Evaluation of AmtDNA Database

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Outline

- AmtDB is a database of ancient human mitochondrial DNA
- AmtDB fills a crucial niche in the field of biological archaeology/anthropology
- AmtDB provides an easy-to-use, simple interface for scientists to be able to find the right sample(s) for their needs
- AmtDB contains high quality information, but may not be the most complete database

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Ancient mtDNA Database (AmtDB)

- Database of ancient mitochondrial DNA
- Built with secondary sources
- Curated by a select group of researchers

AmtDB is a database of ancient human mitochondrial DNA

- Maintenance:
  - Dr. Ehler - Czech Academy of Sciences, Czech Republic
  - Anna Juras - Adam Mickiewicz University, Poland
- Funding:
  - The Ministry of Education, Youth and Sports of the Czech Republic
  - The Polish National Science Center

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AmtDB fills a niche in the field of biological archaeology/anthropology

- No other database exists specifically for ancient human mitochondrial DNA
    - Ancient genetic data from multiple populations and multiple points in time can allow for the study of populations in space and time using phylogenetic and population genetic methods (Ramakrishnan & Hadley, 2009)
- Mitochondrial DNA is particularly useful:
    - Often the only genetic material that can be recovered from samples
    - Particularly suited to population-level studies because of maternal inheritance, high mutation rate, and absence of recombination and population-level variability

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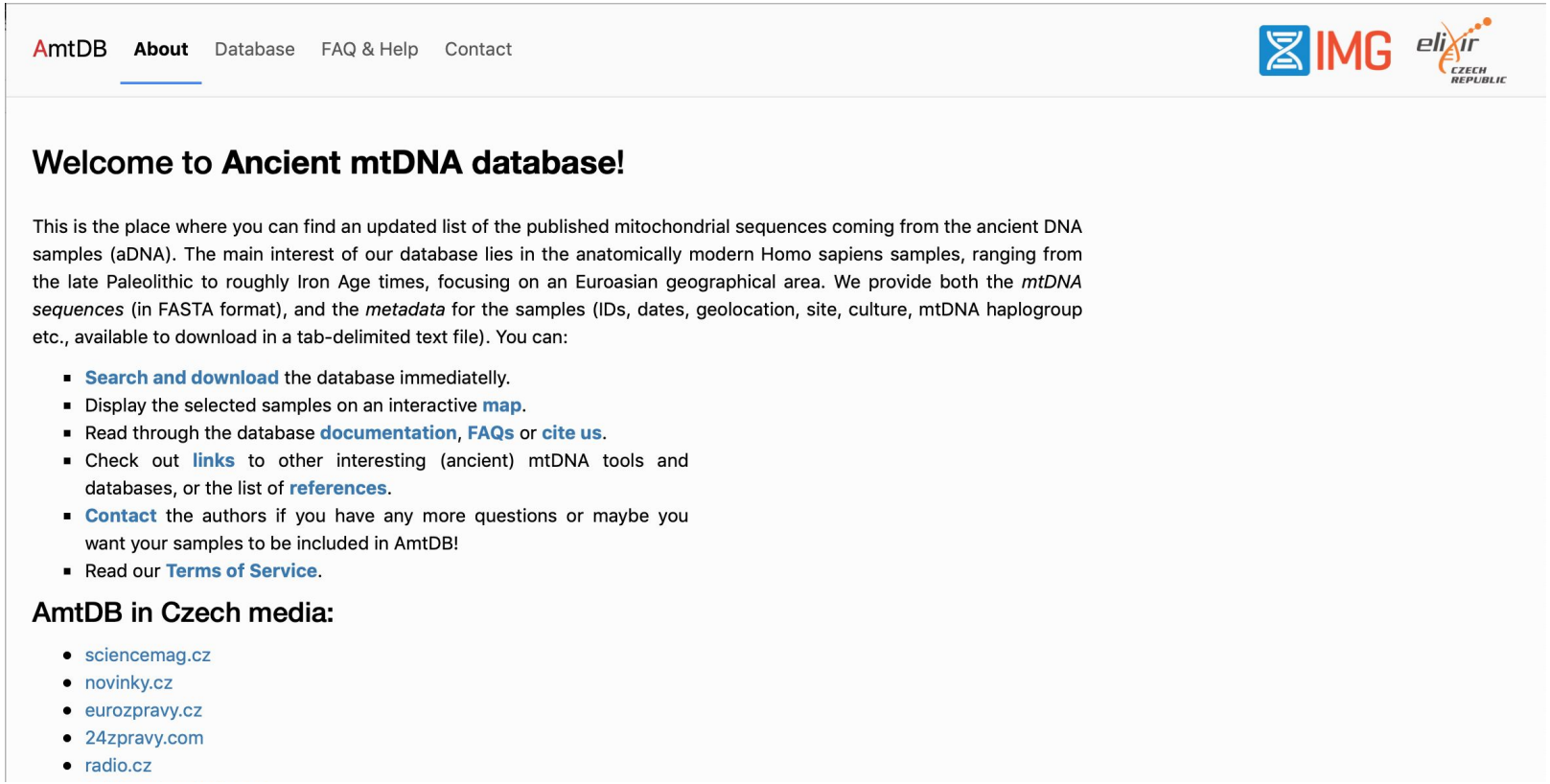
The AmtDB contains important information and links regarding the database



Links to other sites on AmtDB

- The ELIXIR Czech Republic
- The Institute of Molecular Genetics of the Czech Academy of Sciences
- An individual reference to each source of mitochondrial DNA

Search

Paleolithic | Mesolithic | Neolithic | Copper Age | Bronze Age | Iron Age | Middle Ages

Advanced search

Actions

Download FASTA	All	Selected	Separated
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Table | Map

Select all
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Show 50 entries

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Quick filter:

ID	Name	Group	Epoch	Country	Sex	Year from	Year to	Haplogroup	Sequence source	Avg. coverage	References	Download	Map
1	RISE509	BARu	Bronze Age	Russia	F	-2887	-2677	T2c1a2	bam	<NA		FASTA | metadata	
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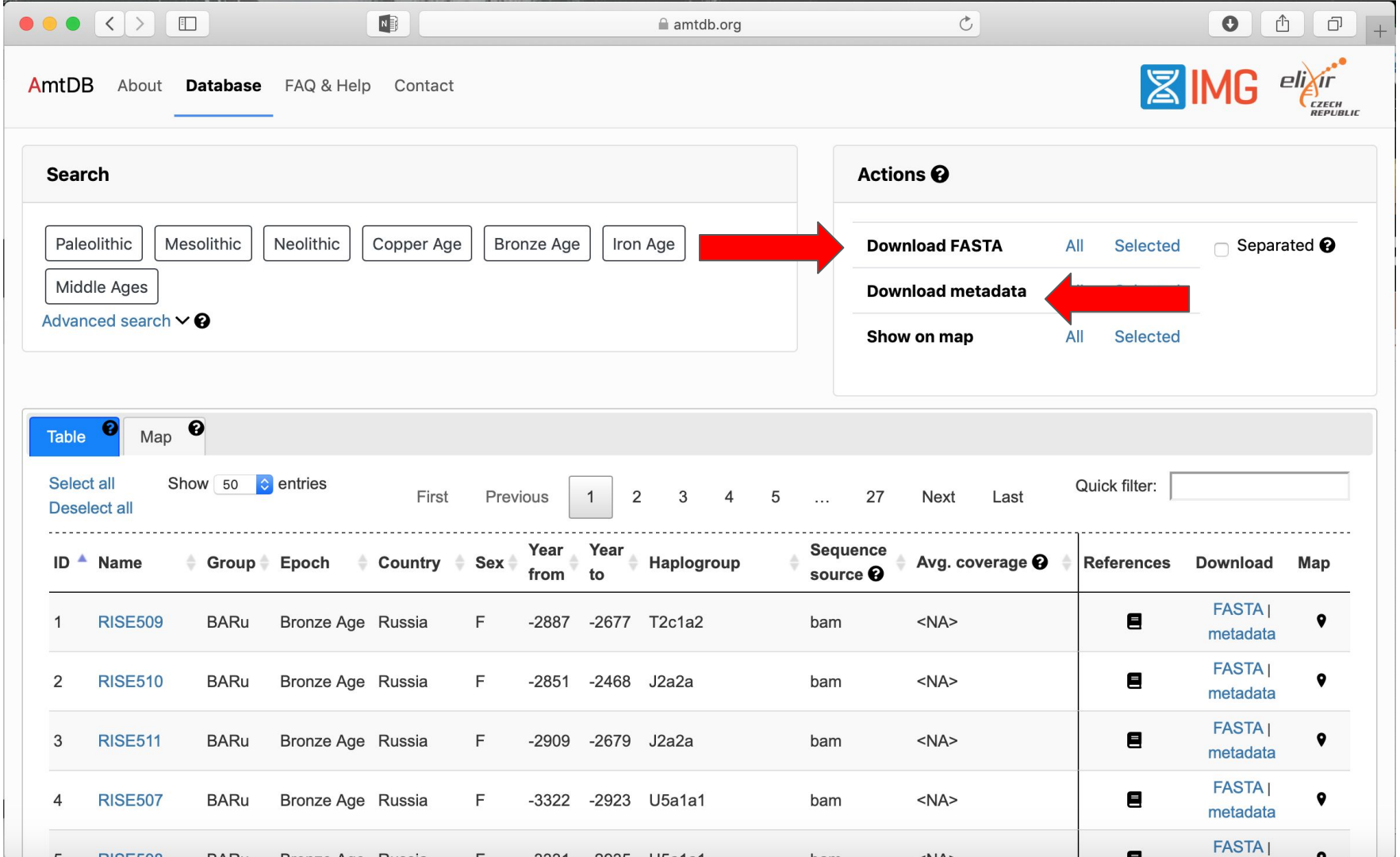
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amtdb.org

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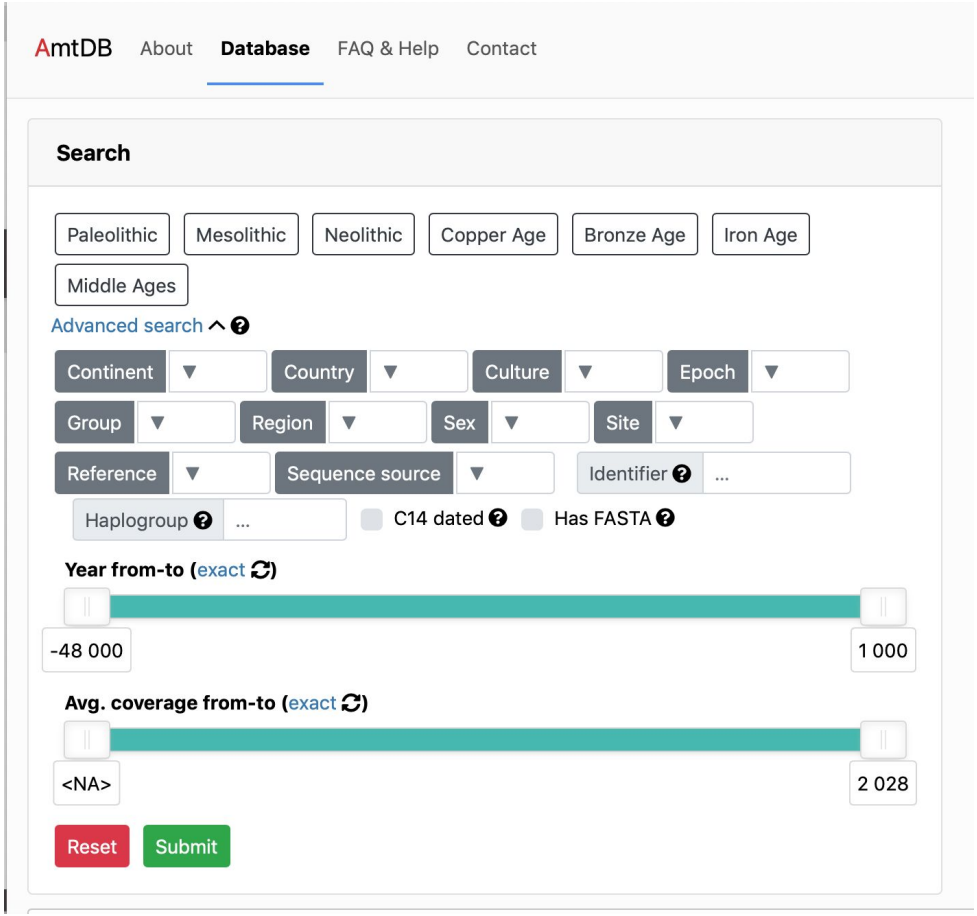
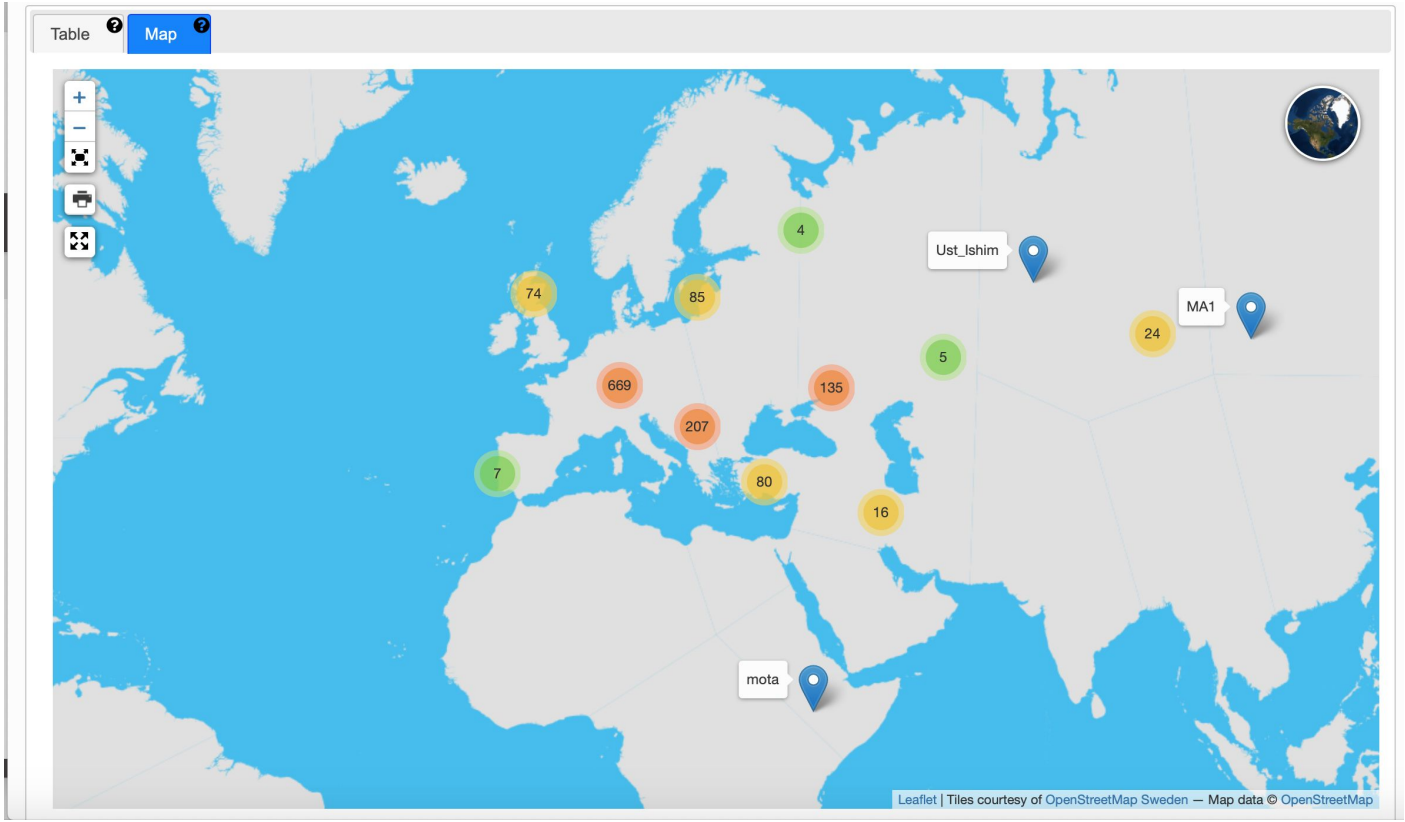
5												FASTA |	

Advance Search

- Allows the data to be narrowed down very specifically
- You can just download the data you need

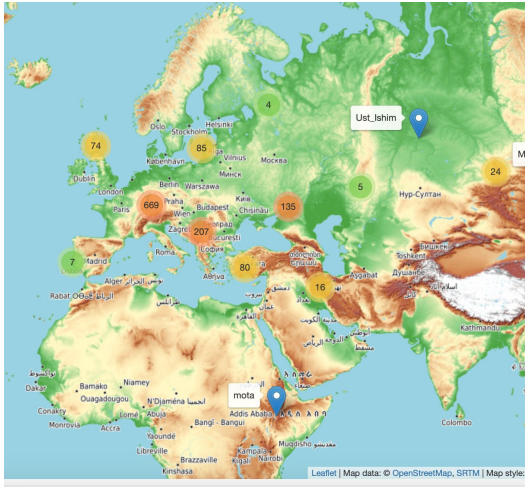


A user may also search for an entry via a map



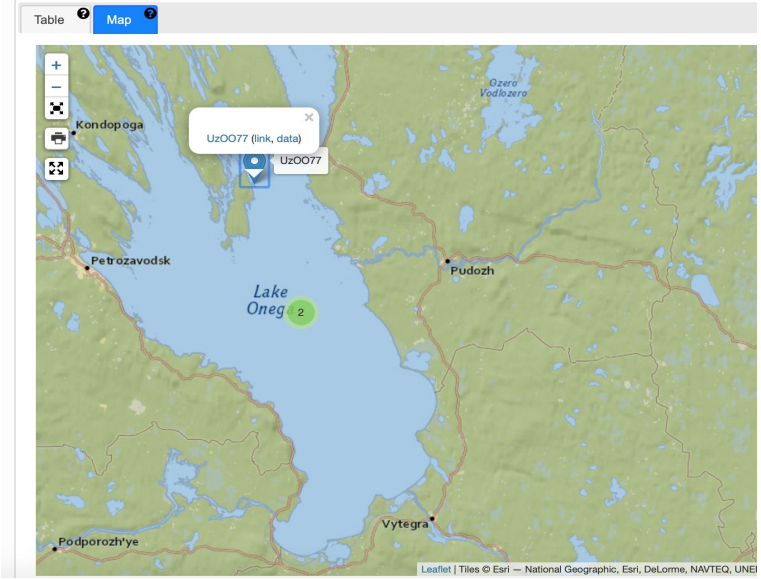
Maps can be easily modulated to display in different formats

- The maps can be changed the samples can be viewed geographically or topically

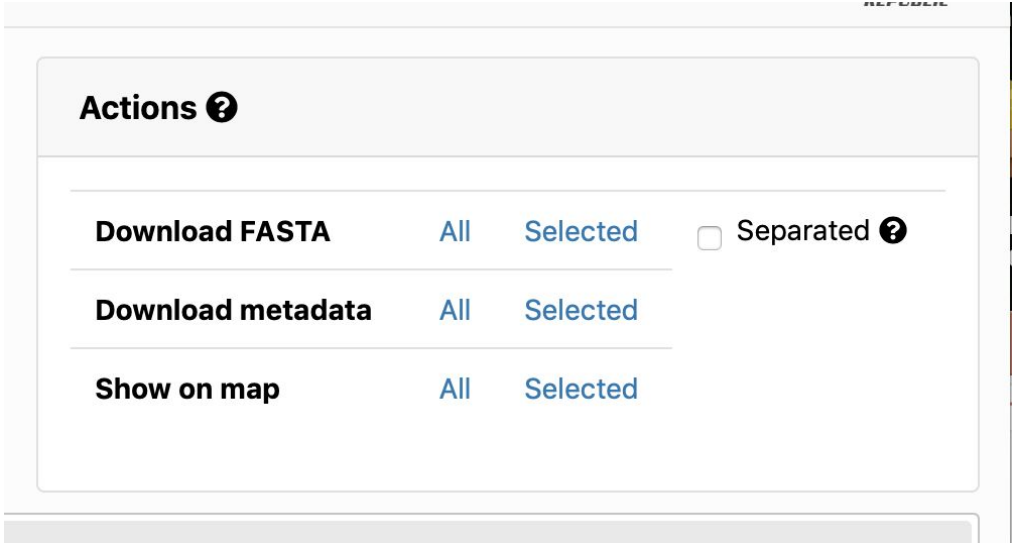


Individual samples can be pinpointed and accessed

You could even select a single mitochondrial DNA sample off the map and access its profile on the site, link to primary data and its journal article



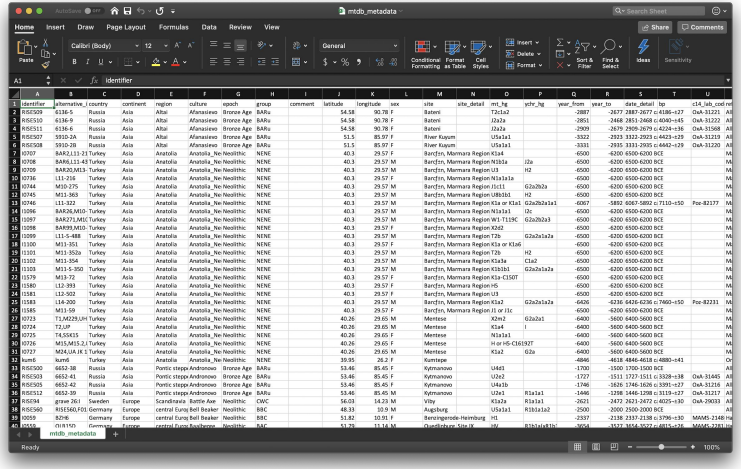
Easily download individual entries or the entire database



Users may download data entries with various options

- Download sequences in the common FASTA (.fasta) format

- Download sequence metadata in a tabular (.csv) format



There are no license agreement or restrictions, simply a disclaimer

AmtDB Terms of Service

The content of the AmtDB is the sole responsibility of researchers at the Institute of Molecular Genetics, Academy of Sciences of the Czech Republic. Authors make no representations or warranties of any kind, express or implied, concerning the content of the database, including, without limitation, warranties of merchantability, fitness for a particular purpose, non-infringement, validity of any intellectual property rights or claims, whether issued or pending, and the absence of latent or other defects, whether or not discoverable.

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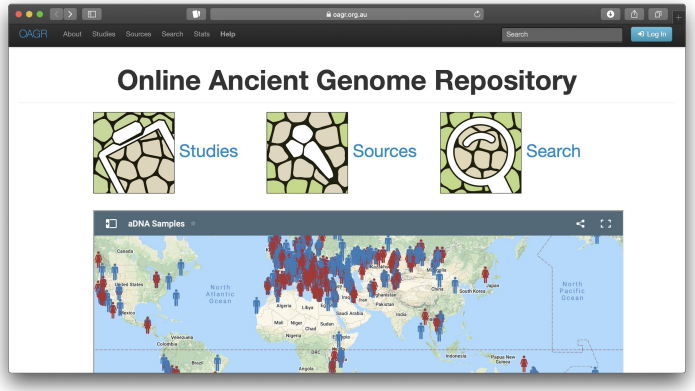
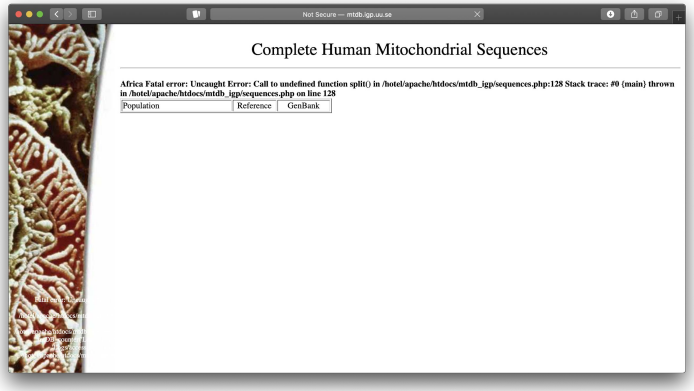
Competitors:



Online Ancient Genome Repository - ancient human genome database maintained by University of Adelaide, Australia



mtDB: Human Mitochondrial Genome Database - maintained by Uppsala University, Swedent

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Lack of data:

In conclusion, AmtDB is a fairly new, but thorough and easy to use database

- The database fills a particular thus-far unfilled niche in its particular area of usage
- The clean and modern interface, along with host of options make it an easy to use database
- Manual curation is to the benefit of the database because of the relatively small size of total samples

Acknowledgements

This week, the two partners for this project are Mihir Samdarshi and Emma Young. Both partners worked with each other outside of class to assist each other in finding and synthesizing the necessary information required to complete this assignment.

We would like to acknowledge Dr. Dahlquist for her instruction on this topic and how to give a presentation.

References

1. Ehler, E., Novotný, J., Juras, A., Chyleński, M., Moravčík, O., & Pačes, J. (2018). AmtDB: a database of ancient human mitochondrial genomes. Nucleic acids research, 47(D1), D29-D32.
2. Ramakrishnan, U., & Hadly, E. A. (2009). Using phylochronology to reveal cryptic population histories: review and synthesis of 29 ancient DNA studies. Molecular Ecology, 18(7), 1310-1330.