGAGTTTGTAAACCCGAA  ACTGAGTGAGCTACTCCAAGACAGCCTATTTATAG  GGCAAACCCGTCTCTGTGGCAAAGAGTGGGAAGA  GCTTTGAGTAGAGGTGACAGACCTACCGAACTCAG  TTATAGCTGGTTGCCCGTGAATTGGATAGAAGTTC  AGCCCCCTGGGTCCCCGACTCATTCACTGTTATCA  CCCTCAGACGCAGCGAGAAACCAGGGATGTTAGT  CAAAGGGGGTACAGCCCCTTTGAACAAGACACAA  CTTTTACAGCAGGATAAAGATCACATTAATTAAG  GACAAATGTTTTAGTGGGCCTAAAAGCAGCCATCT  TTACAGAAAGCGTTAAAGCTCAGACATACGCACCT  CCACATATACCGATACCCCTATCTTAAGCCCCATA  ATTTAACGAGCCCCCTATGCTAACATAGGAACGA  CCATGCTAATATGAGTAATAAGAGAATATTAAGTA  CTCTCTCCTCGCACATGTGTATGTCCGAACGGACC  CCCCACCGACTCTTAACGGCCCCAACAAAAGAGGG</p>
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			AATTGGAATGTGTCATAAACAGACTAGAAAAACAT CCAACCTCAACCCCGTTAACCCACACTGGCGTGCT CCAGAGGAAAGACTAAAAAGGGAAGAAGGAACCTCG GCAAACCTACCCCAAGCCTCGCCTGTTTACCAAAA ACATCGCCTCTTGCAAAACATAAGTATAAGAGGTC CCGCCTGCCCAGTGACAAGATAGTTTAAACGGCCGC GGTATTTTGACCGTGCAAAGGTAGCGTAATCACTT GTCTTTTAAATGAAGACCCGTATGAATGGCATAAC GAGGGCTTAACTGTCTCCTTCCCCCAGTCAATGAA ATTGATCTCCCCGTGCAGAAGCGGGGATAAAATCA TAAGACGAGAAGACCCTATGGAGCTTTAGACGCAA AGACAGATCATGTCAAATACACCTAGTTATAGGCC TGAAC TAAATGAAACCAGTCTTGATGTCTTCGGTT GGGGCGACCATGGGGAACACAAAACCCCCACGTGG AACAGGAGTACACCCCTATCTTCCACCTCCTAC AACTAGAGCAACAGCTCTAATAAGCAGAAATTTCT GACCAAACCTGATCCGGCAACGCCGATCAACGAATC AAGTTACCCTAGGGATAACAGCGCAATCCCCTTTT AGAGCCCATATCGACAAGGGGGTTTACGACCTCGA TGTTGGATCAGGACATCCTAATGGTGCAAGGACAT CCCAATGGTGCAGCCGCTATTAAGGGTTCGTTTGT TCAACGATTAAGTCCACGTGATCTGAGTTCAGA CCGGAGTAATCCAGGTCAGTTTCTATCTATGTTGT GATCTTTTCTAGTACGAAAGGACCGAAAAGAAGAG GCCCATGCCTCTAGCACGCCTCACCCCCACCTAAT GAAAAATCTAAACTAGACAAAAGGGCATGACCAC TTATGTCTGAAGATAACGACGTGTTAGGGTGGCAGA GCCCCGCTAATGCAAAAGACCTAAGCCCTTTCTAC AGAGGTTCAAGTCTCTCCTTAACTATGATTTTCTGA TACTCATTTACGCACATCATCAACCCGTTAGCCCTA ATCGTACCCGTACTATTAGCGGTAGCATTCCTCAC CCTGCTTGAACGAAAAGTGCTTGGCTACATACAAC TTTCGAAAAGGCCCGAATATCGTGGGACCCATGGC CTCCTCCAACCCATCGCCGACGGCGTAAAAC TTTT TATTAAGAACCCGTTTCGACCTTCAACCGCATCTC CCCTCCTCTTCTTCTAGCACCCATACTTGC ACTC
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