

The challenge

Your company has been asked to carry out an ecological survey of a wetlands area and river system to find out which species are living there. You will use environmental DNA (eDNA) to produce a site report.

Working in groups:

1. Identify the species living in your location using comparison of eDNA sequences from the 'Site data files' to the online DNA database.
2. Find out more about your species using the 'River species list'.
3. Complete your 'Site report' sheet.
4. Investigate what impact the species present may have on the ecosystem and feedback your results to the class.

Follow the steps below to identify the species in your location.

1. Open the 'Site data file' document for your location on your computer.
2. Go to <https://blast.ncbi.nlm.nih.gov/>.
3. Click 'Nucleotide BLAST'.

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)

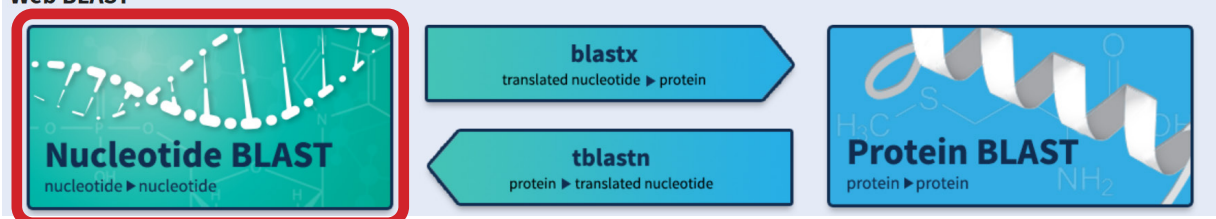
Mon, 17 Mar 2025

Improvements include upgrading to GCP Artifact Registry and better handling of job completion status in kubernetes version 1.30+.

ElasticBLAST 1.4.0 is now available!

[More BLAST news...](#)

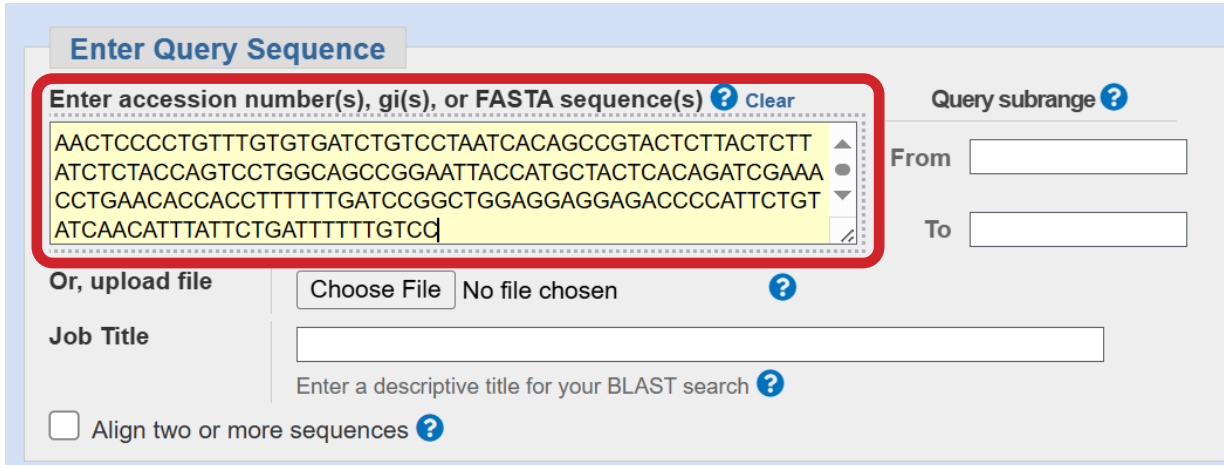
Web BLAST



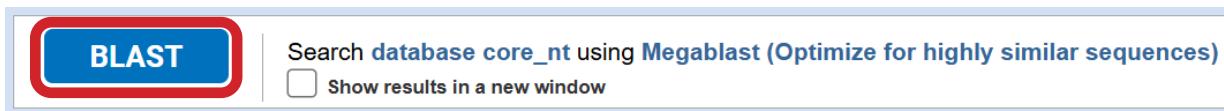
The Web BLAST interface features four main options:

- Nucleotide BLAST**: nucleotide ► nucleotide (highlighted with a red border)
- blastx**: translated nucleotide ► protein
- tblastn**: protein ► translated nucleotide
- Protein BLAST**: protein ► protein

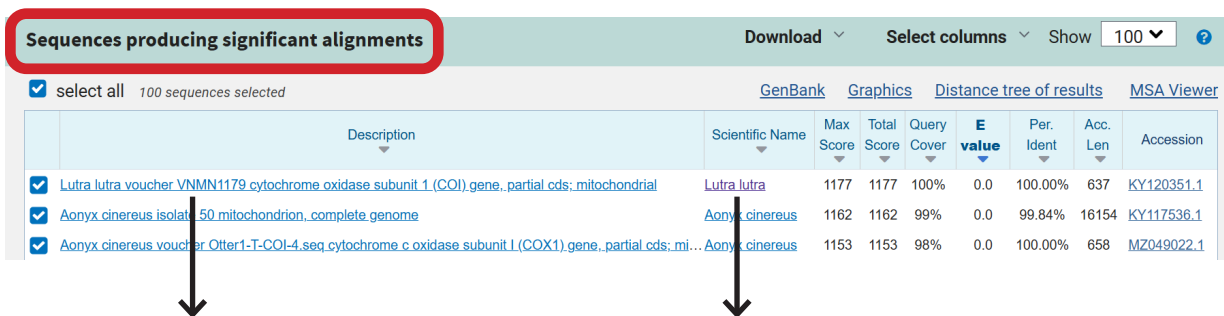
- Copy the DNA sequence for one species and paste it into the 'Enter Query Sequence Box'.



- Click 'BLAST' at the bottom of the page to search the DNA database for a matching sequence.



- On the results page, scroll down to 'Sequences producing significant alignments'. This will show a description of the sample that your eDNA matches and the scientific name of the species.



Sequences producing significant alignments								
Download Select columns Show 100 ?								
<input checked="" type="checkbox"/> select all 100 sequences selected								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Lutra lutra voucher VNMN1179 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Lutra lutra	1177	1177	100%	0.0	100.00%	637	KY120351.1
<input checked="" type="checkbox"/> Aonyx cinereus isolate 50 mitochondrion, complete genome	Aonyx cinereus	1162	1162	99%	0.0	99.84%	16154	KY117536.1
<input checked="" type="checkbox"/> Aonyx cinereus voucher Otter1-T-COI-4 seq cytochrome c oxidase subunit I (COX1) gene, partial cds; mi...	Aonyx cinereus	1153	1153	98%	0.0	100.00%	658	MZ049022.1

Description of sample

Scientific name of species

- Now you have identified a species present at your site, find out its common name, facts about it and its conservation status from the 'River species list'.

8. Put a tick on your 'Site report' sheet to record the species' presence.
9. Repeat steps 3-8 to identify which species each DNA sequence comes from and to complete the table on your 'Site report' sheet.
10. Consider the impact each species at your site may have on the ecosystem. Find out more about each species using the 'River species list'.
 - Which are predators?
 - Are there any endangered species present?
 - Are there any invasive species present?
 - Are any species indicators of good water quality?
11. Record your findings on the second side of your 'Site report' sheet.