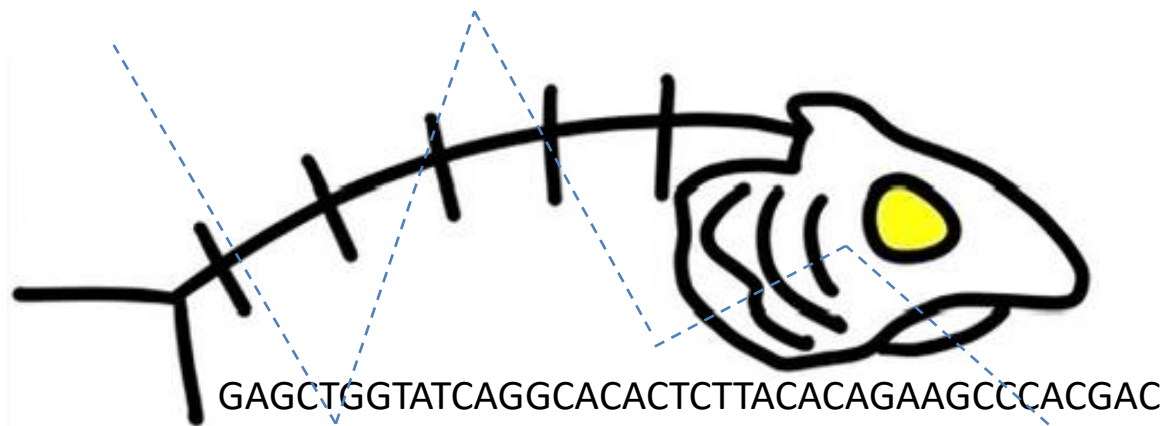
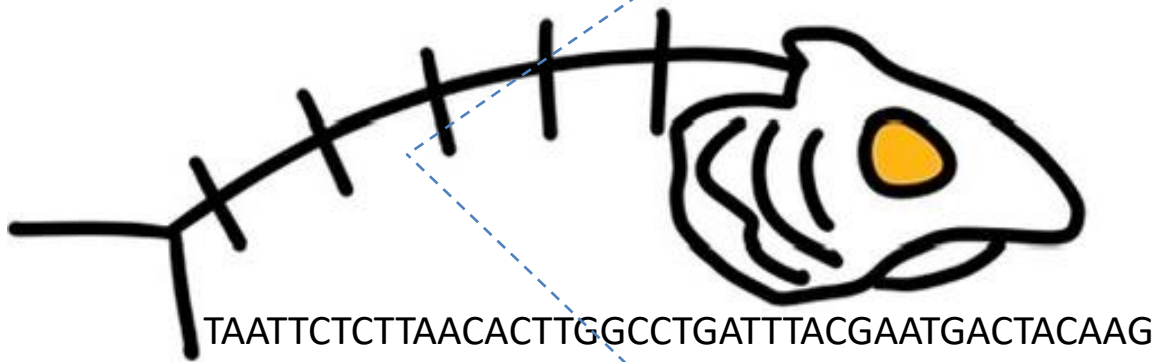
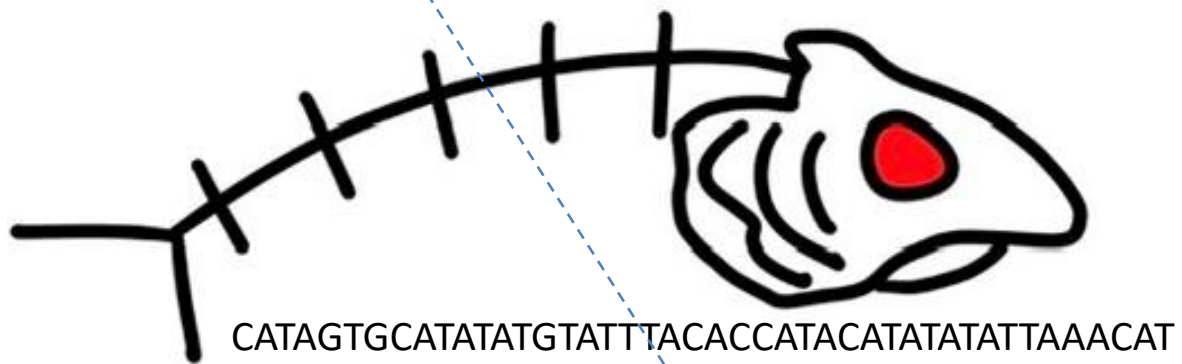
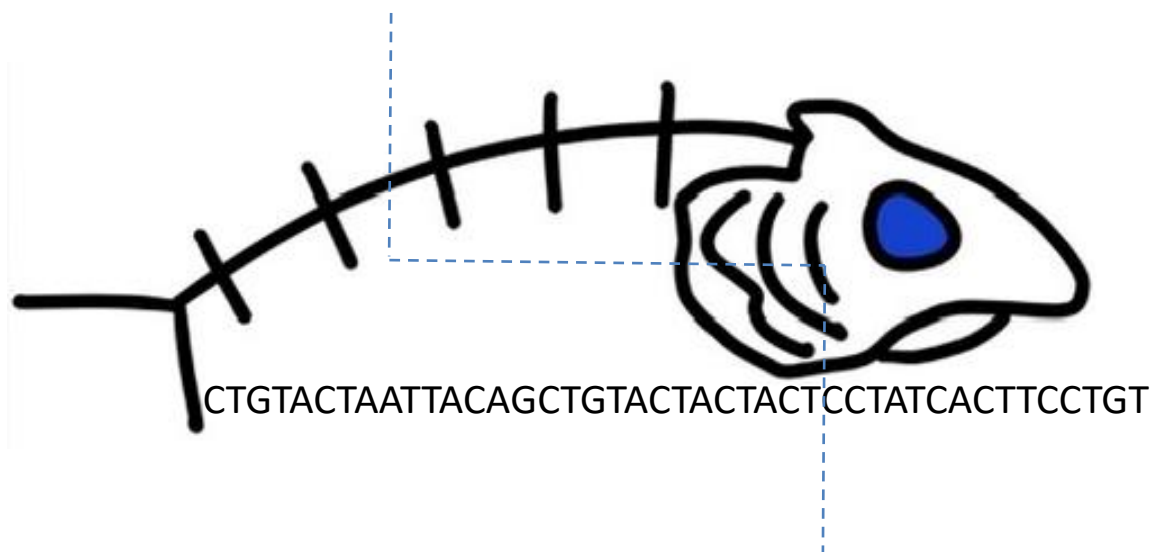
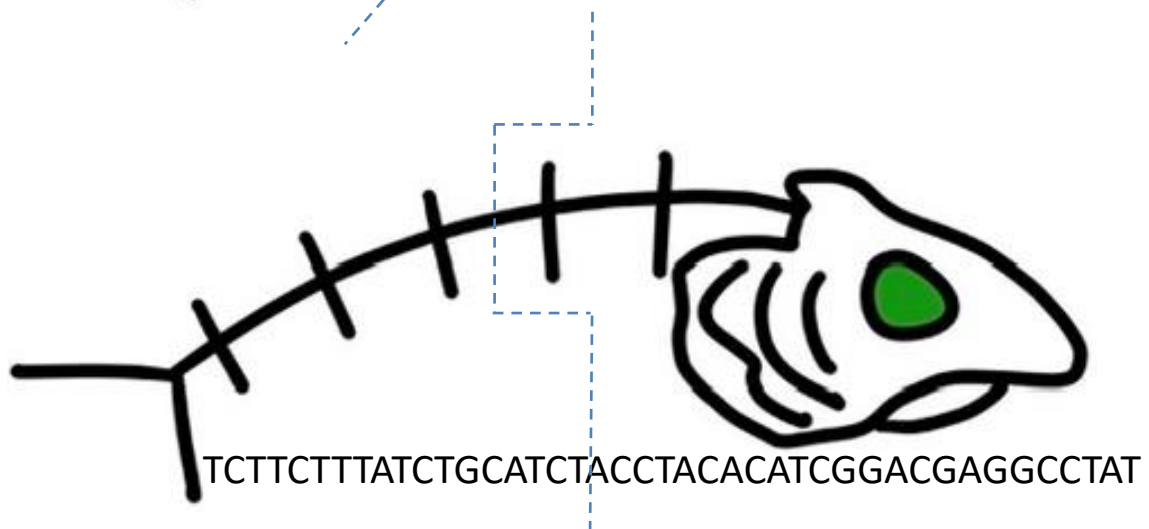
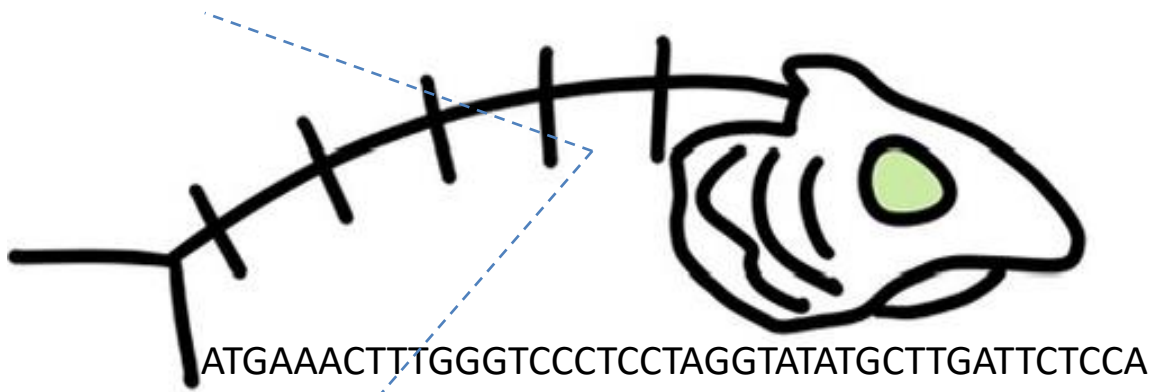
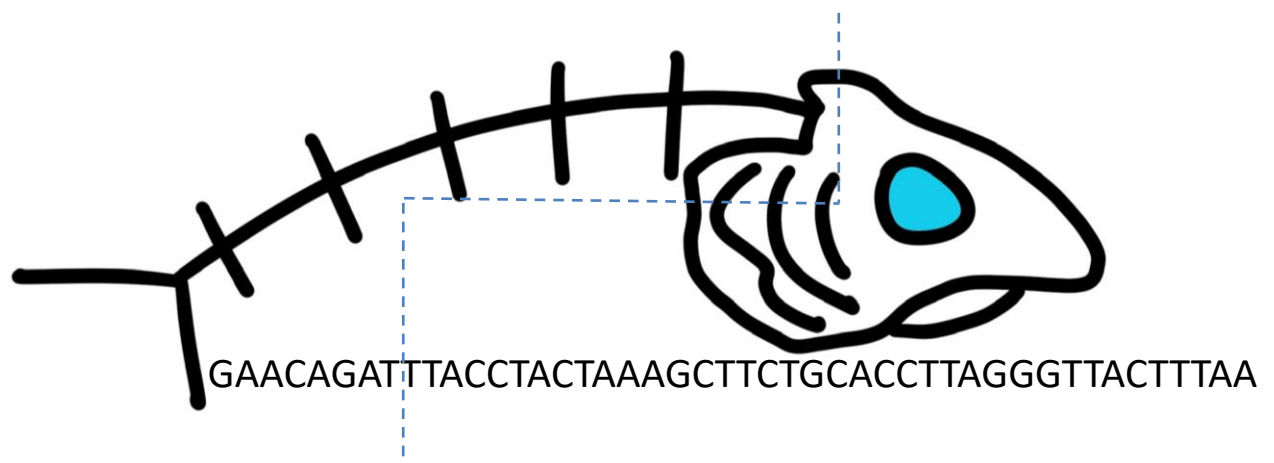
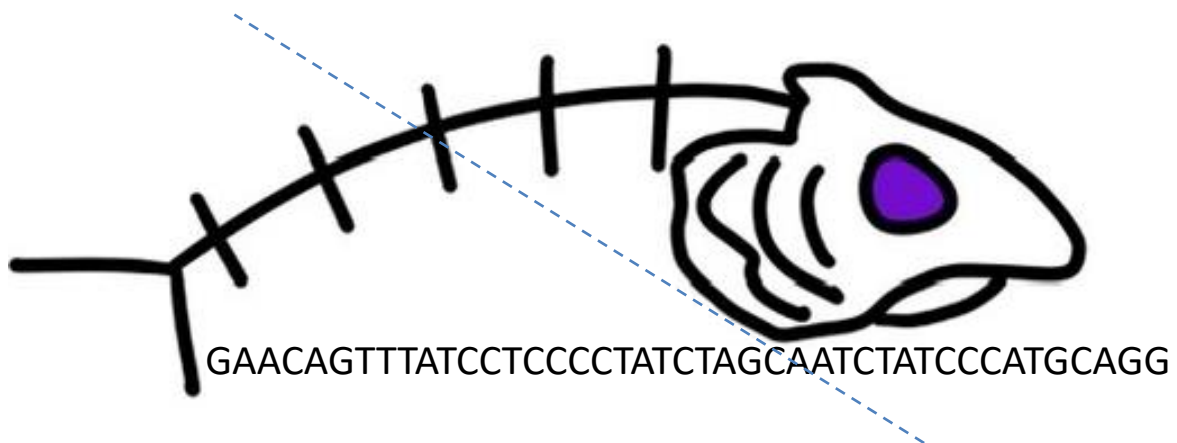
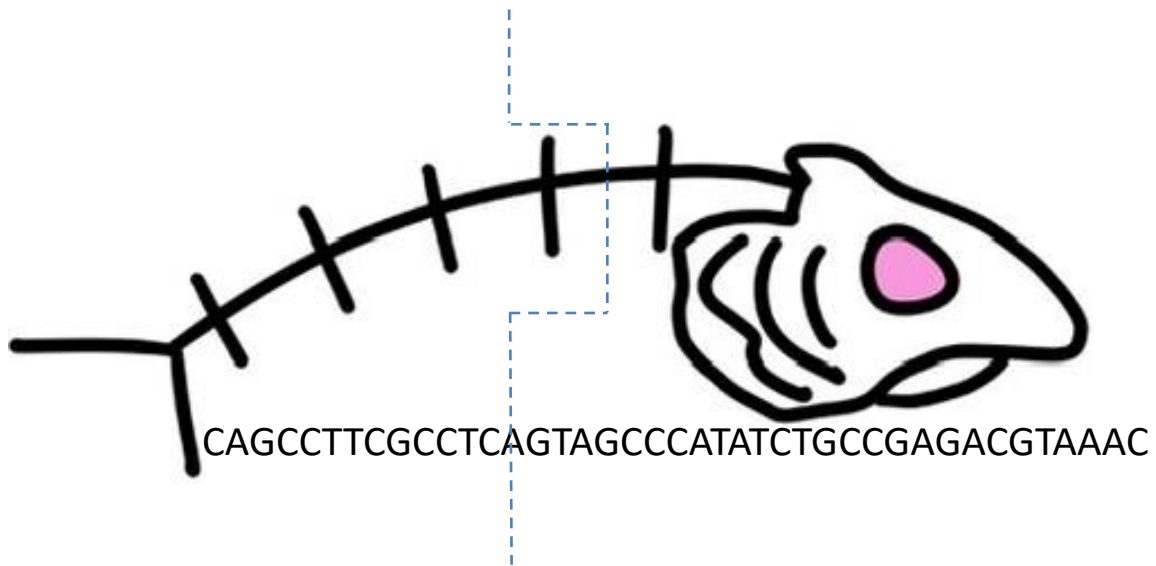


## Handout 1. Fish to Cut Out







## Worksheet 1. Student Worksheet

Name

Assessment

Class period

Date

Eye color of organism

1. What is the DNA sequence you picked?

**NCBI BLAST website:** <https://blast.ncbi.nlm.nih.gov/Blast.cgi>

Go to NCBI GenBank, nucleotide BLAST. Search the sequence and answer the following questions:

2. What is the first scientific name that comes up? They are in the second column.

3. Are the first three scientific names the same species?

4. Keep scrolling down the page. Are there other species listed that are different from the top result? If not, list the English common name of your species. If yes, list the other scientific names and determine the English common name for those species, in addition to your species.

5. If there are other species that are listed in the results, why do you think the results show other species besides the correct species identification?

6. How can using DNA and genetics be useful in learning about the food web?

**Worksheet 2. Advanced Student Worksheet Supplement – use the DNA sequence from the organism in Worksheet 1**

Name	Assessment	Class period
Date	Eye color of organism	

1. What is the transcribed sequence? (DNA to RNA)

2. What is the translated sequence? (RNA to protein)

Go to NCBI GenBank, protein BLAST. Search the protein sequence and answer the following questions:

3. What are the first three proteins that come up?

4. Pick one of them. Click on one of the description rows with the name of the protein (first column). What is the Query sequence and the Subject of the protein?

5. For the protein you picked, what is the main function of this gene? Tip: use [www.uniprot.org](http://www.uniprot.org) or <https://www.ebi.ac.uk/interpro/entry/InterPro/#table> to learn more about the protein. Google scholar is also a good source to find information about proteins.

6. In these searches, there are likely new vocabulary words. List three of them and provide the definition.

Sequences producing significant alignments					Download	Select columns	Show	100	?
<input checked="" type="checkbox"/> select all 100 sequences selected					<a href="#">GenBank</a>	<a href="#">Graphics</a>	<a href="#">Distance tree of results</a>	<a href="#">MSA Viewer</a>	
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	<a href="#">Auxis thazard haplotype 256 tRNA-Pro gene and D-loop, partial sequence: mitochondrial</a>	<a href="#">Auxis thazard</a>	82.4	82.4	100%	1e-12	100.00%	441	<a href="#">JN398926.1</a>
<input checked="" type="checkbox"/>	<a href="#">Auxis thazard haplotype 215 tRNA-Pro gene and D-loop, partial sequence: mitochondrial</a>	<a href="#">Auxis thazard</a>	82.4	82.4	100%	1e-12	100.00%	444	<a href="#">JN398885.1</a>
<input checked="" type="checkbox"/>	<a href="#">Auxis thazard haplotype 148 tRNA-Pro gene and D-loop, partial sequence: mitochondrial</a>	<a href="#">Auxis thazard</a>	82.4	82.4	100%	1e-12	100.00%	450	<a href="#">JN398818.1</a>

Orange species:

Sequences producing significant alignments					Download	Select columns	Show	100	?
<input checked="" type="checkbox"/> select all 3 sequences selected					<a href="#">GenBank</a>	<a href="#">Graphics</a>	<a href="#">Distance tree of results</a>	<a href="#">MSA Viewer</a>	
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	<a href="#">Euthynnus alletteratus mitochondrion, complete genome</a>	<a href="#">Euthynnus alletteratus</a>	78.7	78.7	100%	2e-11	100.00%	16520	<a href="#">NC_004530.1</a>
<input checked="" type="checkbox"/>	<a href="#">Euthynnus alletteratus voucher USNM 421831 mitochondrion, complete genome</a>	<a href="#">Euthynnus alletteratus</a>	78.7	78.7	100%	2e-11	100.00%	16520	<a href="#">MW232424.1</a>
<input checked="" type="checkbox"/>	<a href="#">Euthynnus alletteratus mitochondrial DNA, complete genome</a>	<a href="#">Euthynnus alletteratus</a>	78.7	78.7	100%	2e-11	100.00%	16523	<a href="#">AP006829.1</a>

Yellow species:

Sequences producing significant alignments					Download	Select columns	Show	100	?
<input checked="" type="checkbox"/> select all 56 sequences selected					<a href="#">GenBank</a>	<a href="#">Graphics</a>	<a href="#">Distance tree of results</a>	<a href="#">MSA Viewer</a>	
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	<a href="#">Scomber colias mitochondrial DNA, tRNA-Pro, control region and tRNA-Phe region, haplotype: ScoCRH42</a>	<a href="#">Scomber colias</a>	75.0	75.0	100%	2e-10	100.00%	1249	<a href="#">AB361536.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomber colias mitochondrial DNA, tRNA-Pro, control region and tRNA-Phe region, haplotype: ScoCRH2</a>	<a href="#">Scomber colias</a>	75.0	75.0	100%	2e-10	100.00%	1250	<a href="#">AB361496.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomber colias mitochondrial DNA, tRNA-Pro, control region and tRNA-Phe region, haplotype: ScoCRH4</a>	<a href="#">Scomber colias</a>	75.0	75.0	100%	2e-10	100.00%	1250	<a href="#">AB361499.1</a>

Light Green species:

Sequences producing significant alignments					Download	Select columns	Show	100	?
<input checked="" type="checkbox"/> select all 2 sequences selected					<a href="#">GenBank</a>	<a href="#">Graphics</a>	<a href="#">Distance tree of results</a>	<a href="#">MSA Viewer</a>	
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	<a href="#">Stephanolepis hispidus cytochrome b (cytb) gene, complete cds: mitochondrial</a>	<a href="#">Stephanolepis hispida</a>	78.7	78.7	100%	2e-11	100.00%	1141	<a href="#">HM049967.1</a>
<input checked="" type="checkbox"/>	<a href="#">Stephanolepis hispidus cytochrome b (cytb) gene, complete cds: mitochondrial</a>	<a href="#">Stephanolepis hispida</a>	78.7	78.7	100%	2e-11	100.00%	1141	<a href="#">DQ198008.1</a>

Dark Green species:

Sequences producing significant alignments					Download	Select columns	Show	100	?
<input checked="" type="checkbox"/> select all 100 sequences selected					<a href="#">GenBank</a>	<a href="#">Graphics</a>	<a href="#">Distance tree of results</a>	<a href="#">MSA Viewer</a>	
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	<a href="#">Pomatomus saltatrix voucher RSA04 cytochrome b gene, partial cds: mitochondrial</a>	<a href="#">Unknown</a>	78.7	78.7	100%	2e-11	100.00%	1078	<a href="#">KX196672.1</a>
<input checked="" type="checkbox"/>	<a href="#">Pomatomus saltatrix voucher RSA33 cytochrome b gene, partial cds: mitochondrial</a>	<a href="#">Unknown</a>	78.7	78.7	100%	2e-11	100.00%	1078	<a href="#">KX196701.1</a>
<input checked="" type="checkbox"/>	<a href="#">Pomatomus saltatrix voucher ANG08 cytochrome b gene, partial cds: mitochondrial</a>	<a href="#">Unknown</a>	78.7	78.7	100%	2e-11	100.00%	1078	<a href="#">KX196711.1</a>

Dark Blue species: