2022
F.I.R.S.T Workshop

PubMed and Bio-Resources Databases of NTU Library

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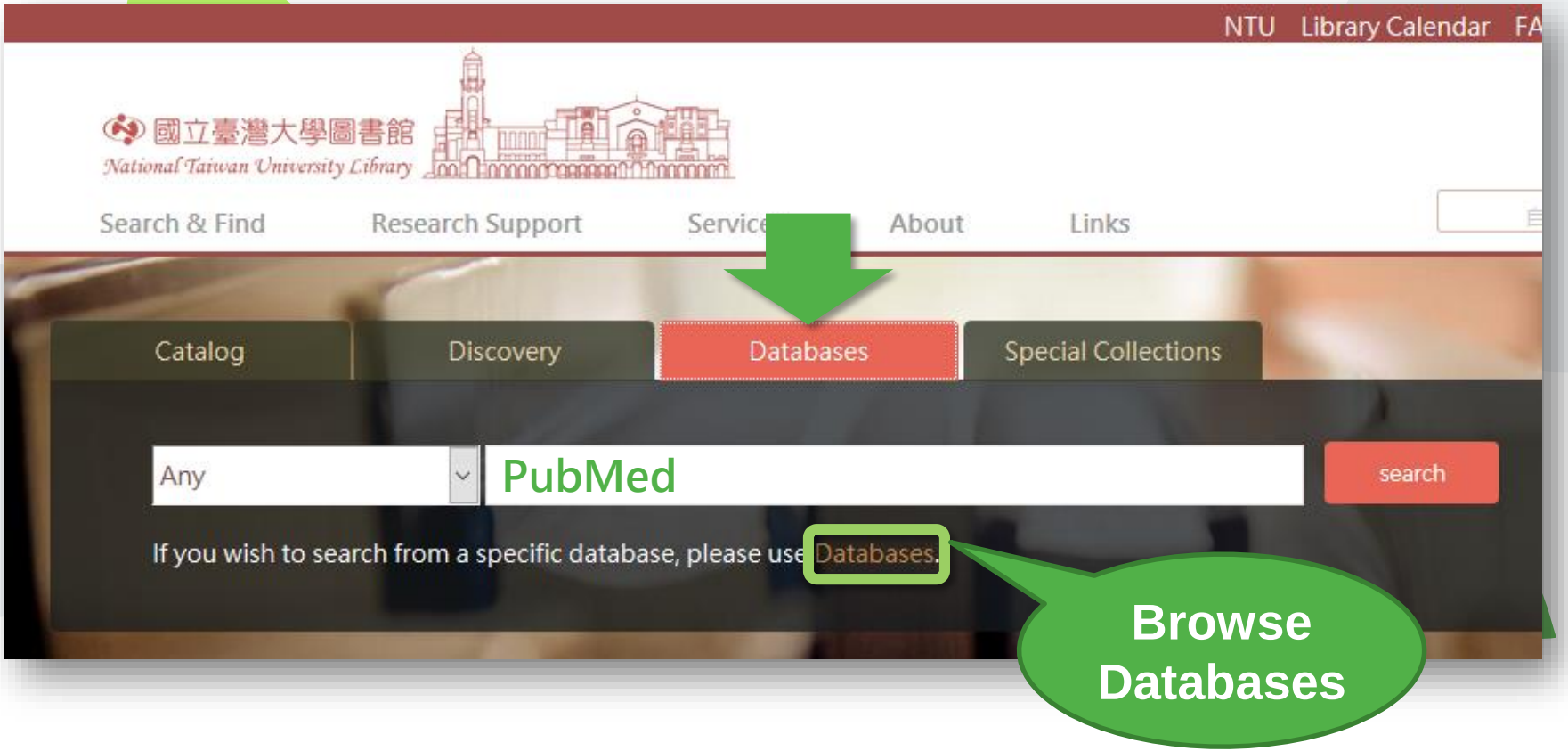
Subject Service Division,
National Taiwan University Library

In this talk

1. How to search databases?
2. Search Strategies and Techniques
3. PubMed
4. General Bio-Resources Databases
5. Open Access Resources

1.
How to search databases?

Databases


NTU Library Calendar FA
國立臺灣大學圖書館
National Taiwan University Library
Search & Find
Research Support
Service
About
Links
Catalog
Discovery
Databases
Special Collections
Any
PubMed
search
If you wish to search from a specific database, please use Databases.
Browse Databases

Sign in to get complete results and to request items Sign in

General databases often used

Databases by Category / Titles / Content Type

- Browse by Subject
- Browse by Titles
- Content Type
- Trial

Click “>” to show more

Related Links

- View All
- Database APP
- Off-campus Internet Connection

Top picks

- Web of Science
- Scopus
- JSTOR
- Academic Search Complete
- Airiti library
- CNKI

Feature Databases

Arts & Humanities

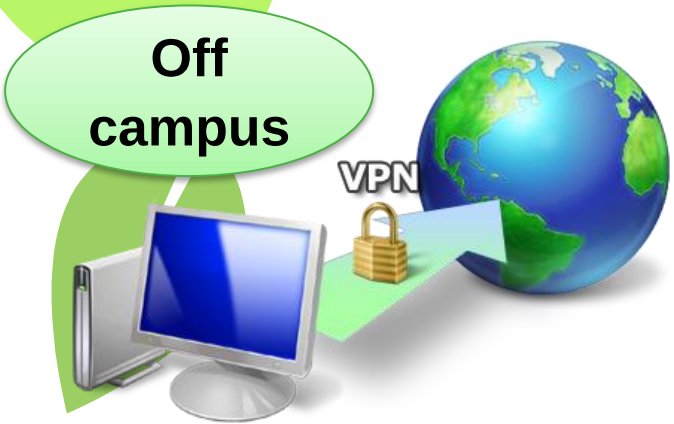
Art ; History ; Linguistics ; Literature ; Music ; Philosophy ; Religi
; Theatre／Movies

Life Sciences & Medicine

Agriculture ; Biological Sciences ; Medical Science ; Nursing
; Pharmacy / Pharmacology ; Public Health ; Zoology

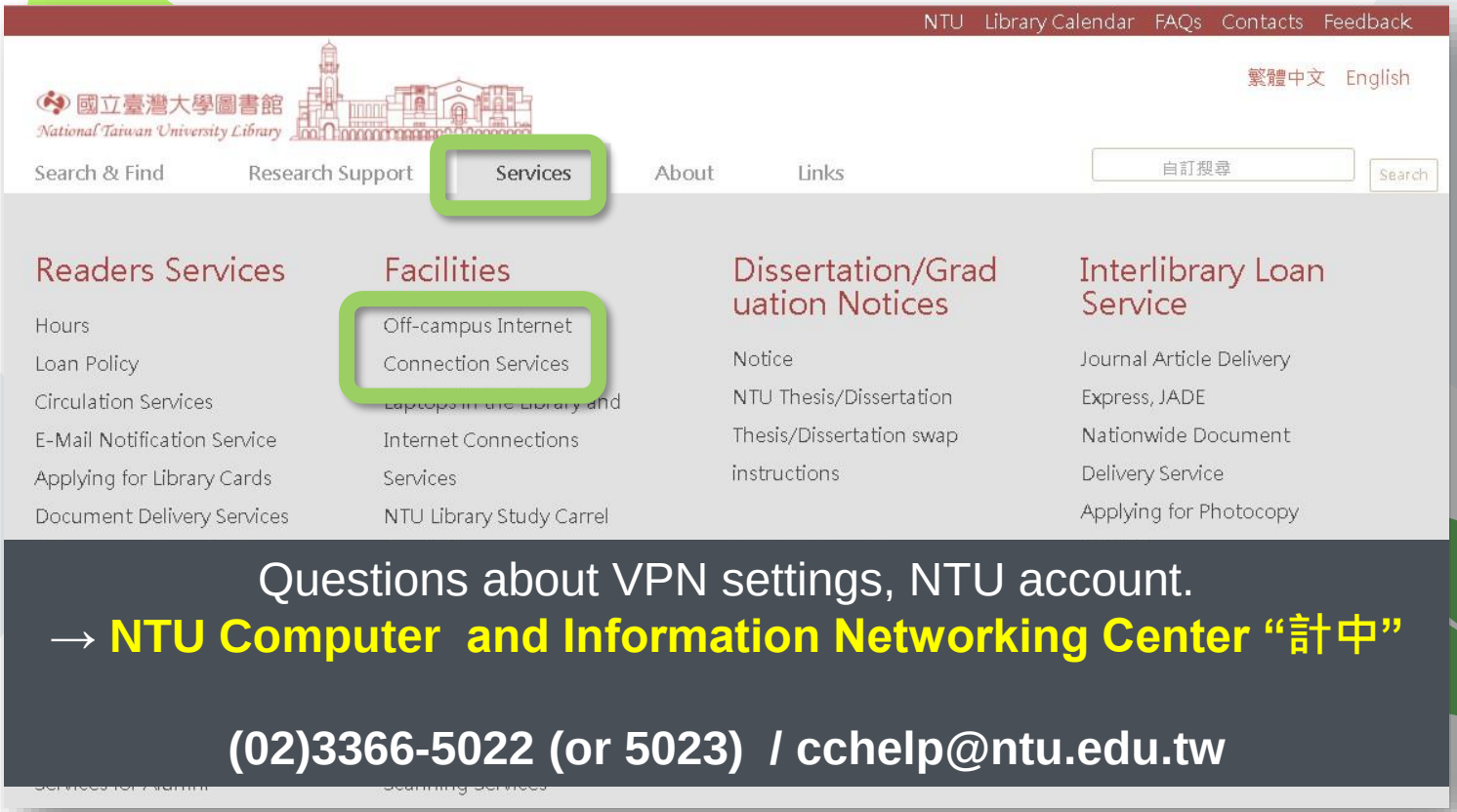
Important databases of each subject

Off-campus internet connection services (VPN, Virtual Private Network)



NTU IP address 140.112.*.*

Off-campus internet connection services (VPN, Virtual Private Network)

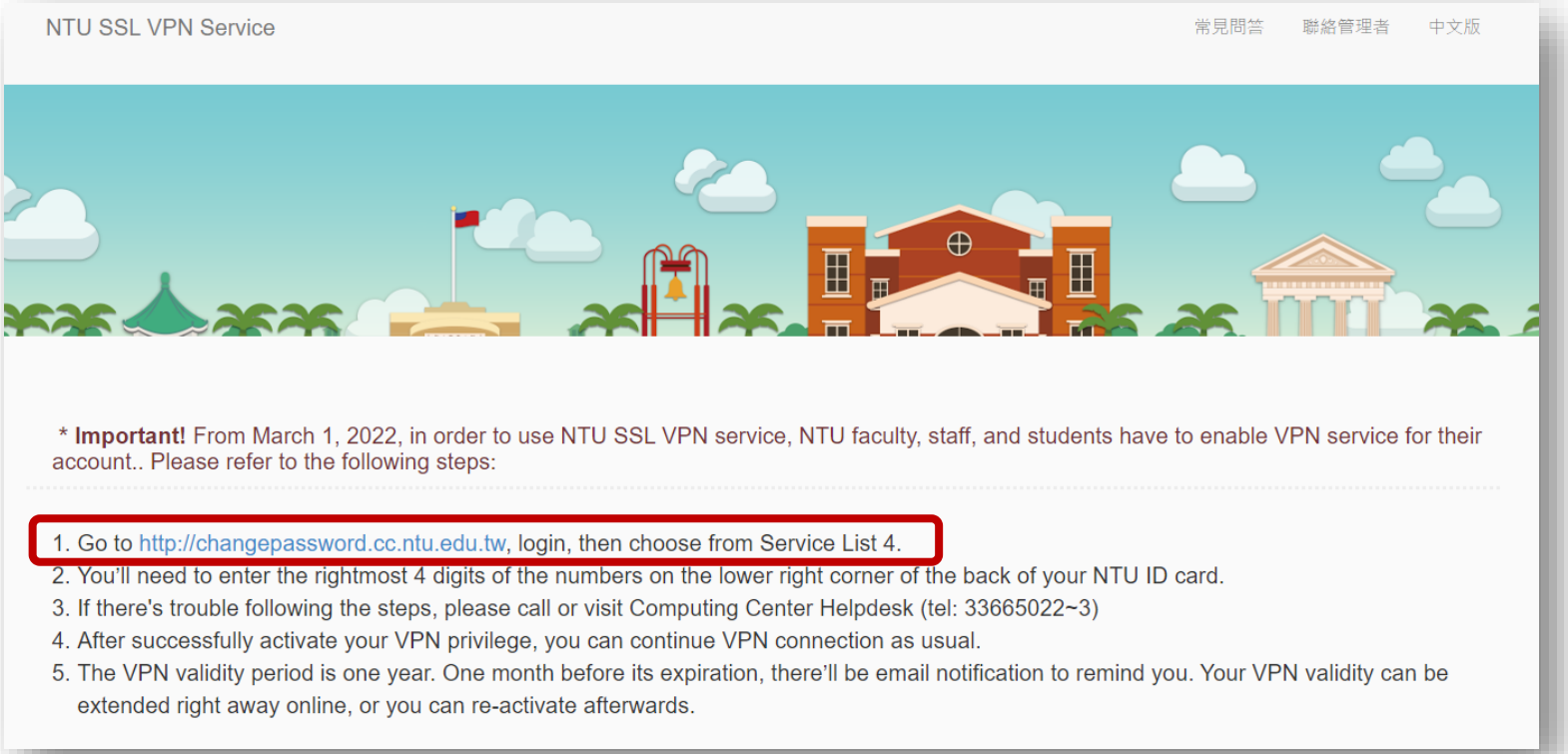


Questions about VPN settings, NTU account.

→ **NTU Computer and Information Networking Center "計中"**

(02)3366-5022 (or 5023) / cchelp@ntu.edu.tw

How to apply for VPN?



https://ccnet.ntu.edu.tw/vpn/PulseSecure-eng.html

How to apply for VPN?

親愛的 [redacted] 您好，您來自 [redacted]

您的帳號資訊(Your Account Info)

名稱(Username)	[redacted]
種類(Type)	職員 Staff
狀態(Status)	在校/在職/正常 Normal/Activated
前次密碼更改(Password last modified)	[redacted]

計算機中心所提供之服務如下(Services List)：

1. 密碼修改(Change Password)
2. 設定 Eduroam 密碼
3. 設定 G Suite(Google Apps)服務
4. 進階功能 - 啟用 SSLVPN 校外連線服務

登出

進階服務 設定網頁 [English Version]

Instruction of English Version

相關說明

- 計中部分服務，具備高資安保護考量，因此列為「進階服務」。
- 目前進階服務包括：SSLVPN（校外連線）
- 申請啟用「進階服務」，需進行第二層身份驗證。
- 請拿出您的職員證/學生證，翻到背面，找出右下角一連串數字，需要最末四碼。[Sample Pictures]
- 服務對象
  - 僅限本校人事室控管人員、具備學籍學生。
  - 不包含附設單位，如：台大醫院、動物醫院、實驗林、山地農場等。
  - 不包含「新生未繳費休學者」。
  - 不包含「新生未取得學生證者」。（新生完成註冊，開學後即可取得學生證。）
- 如不確定卡片是否有效，請刷卡進入就近館舍，以驗證卡片有效性。
- 若曾掛失卡片，請儘速補辦新卡。

請輸入證件背面末四碼 [ ] 申請驗證

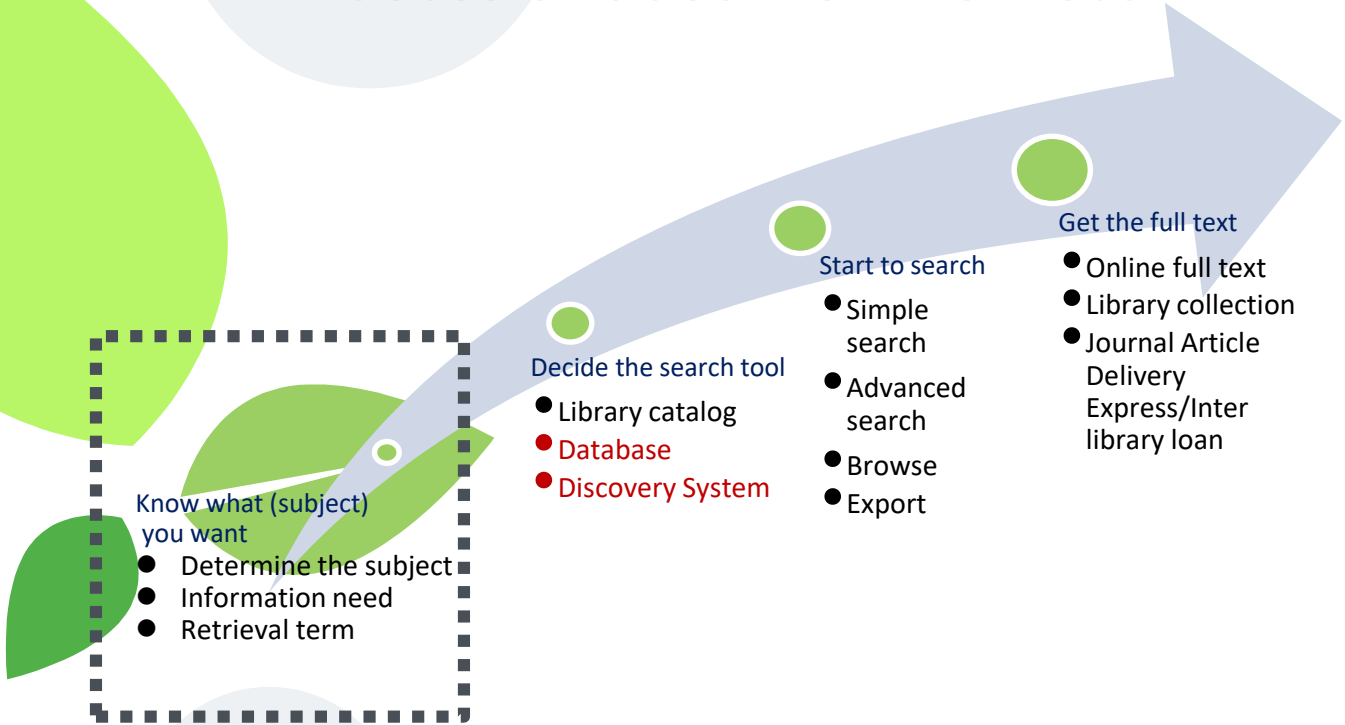
回到上一頁

XXXXXXXX
XX

the last 4 digit of the code at the back of your NTU student ID card

2.
Search Strategies and Techniques

Process of document retrieval



Concept on your mind → Retrieval term

- **Extract keywords**
  - Opinion, concept, and proper noun
  - Prefix and suffix change, such as part of speech, singular and plural, or abbreviation
  - Use different languages
  - Find the hierarchical relationship between words

A Review on Polymeric Membranes and Hydrogels Prepared by Vapor-Induced Phase Separation Process

ANTOINE VENAULT,[1] YUNG CHANG,[1,2] DA-MING WANG,[2,3] AND DENIS BOUYER[4]

[1]Department of Chemical Engineering, Chung Yuan Christian University, Chung-Li, Taiwan
[2]R&D Center for Membrane Technology, Chung Yuan Christian University, Chung-Li, Taiwan
[3]Department of Chemical Engineering, National Taiwan University, Taipei, Taiwan
[4]Institut Européen des Membranes, Université Montpellier 2, Montpellier, France

In 1918, Zsigmondy and Bachmann presented a new method to induce phase s... of a homogeneous polymeric solution from a vapor phase. The so-called vapor... phase separation (VIPS) was born. In a century, the body of knowledge on... membranes and hydrogels prepared by VIPS has grown importantly, which suggests... the need for a critical review. Slowness of mass transfers involved in VIPS, attributed to the resistance at the gaseous phase/liquid phase interface, permits reaching better control of polymer membrane formation than with the popular wet-immersion process. As a result, a broad variety of morphologies can be obtained and well controlled. The control of testing conditions and formulation parameters also permits tuning and tailoring morphologies, which arises in various membranes properties, and led scientists to investigate the possibility of forecasting mass transfers in VIPS. Therefore, at the end of the twentieth century, first models were developed to describe this process, and validated by comparing simulated data to experimental results. Afterwards, studies demonstrated the possibility of predicting membrane morphologies from the knowledge of operating conditions. This article aims at reviewing the work done so far reporting this process to prepare polymer membranes and hydrogels. The experimental set-ups will be introduced as well as the different polymer/solvent/nonsolvent and polymer/additive(s)/solvent/nonsolvent systems used and the morphologies obtained. The effect of testing conditions and formulation parameters on the structure of the matrices will be subsequently discussed. Close attention will be given to the fundamental theory of VIPS before moving onto the potential applications of such polymer matrices.

Keywords VIPS process, polymer membranes, hydrogels, morphology control, testing conditions, VIPS simulation

Keywords from the Articles

Selection history modulates working memory capacity (Article) (Open A...

Kuo, B.-C.

Department of Psychology, National Taiwan University, Taipei, Taiwan

Abstract

Recent studies have shown that past selection history affects the allocation of attention on target sele... whether context-driven selection history can modulate the efficacy of attention allocation on working... representations. This study tests the influences of selection history on WM capacity. A display of one i... items (high load) was shown for the participants to hold in WM in a delayed response task. Participan... probe item was in the memory display or not. Selection history was defined as the number of items a... task context within a block, manipulated by the stimulus set-size in the contexts with fewer possible s... ...nuli (8-item or 9-item context) from which the memorized content was ... ...was estimated to reflect the number of items that can be held in WM. A... ...aled that the capacity was significantly reduced in the context with more ... ...le stimuli. Moreover, the reduction in capacity was significant for high W... when the focus was on only a single item. Together, these findings indicate that context-driven select... attention influence WM capacity. © 2016 Kuo.

Retrieval term

SciVal Topic Prominence

Topic: Memory, Short-Term | Memory | Contralateral delay

Prominence percentile: 97.566

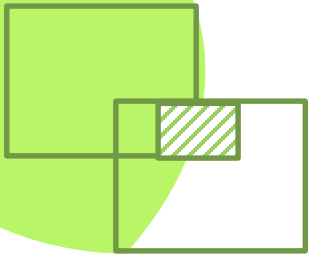
Author keywords

Attention | Limited capacity | Selection history | Top-down control | Working memory

https://www.youtube.com/watch?v=LTJygQwYV84

Boolean Operators

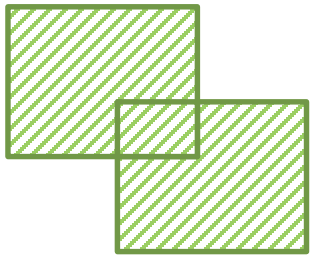
AND
find result of both words



a study of attitudes and behaviors of idolatry among fans of popular songs.

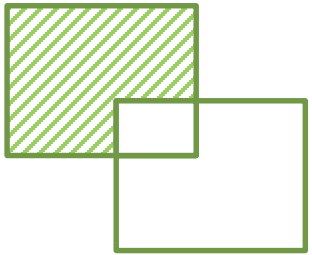
attitude
AND behavior
AND idolatry
AND popular songs

OR
find either keyword



bike
OR bicycle
OR cycling
OR two-wheeler

NOT
exclude words from the search

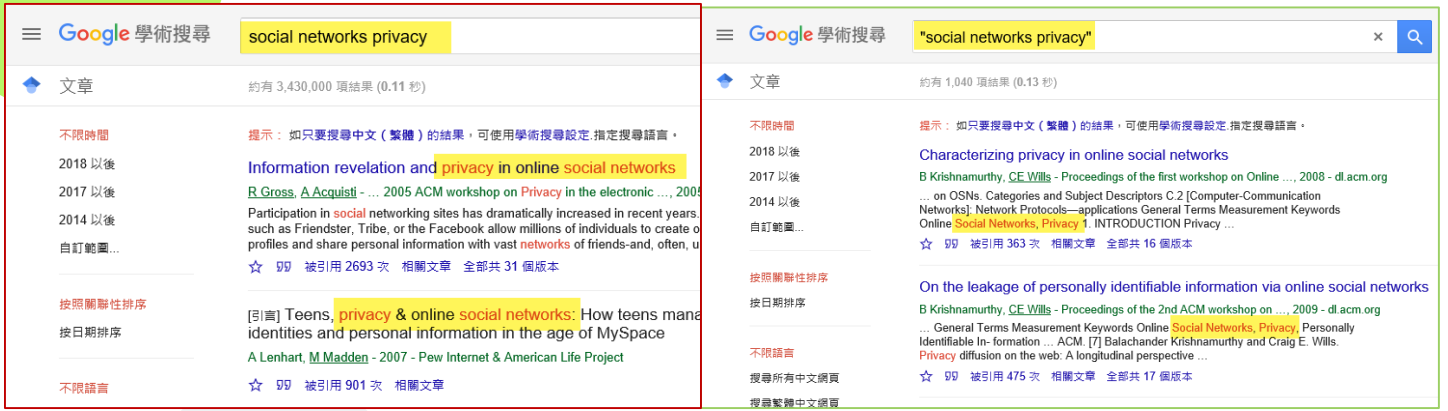


a study on genetic engineering of human cloning

cloning NOT sheep

Exact Phrase Search

- Use double quotation“ “ to search phrases. Every word is grouped together, not separate.
- For example, if you type “social networks privacy “, you wouldn’t get privacy in online social networks.



Truncation / Wildcard Character

- The asterisk (*) is the Truncation character, used to replace one or more characters.
- It is used at the end of a root word, when you want to search for variable endings of a root word.

Retrieval term	Search results
fiction*	fiction
	fictions
educat*	educate
	educated
	education
	educational
	educator

Each database use the truncation character differently. Look for the "Help" of each database.

Truncation / Wildcard Character

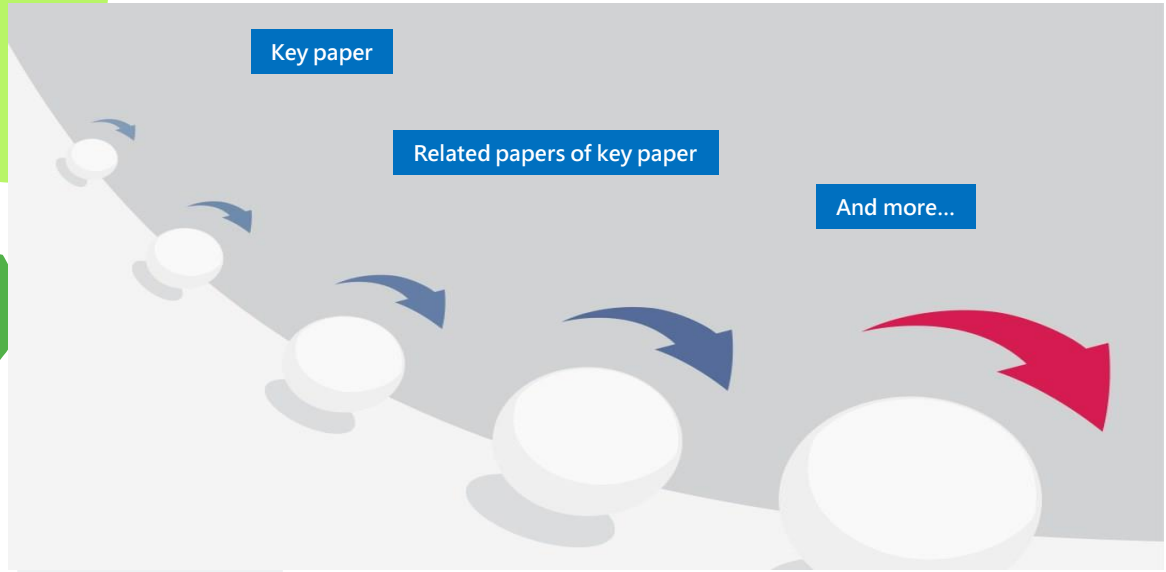
- The question mark (?) is the Wildcard character, used to replace any single character, either inside or at the right end of the word.
- It is useful when there are variable spellings for a word, and you want to search for all variants simultaneously.

Retrieval term	Search results
Wom?n	Woman
	Women
Re?d	Read
	Reed
Col?r	Color
	Colour

Each database uses the wildcard character differently. Look for the "Help" of each database.

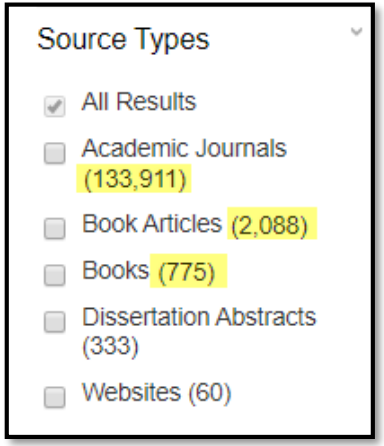
Snowball Method

- Read related references to extend search results
- Use "call number" to find more similar subjects



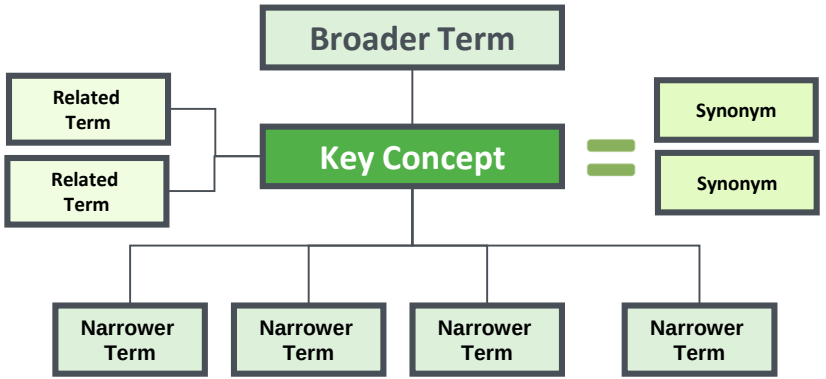
Refine Results

- Results are classified again based on different attributes to decrease search scope
  - subject, author, organization, document type, publication year, source title and so on
- With the amount of articles for each filtered item

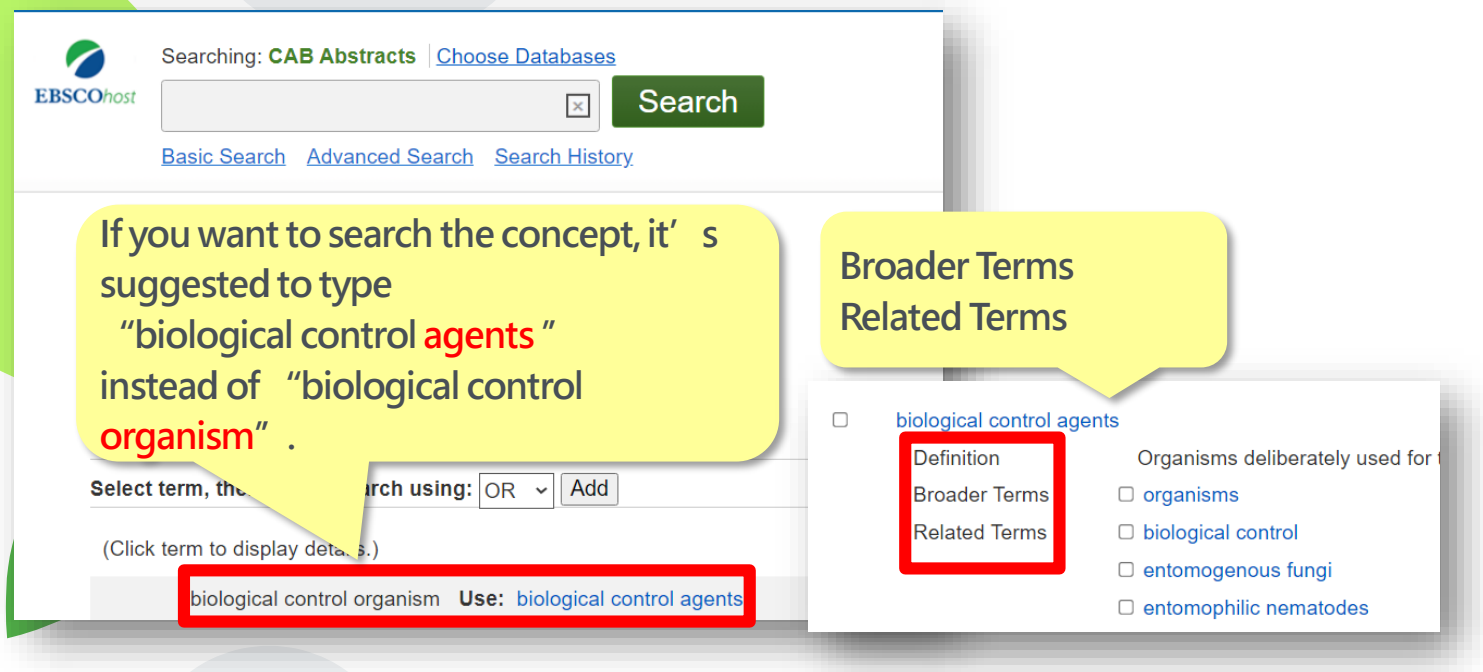


Thesaurus (in the context of information retrieval)

- A thesaurus is an alphabetical listing of all the subject terms in a single database, used to classify and organize information for that database. The thesaurus shows relationships between terms such as **synonyms** or **related terms**, and hierarchical arrangements such as **broader terms**, or **narrower terms**.

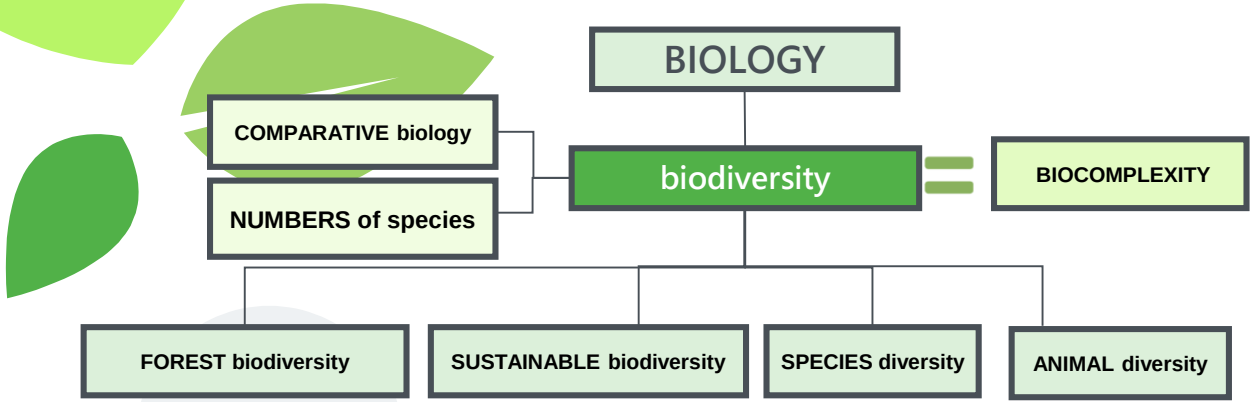


Thesaurus e.g. **CAB Abstracts** [EBSCOhost]

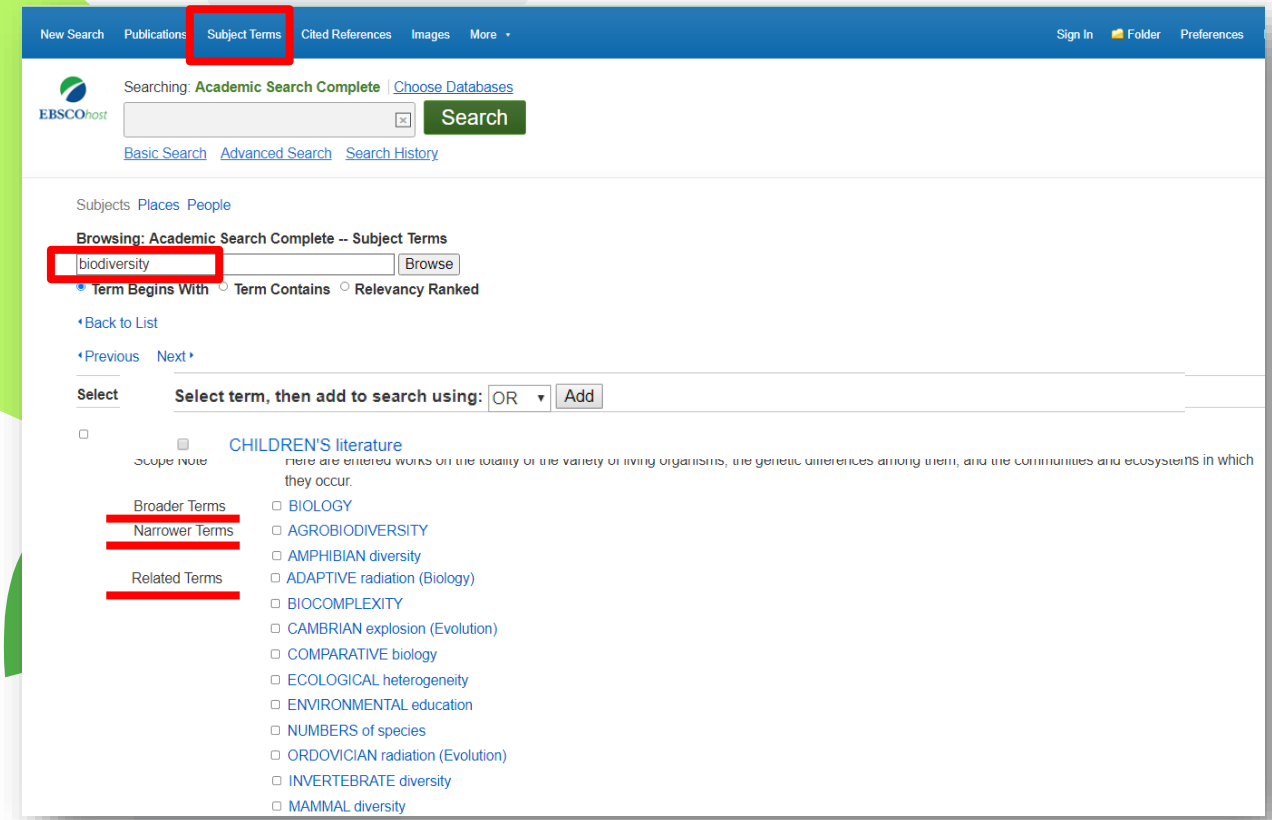


Subject Headings

- In addition to “author keywords”, experts would define more precise terms to documents.
- a type of standardized “tag” used to index and organize resources on the same topic



Subject Headings e.g. ASC [EBSCOhost]



Thesaurus & Subject Headings

- Main Purposes

Related Terms

- You want to explore a topic, but you don’ t have any idea.

Narrower Terms

- You will have to decrease the search scope with precise keywords if you get too many results,

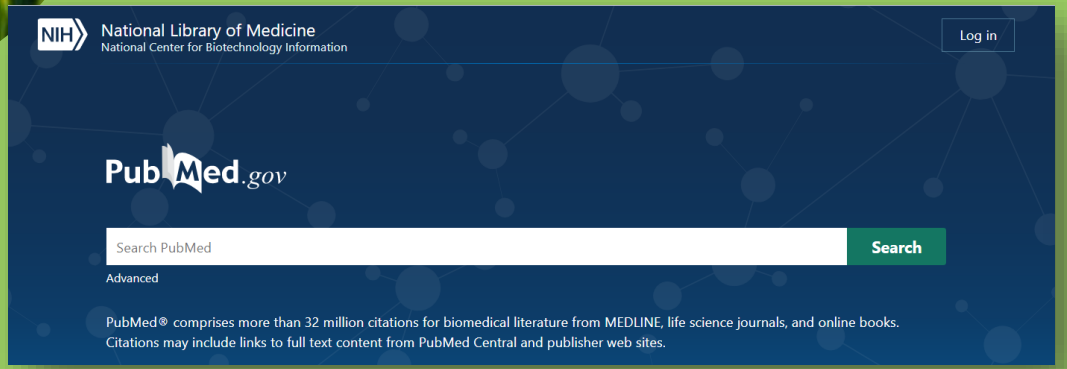
Broader Terms

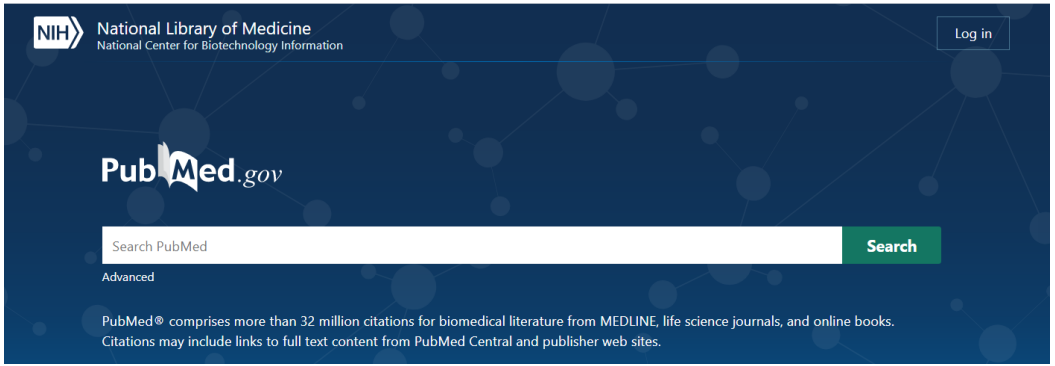
- If you only get few articles, you would have to expand search scope.

Synonyms

- Use similar words and retrieve target articles you may lost.

3. PubMed

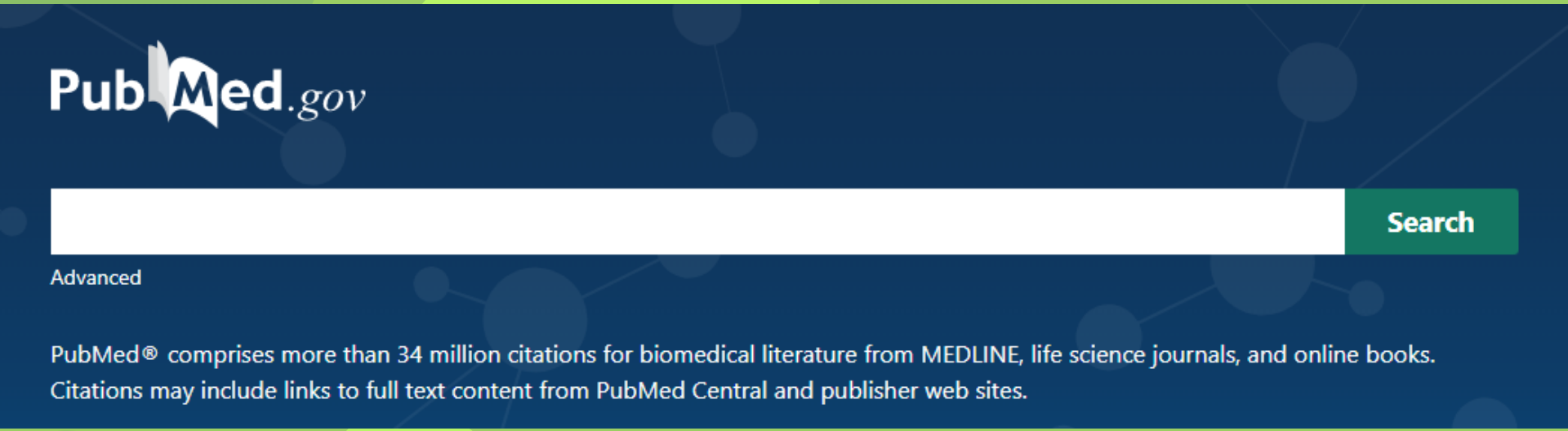

NIH
National Library of Medicine
National Center for Biotechnology Information
Log in
PubMed.gov
Search PubMed
Search
Advanced
PubMed® comprises more than 32 million citations for biomedical literature from MEDLINE, life science journals, and online books.
Citations may include links to full text content from PubMed Central and publisher web sites.



PubMed

- A free resource supporting the search and retrieval of **biomedical and life sciences literature**
- Developed and maintained by the National Center for Biotechnology Information (NCBI), at the U.S. National Library of Medicine (NLM)
- Contains more than 32 million citations and abstracts of biomedical literature back to the 1950s.
- **Includes links to many sites providing full text articles** and other related resources.

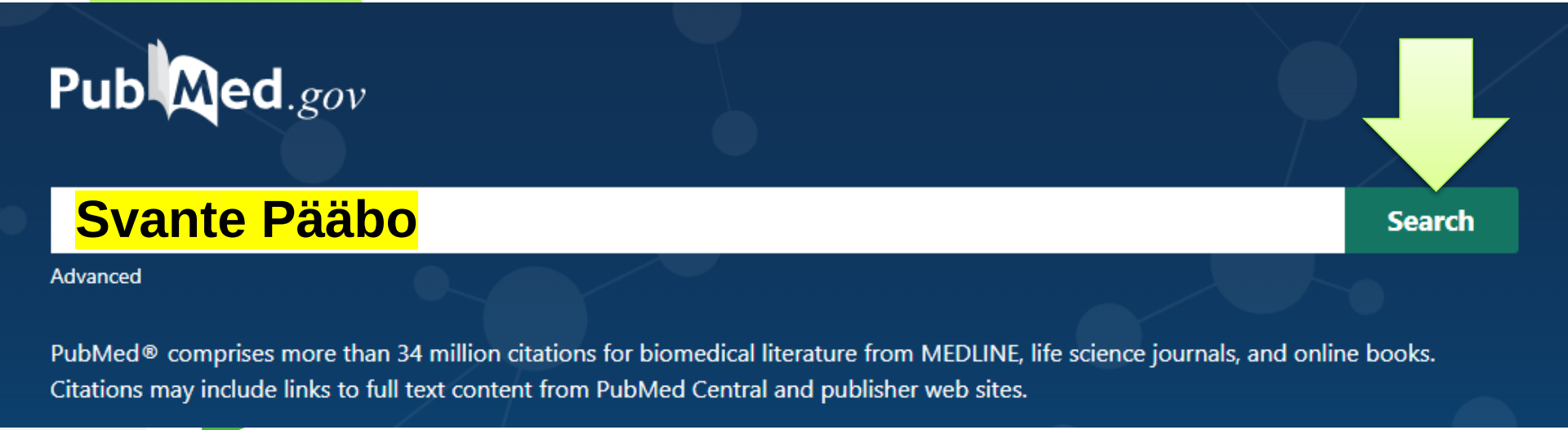
How to Search for PubMed



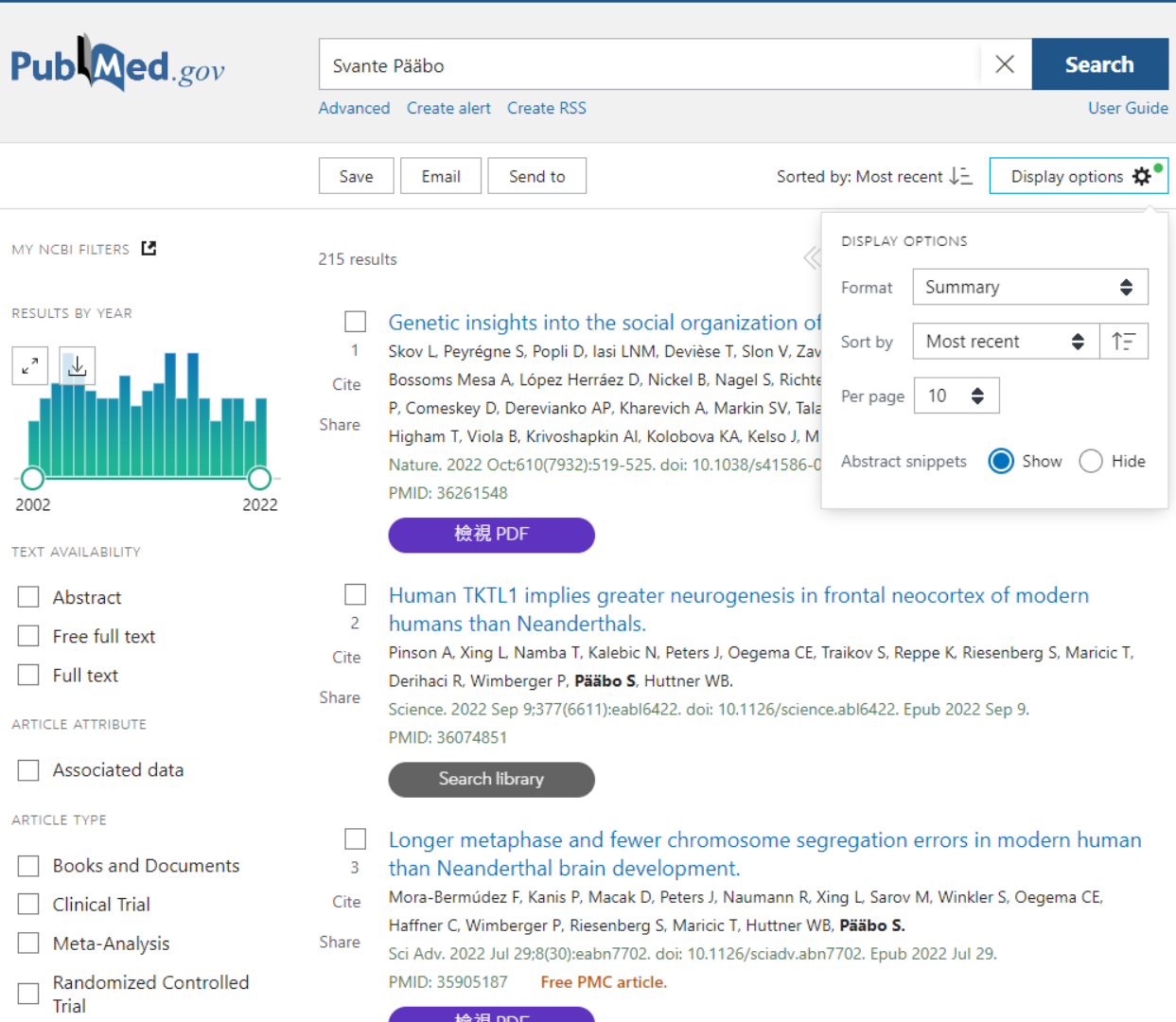
Example

The 2022 Nobel Prize for Physiology and Medicine was awarded to Swedish scientist Svante Pääbo for Neanderthal Genome Sequencing.

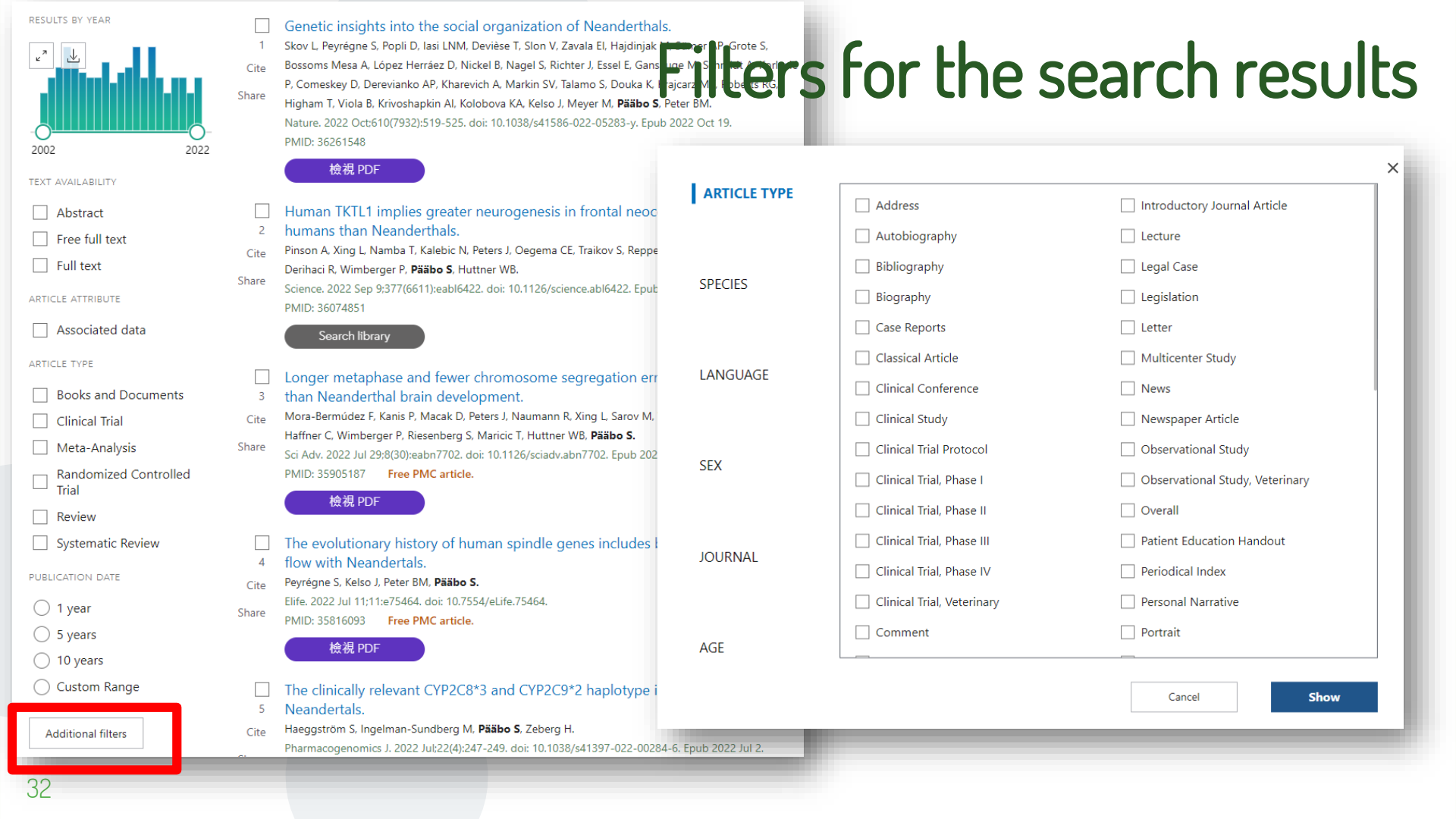
Search for Author



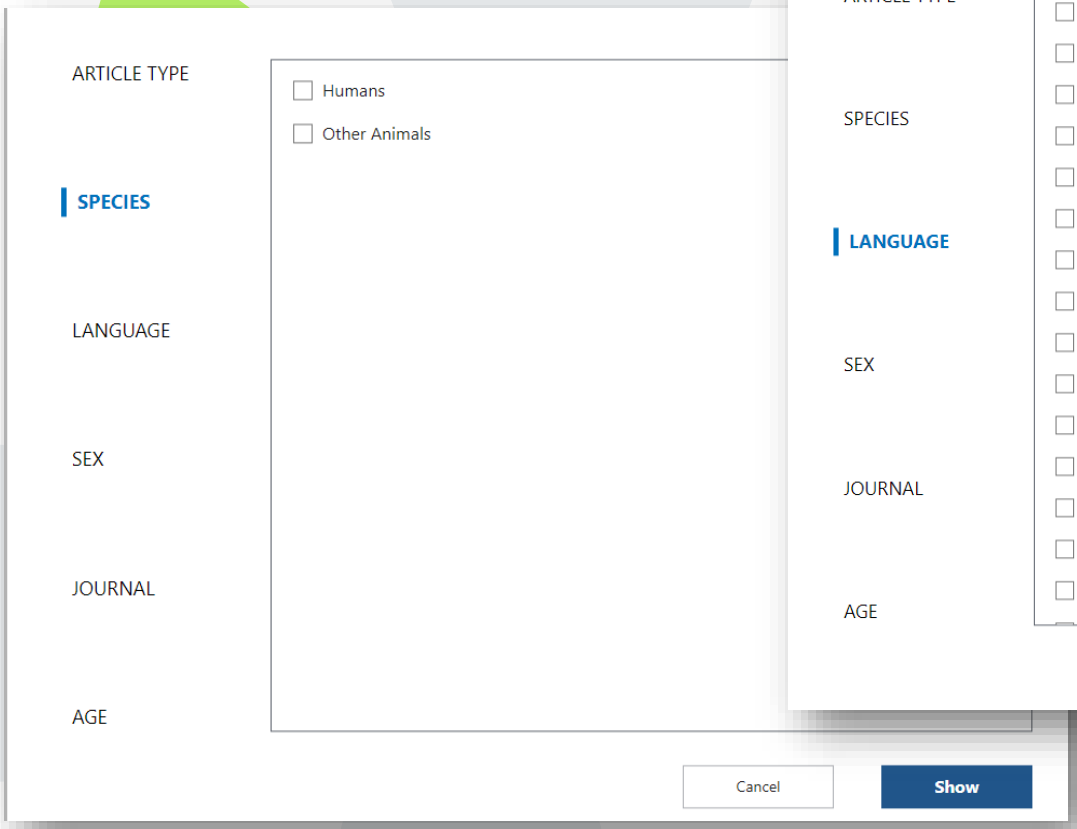
Display option

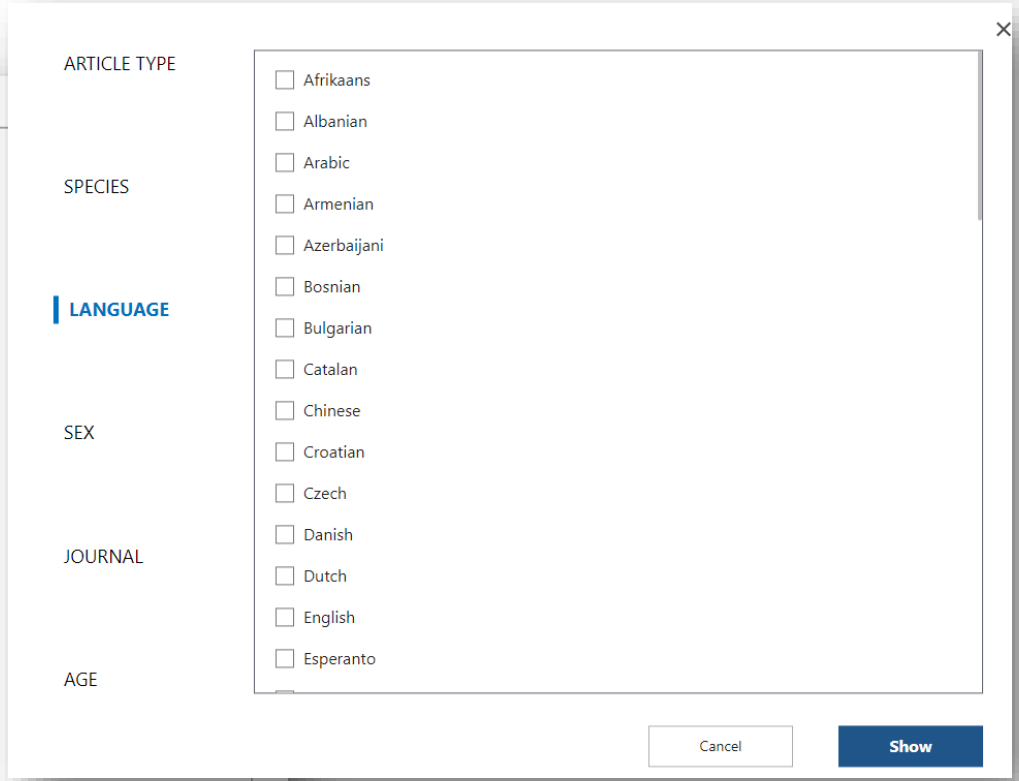


Filters for the search results

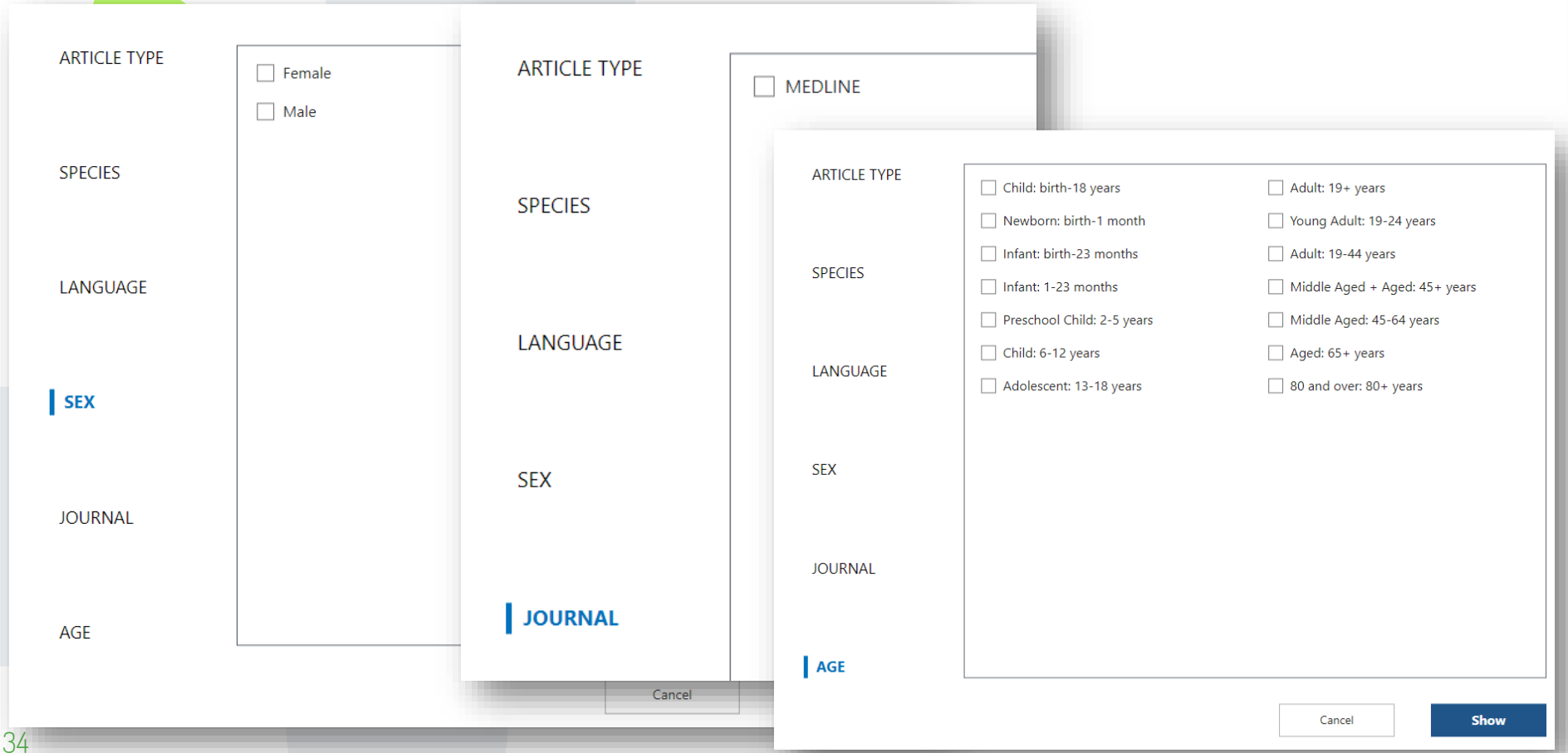


Additional filter





Additional filter



Search for keywords

PubMed.gov

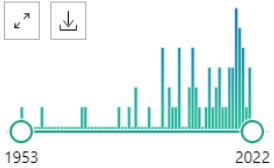
"ancient bones" Search

Advanced Create alert Create RSS User Guide

Save Email Send to Sorted by: Most recent Display options

MY NCBI FILTERS

RESULTS BY YEAR



TEXT AVAILABILITY

- Abstract
- Free full text
- Full text

ARTICLE ATTRIBUTE

- Associated data

ARTICLE TYPE

- Books and Documents
- Clinical Trial
- Meta-Analysis
- Randomized Controlled Trial
- Review
- Systematic Review

60 results Page 1 of 6

1 Cite Share

A method for the temperature-controlled extraction of DNA from **ancient bones**.

Essel E, Korlević P, Meyer M.

Biotechniques. 2021 Jul;71(1):382-386. doi: 10.2144/btn-2021-0025. Epub 2021 Jun 24.

PMID: 34164993 Free article.

An evaluation of the effectiveness of the method using a set of three **ancient bones** resulted in between 1.6- and 32-fold enrichment of endogenous DNA compared with regular DNA extraction. For two **bones**, the method outperformed previous methods of decontaminat ...

Search library

2 Cite Share

Near-infrared hyperspectral imaging (NIR-HSI) and normalized difference image (NDI) data processing: An advanced method to map collagen in archaeological **bones**.

Lugli F, Sciutto G, Oliveri P, Malegori C, Prati S, Gatti L, Silvestrini S, Romandini M, Catelli E, Casale M, Talamo S, Iacumin P, Benazzi S, Mazzeo R.

Talanta. 2021 May 1;226:122126. doi: 10.1016/j.talanta.2021.122126. Epub 2021 Jan 26.

PMID: 33676680

The developed approach addresses an urgent issue of the analytical chemistry applied to bioarcheology researches, which rely on well-preserved collagen in **bones** to obtain key information on chronology, paleoecology and taxonomy. ...NIR-HSI pre-screening allows researchers ...

Search library

3 Cite Share

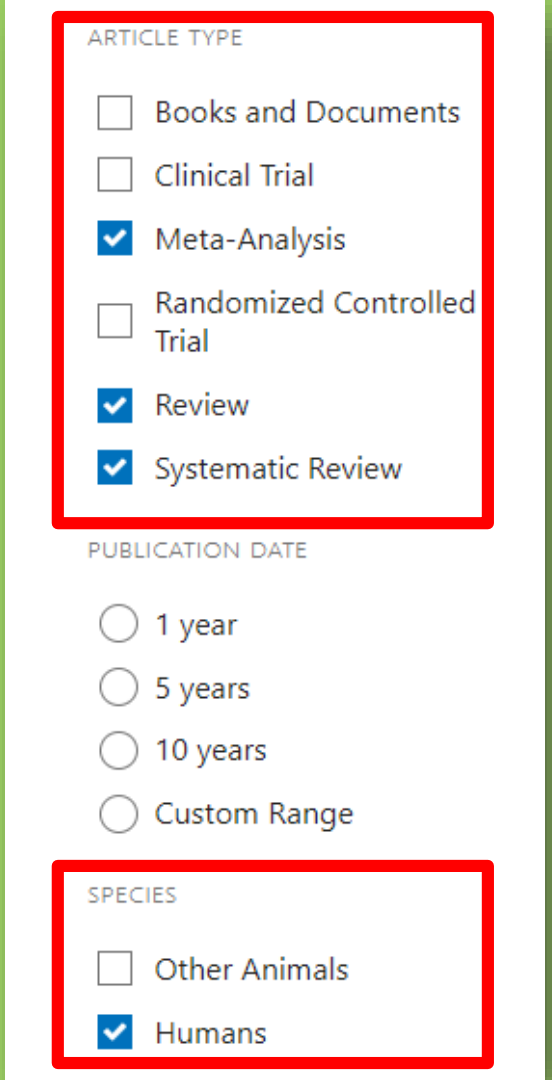
Comparison of bone demineralisation procedures for DNA recovery from burned remains.

Mckinnon M, Higgins D.

Forensic Sci Int Genet. 2021 Mar;51:102448. doi: 10.1016/j.fsigen.2020.102448. Epub 2020 Dec 26.

PMID: 33373911

Recovering DNA from modern incinerated **bones** can be challenging and may require alteration of



Meta-Analysis: Technique that statistically combines the results of quantitative studies to provide a more precise effect of the results

Review: Published materials that provide an examination of recent or current literature. Can cover a wide range of subjects at various levels of completeness and comprehensiveness. It may include research findings.

Systematic Review: Seeks to systematically search for, appraise, and synthesize research evidence, often adhering to guidelines on the conduct of a review

Biotechniques. 2021 Jul;71(1):382-386. doi: 10.2144/btn-2021-0025. Epub 2021 Jun 24.

A method for the temperature-controlled extraction of DNA from ancient bones

Elena Essel [1], Petra Korlević [1 2], Matthias Meyer [1]

Affiliations + expand

PMID: 34164993 DOI: 10.2144/btn-2021-0025

Free article

Abstract

Contamination with microbial and other exogenous DNA poses a significant challenge in the generation of genome-wide sequence data from ancient skeletal remains. Here we describe a method for separating ancient DNA into multiple fractions during DNA extraction by sequential temperature-controlled release of DNA into sodium phosphate buffer. An evaluation of the effectiveness of the method using a set of three ancient bones resulted in between 1.6- and 32-fold enrichment of endogenous DNA compared with regular DNA extraction. For two bones, the method outperformed previous methods of decontaminating ancient bones, including hypochlorite treatment, which resulted in near-complete destruction of DNA in the worst-preserved sample. This extraction method expands the spectrum of methods available for depleting contaminant DNA from ancient skeletal remains.

Keywords: ancient DNA; archaeological material; contamination removal; endogenous DNA; sequential DNA extraction.

Similar articles

Pretreatment: Improving Endogenous Ancient DNA Yields Using a Simple Enzymatic Predigestion Step.
Schroeder H, de Barros Damgaard P, Allentoft ME.
Methods Mol Biol. 2019;1963:21-24. doi: 10.1007/978-1-4939-9176-1_3.
PMID: 30875040

The influence of sample quantity and lysis parameters on the success of ancient DNA extraction from skeletal remains.
Euskirchen A, Hartmann L, Mazanec J, Wittmeier P, Hummel S.
Biotechniques. 2021 Jul;71(1):376-381. doi: 10.2144/btn-2020-0169. Epub 2021 Jun 30.
PMID: 34187204

Benchmark

BioTechniques

A method for the temperature-controlled extraction of DNA from ancient bones

Elena Essel*[,1], Petra Korlević[1,2] & Matthias Meyer[1]

*[1]Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig, D-04103, Germany; [2]Wellcome Genome Campus, European Bioinformatics Institute (EMBL-EBI), Hinxton, Cambridgeshire, CB10 1SD, UK; *Author for correspondence: Tel.: +49 341 3550 530; elena_essel@eva.mpg.de*

BioTechniques 71: 383–386 (July 2021) 10.2144/btn-2021-0025

First draft submitted: 18 March 2021; Accepted for publication: 8 June 2021; Published online: 24 June 2021

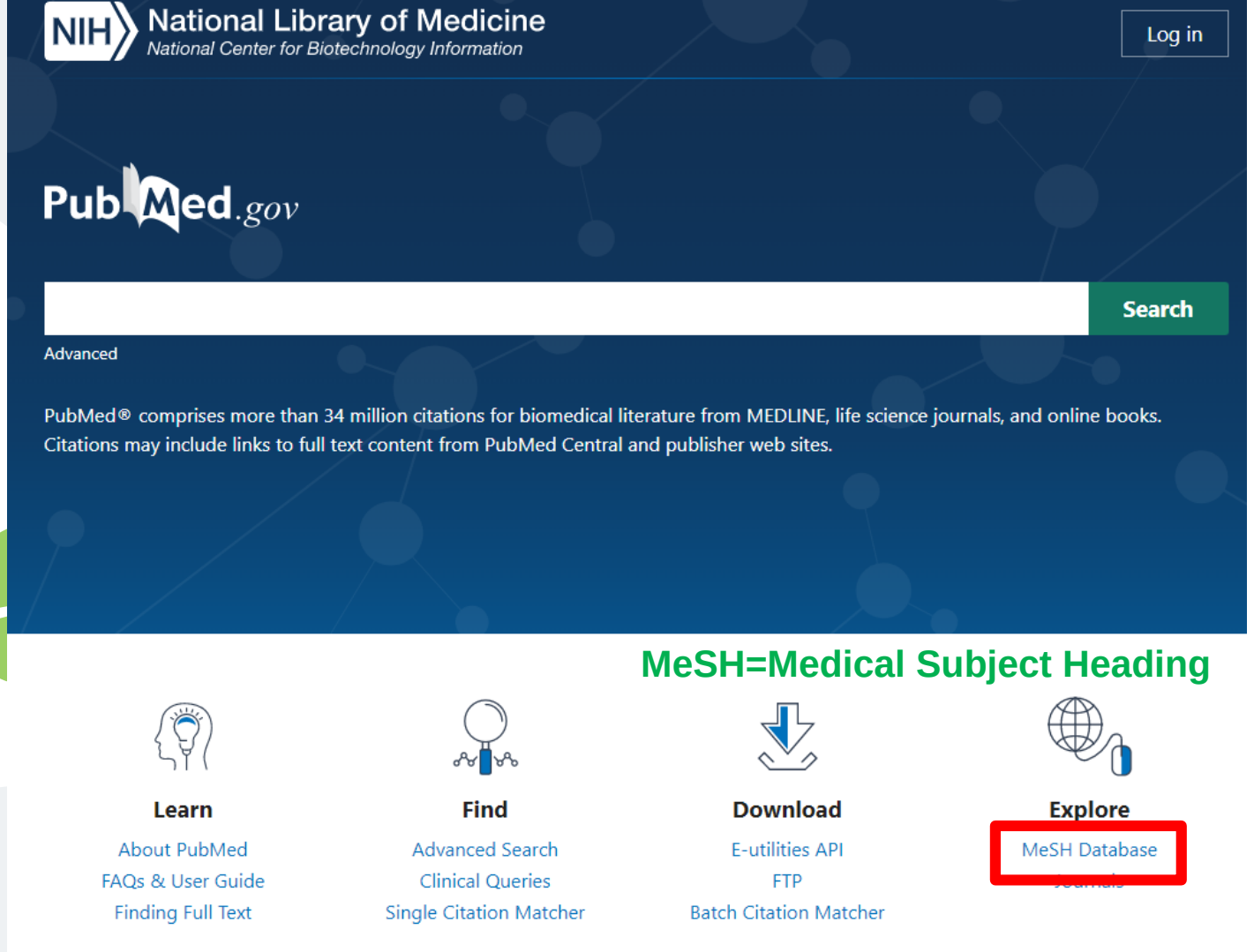
ABSTRACT

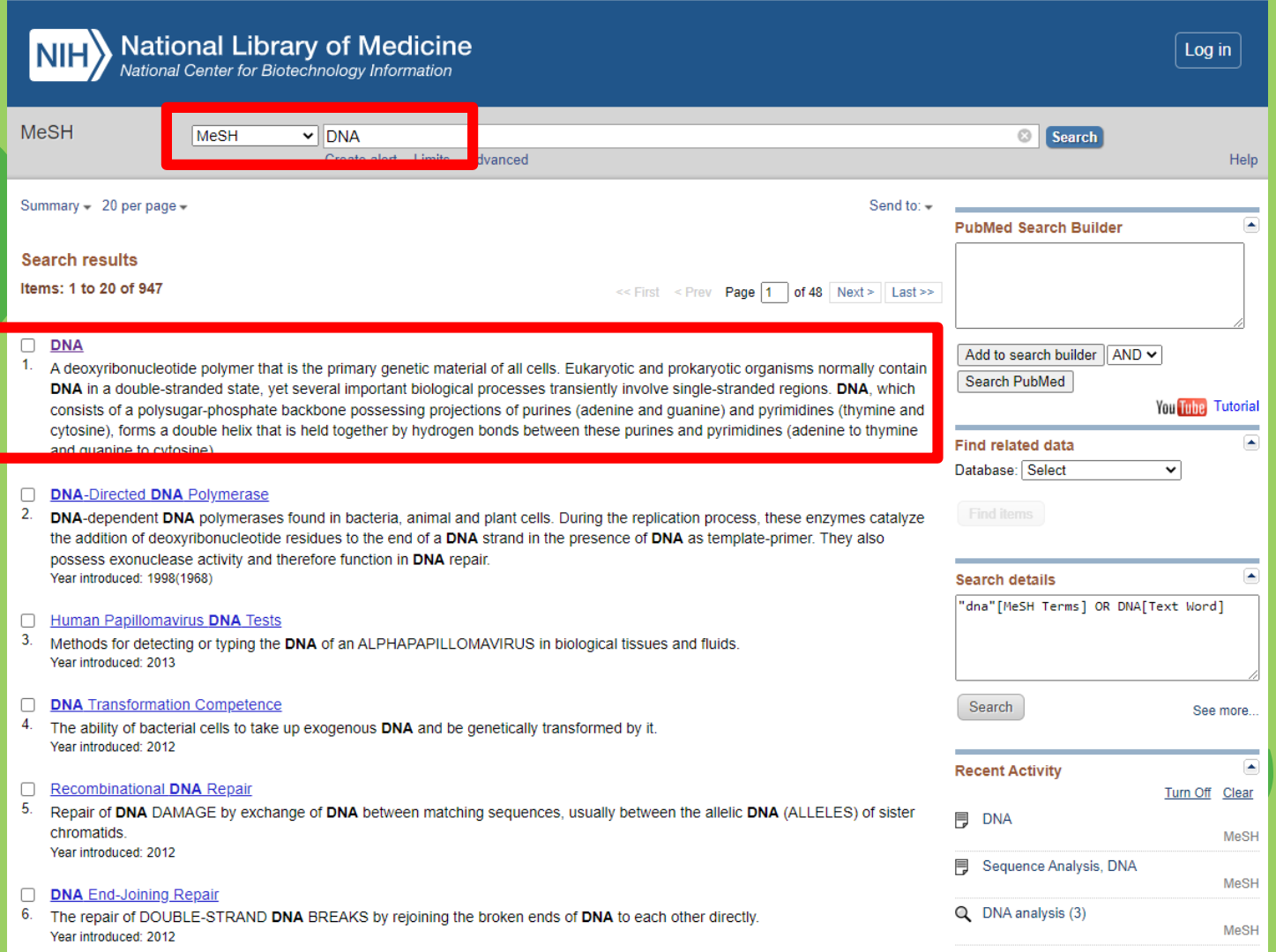
Contamination with microbial and other exogenous DNA poses a significant challenge in the generation of genome-wide sequence data from ancient skeletal remains. Here we describe a method for separating ancient DNA into multiple fractions during DNA extraction by sequential temperature-controlled release of DNA into sodium phosphate buffer. An evaluation of the effectiveness of the method using a set of three ancient bones resulted in between 1.6- and 32-fold enrichment of endogenous DNA compared with regular DNA extraction. For two bones, the method outperformed previous methods of decontaminating ancient bones, including hypochlorite treatment, which resulted in near-complete destruction of DNA in the worst-preserved sample. This extraction method expands the spectrum of methods available for depleting contaminant DNA from ancient skeletal remains.

METHOD SUMMARY

The authors present a decontamination method for poorly preserved ancient bones that relies on a temperature-controlled sequential release of

Search for MeSH

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DNA
1. A deoxyribonucleotide polymer that is the primary genetic material of all cells. Eukaryotic and prokaryotic organisms normally contain DNA in a double-stranded state, yet several important biological processes transiently involve single-stranded regions. DNA, which consists of a polysugar-phosphate backbone possessing projections of purines (adenine and guanine) and pyrimidines (thymine and cytosine), forms a double helix that is held together by hydrogen bonds between these purines and pyrimidines (adenine to thymine and guanine to cytosine)
DNA-Directed DNA Polymerase
2. DNA-dependent DNA polymerases found in bacteria, animal and plant cells. During the replication process, these enzymes catalyze the addition of deoxyribonucleotide residues to the end of a DNA strand in the presence of DNA as template-primer. They also possess exonuclease activity and therefore function in DNA repair.
Year introduced: 1998(1968)
Human Papillomavirus DNA Tests
3. Methods for detecting or typing the DNA of an ALPHAPAPILLOMAVIRUS in biological tissues and fluids.
Year introduced: 2013
DNA Transformation Competence
4. The ability of bacterial cells to take up exogenous DNA and be genetically transformed by it.
Year introduced: 2012
Recombinational DNA Repair
5. Repair of DNA DAMAGE by exchange of DNA between matching sequences, usually between the allelic DNA (ALLELES) of sister chromatids.
Year introduced: 2012
DNA End-Joining Repair
6. The repair of DOUBLE-STRAND DNA BREAKS by rejoining the broken ends of DNA to each other directly.
Year introduced: 2012
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Sequence Analysis, DNA
MeSH
DNA analysis (3)
MeSH

See Also:

- Genetic Code
- Nucleic Acid Denaturation
- Nucleic Acid Hybridization
- Repetitive Sequences, Nucleic Acid
- DNA Primers

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Nucleic Acids
DNA
DNA Adducts
DNA Transposable Elements
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DNA, Algal
DNA, Ancient
DNA, Antisense
Oligodeoxyribonucleotides, Antisense
DNA, Archaeal
DNA, B-Form
DNA, Bacterial
DNA, C-Form
DNA, Catalytic
DNA, Circular
DNA, Catenated
DNA, Chloroplast
DNA, Mitochondrial +
DNA, Superhelical
DNA, Concatenated
DNA, Cruciform
DNA, Environmental
DNA, Fungal
DNA, Helminth
DNA, Intergenic
DNA, Ribosomal Spacer
DNA, Neoplasm
Circulating Tumor DNA
DNA, Plant
DNA, Chloroplast
DNA, Protozoan
DNA, Kinetoplast
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DNA

A deoxyribonucleotide polymer that is the primary genetic material of all cells. Eukaryotic and prokaryotic organisms normally contain DNA in a double-stranded state, yet several important biological processes transiently involve single-stranded regions. DNA, which consists of a polysugar-phosphate backbone possessing projections of purines (adenine and guanine) and pyrimidines (thymine and cytosine), forms a double helix that is held together by hydrogen bonds between these purines and pyrimidines (adenine to thymine and guanine to cytosine).

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☐ adverse effects	☐ drug effects	☑ physiology
☐ agonists	☐ economics	☐ poisoning
☐ analogs and derivatives	☐ embryology	☐ radiation effects
☑ analysis	☑ ethics	☐ standards
☐ anatomy and histology	☑ etiology	☑ statistics and numerical data
☐ antagonists and inhibitors	☑ genetics	☐ supply and distribution
☑ biosynthesis	☐ history	☐ therapeutic use
☐ blood	☐ immunology	☐ therapy
☐ cerebrospinal fluid	☐ isolation and purification	☐ toxicity
☑ chemical synthesis	☐ metabolism	☐ ultrastructure
☐ chemistry	☐ microbiology	☐ urine
☑ classification	☐ organization and administration	☐ virology
☐ cytology	☐ pharmacokinetics	

PubMed Search Builder

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( "DNA/analysis"[Mesh] OR
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"DNA/classification"[Mesh] OR
"DNA/ethics"[Mesh] OR
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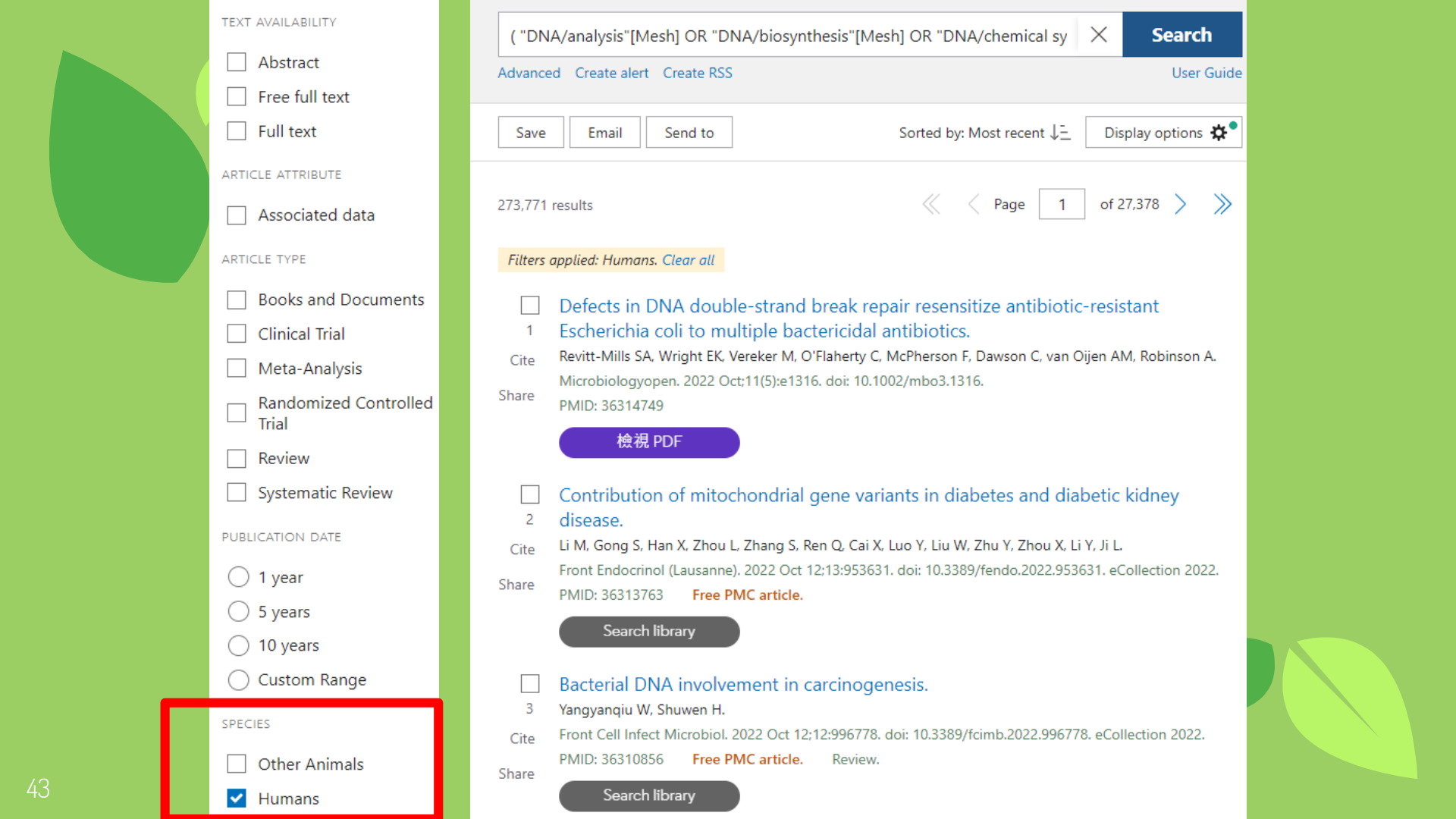
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1
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Revitt-Mills SA, Wright EK, Vereker M, O'Flaherty C, McPherson F, Dawson C, van Oijen AM, Robinson A.
Microbiologyopen. 2022 Oct;11(5):e1316. doi: 10.1002/mbo3.1316.
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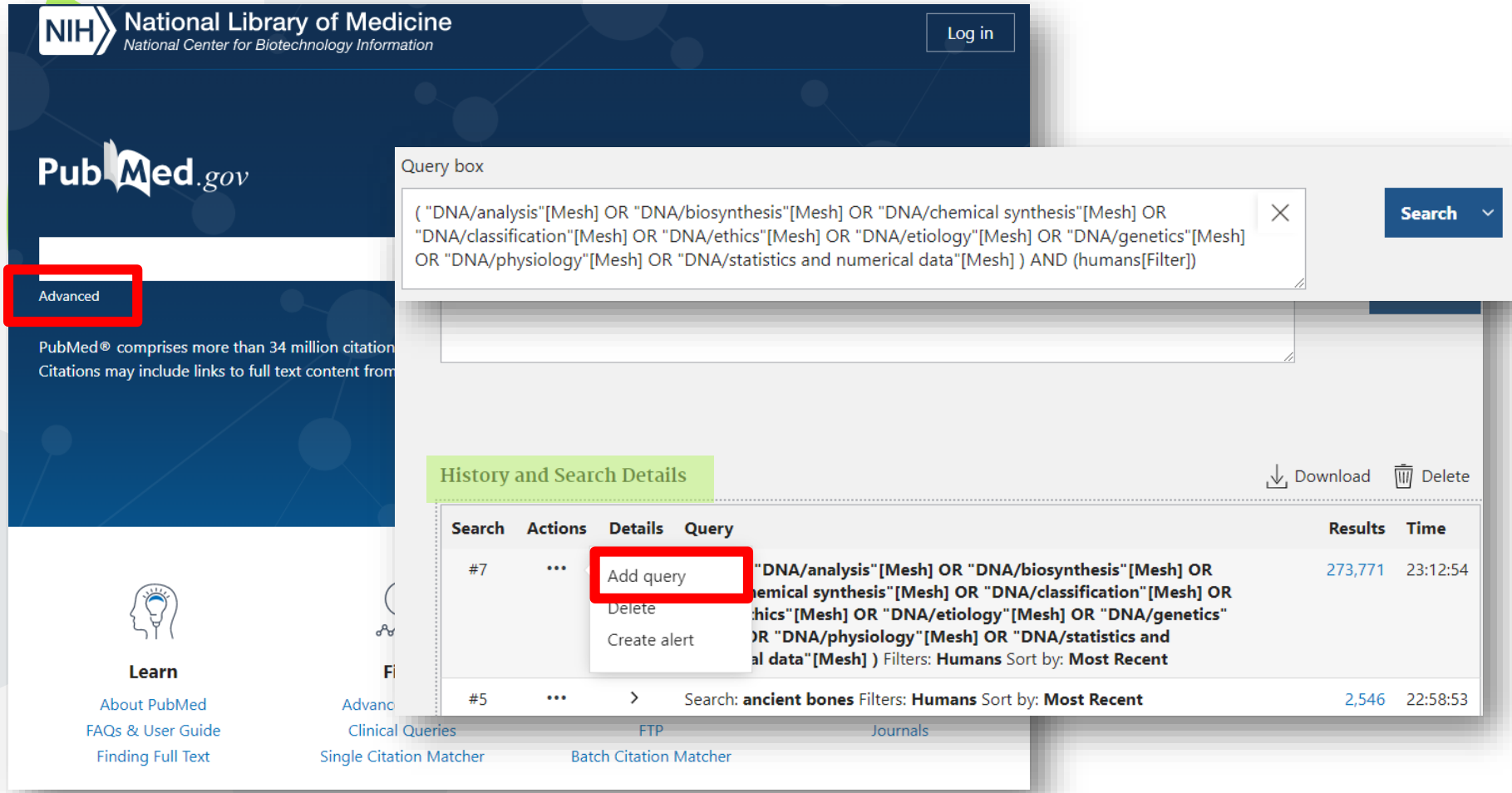

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(("DNA/analysis"[Mesh] OR "DNA/biosynthesis"[Mesh] OR "DNA/chemical synthesis"[Mesh] OR "DNA/classification"[Mesh] OR "DNA/ethics"[Mesh] OR "DNA/etiology"[Mesh] OR "DNA/genetics"[Mesh] OR "DNA/physiology"[Mesh] OR "DNA/statistics and numerical data"[Mesh]) AND (humans[Filter])) AND (ancient bones AND (humans[Filter]))

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#5	•••		**ncient bones** Filters: **Humans** Sort by: **Most Recent**	2,546	22:58:53
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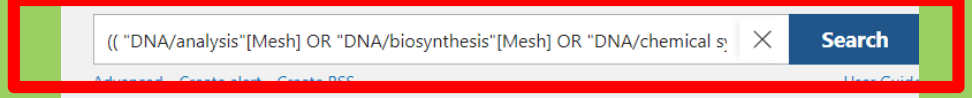

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The petrous **bone** contains high concentrations of osteocytes: One possible reason why **ancient** DNA is better preserved in this **bone**.

Ibrahim J, Brumfeld V, Addadi Y, Rubin S, Weiner S, Boaretto E.

PLoS One. 2022 Oct 25;17(10):e0269348. doi: 10.1371/journal.pone.0269348. eCollection 2022.

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These studies have been aided enormously by the discovery that **ancient** DNA is relatively well preserved in the petrous **bone** compared to most other **bones**. ...We therefore confirm and significantly expand upon previous observations of osteocytic lacuna concentr ...

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Ancient DNA analysis from epoxy resin Biodur®-embedded **bones**.

Flux AL, Schultz M, Hummel S.

Biotechniques. 2022 Sep;73(3):113-122. doi: 10.2144/btn-2022-0056. Epub 2022 Sep 6.

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For microscopic investigation, archaeological **bone** samples are often embedded in Biodur() epoxy resin. This study wants to test whether it is possible to extract DNA suitable for PCR amplification from this sample type. ...Seven out of eight Biodur-embedded femur samples r ...

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Eye and Hair Color Prediction of **Ancient** and Second World War Skeletal Remains Using a Forensic PCR-MPS Approach.

Zupanič Pajnič I, Zupanc T, Leskovar T, Črešnar M, Fattorini P.

Genes (Basel). 2022 Aug 12;13(8):1432. doi: 10.3390/genes13081432.

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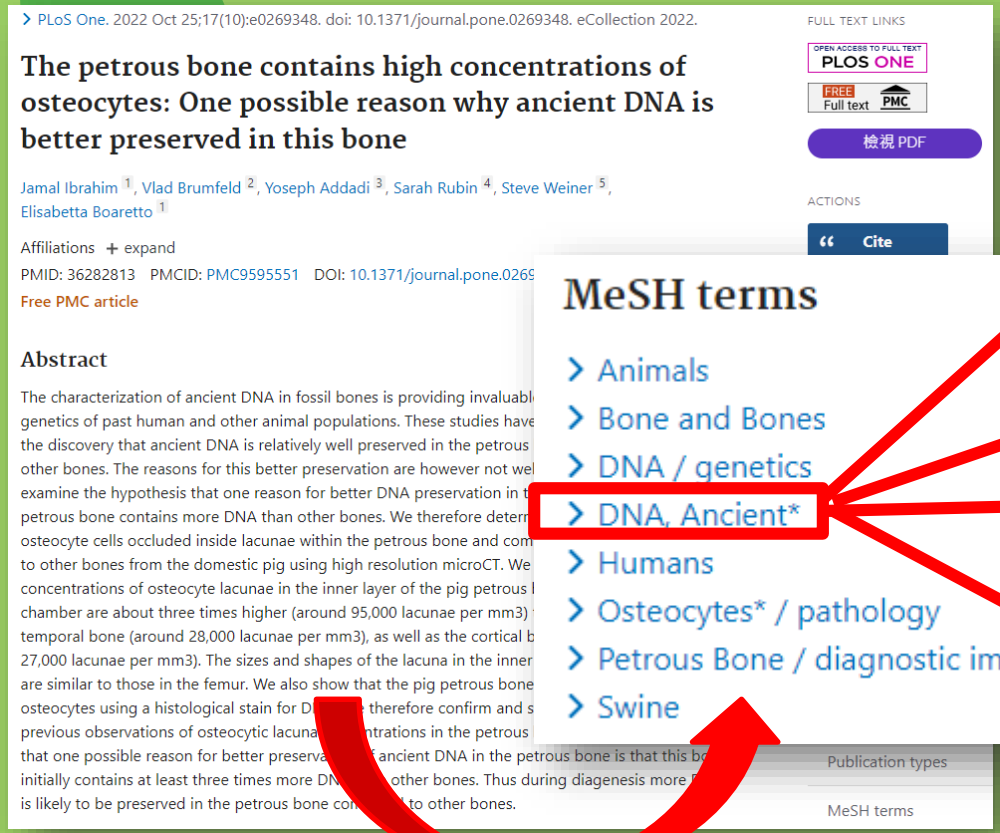
Consensus typing was achieved for about 91.7% of the markers in 10 out of 11 **ancient** skeletons, and the HIrisPlex-**S** webtool was then used to generate phenotypic predictions. Full predictions were

Snowball search with MeSH



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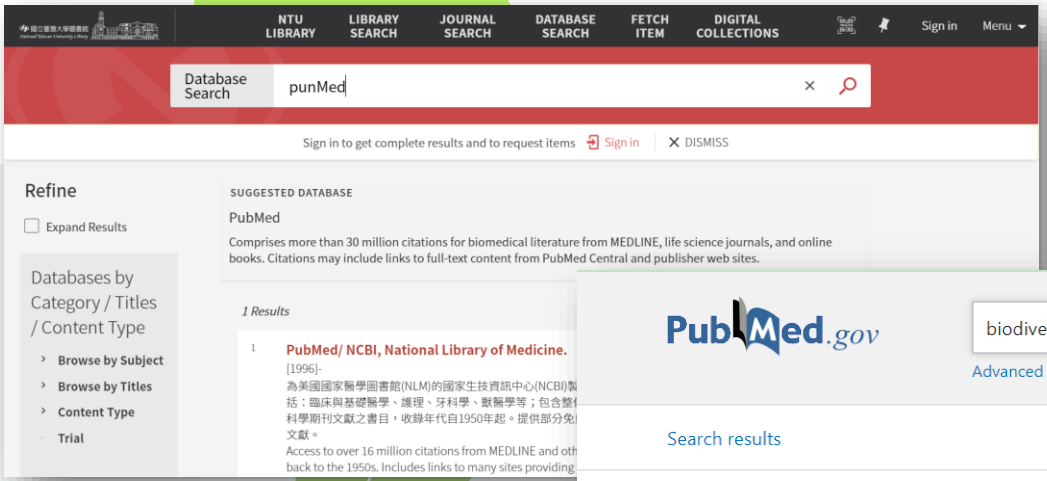

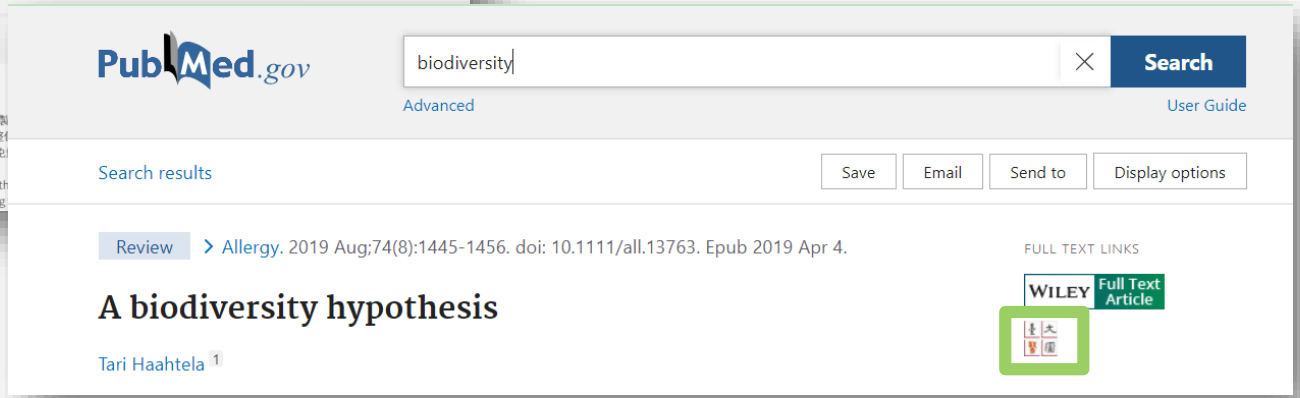

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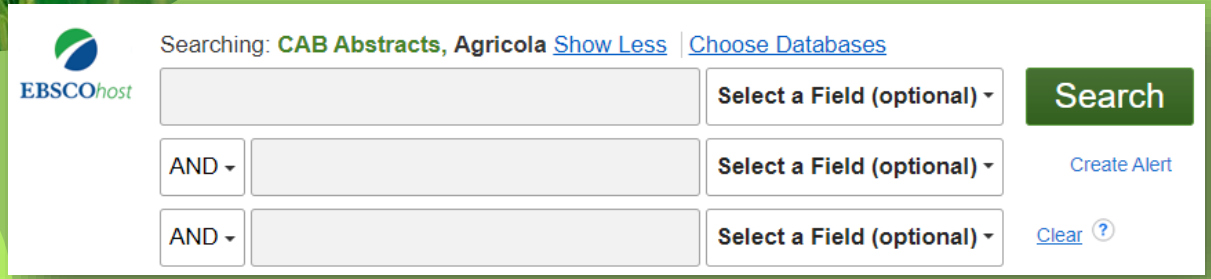

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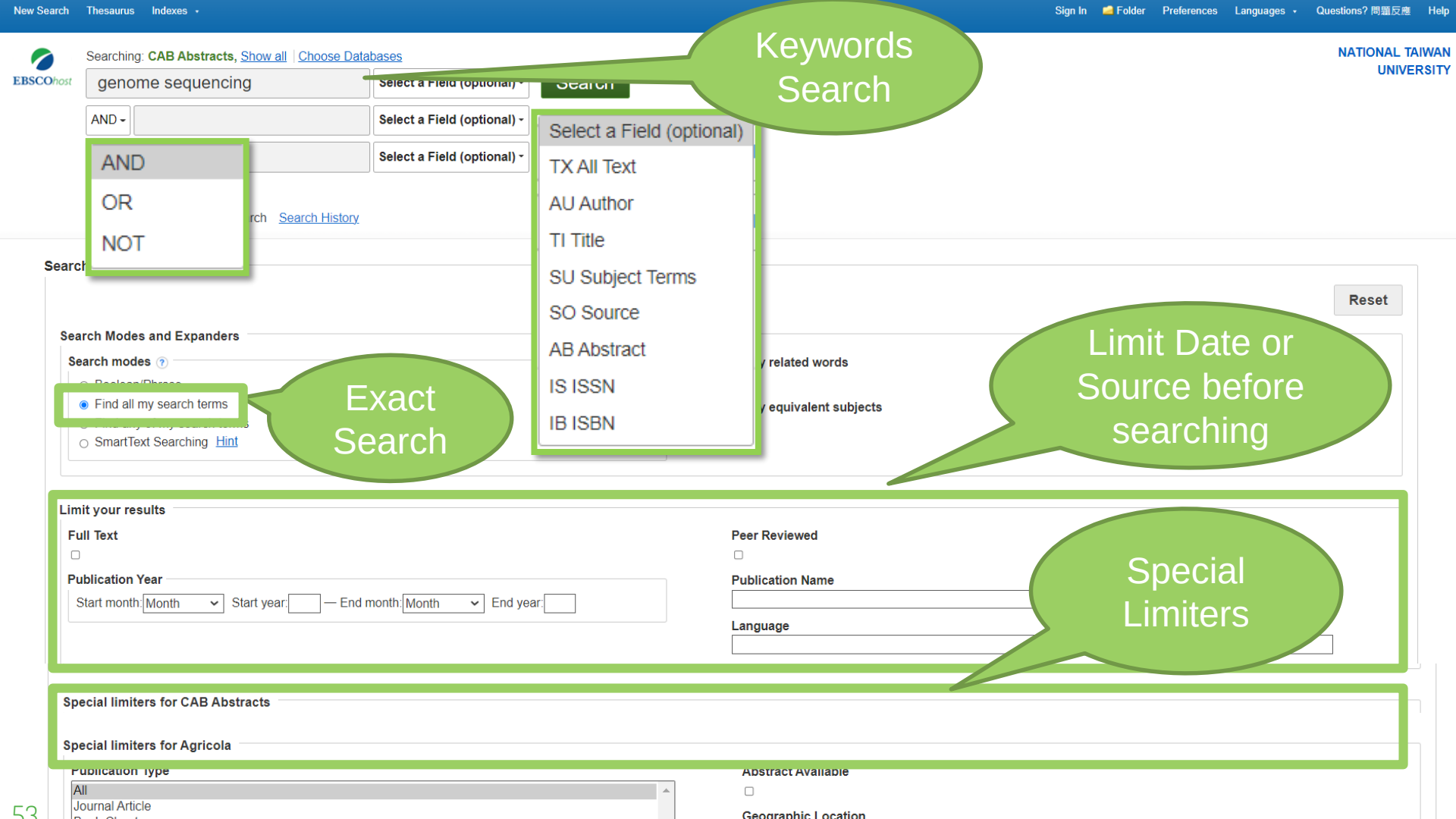
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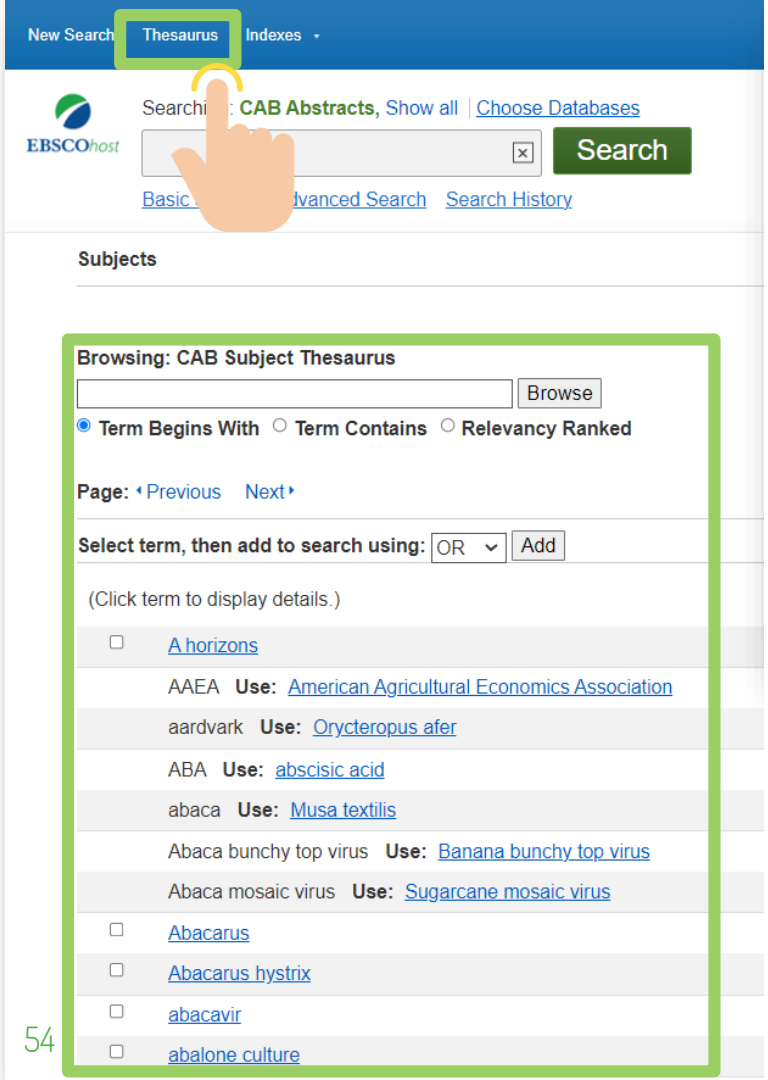
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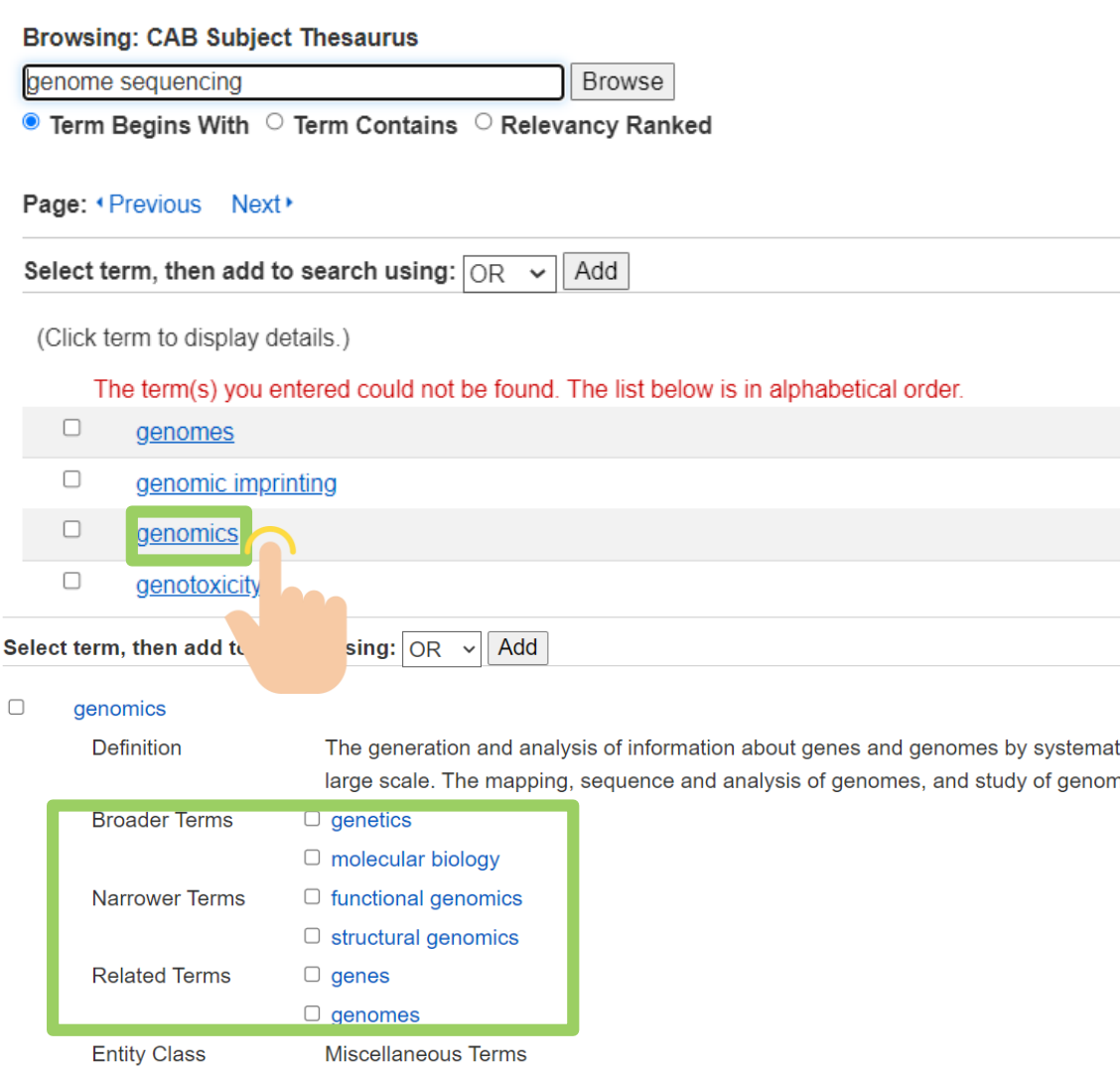
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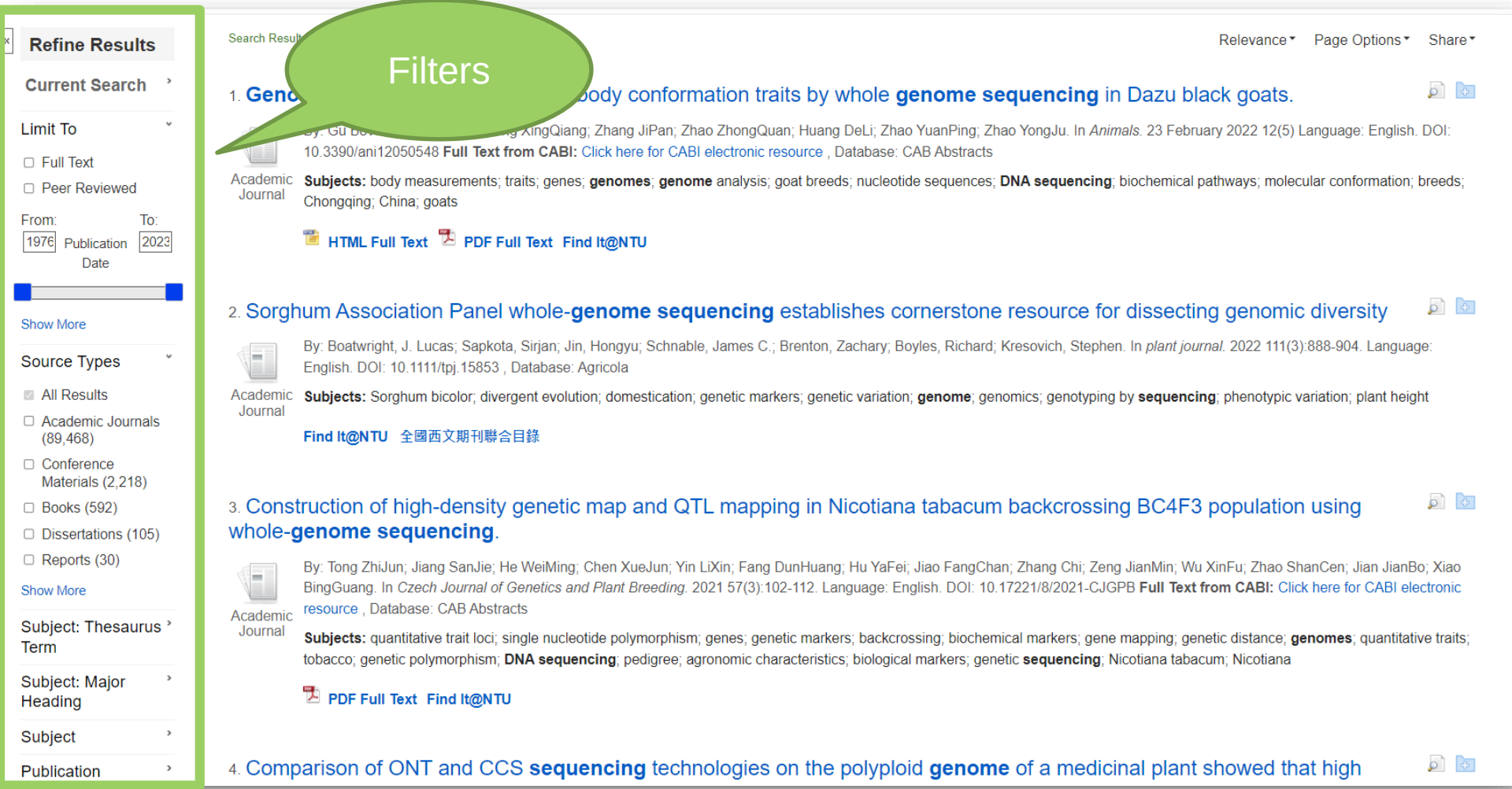
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XingQiang; Zhang JiPan; Zhao ZhongQuan; Huang DeLi; Zhao YuanPing; Zhao YongJu. In Animals. 23 February 2022 12(5) Language: English. DOI: 10.3390/ani12050548 Full Text from CABI: Click here for CABI electronic resource , Database: CAB Abstracts
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Subjects: body measurements; traits; genes; genomes; genome analysis; goat breeds; nucleotide sequences; DNA sequencing; biochemical pathways; molecular conformation; breeds; Chongqing; China; goats
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2. Sorghum Association Panel whole-genome sequencing establishes cornerstone resource for dissecting genomic diversity
By: Boatwright, J. Lucas; Sapkota, Sirjan; Jin, Hongyu; Schnable, James C.; Brenton, Zachary; Boyles, Richard; Kresovich, Stephen. In plant journal. 2022 111(3):888-904. Language: English. DOI: 10.1111/tpj.15853 , Database: Agricola
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3. Construction of high-density genetic map and QTL mapping in Nicotiana tabacum backcrossing BC4F3 population using whole-genome sequencing.
By: Tong ZhiJun; Jiang SanJie; He WeiMing; Chen XueJun; Yin LiXin; Fang DunHuang; Hu YaFei; Jiao FangChan; Zhang Chi; Zeng JianMin; Wu XinFu; Zhao ShanCen; Jian JianBo; Xiao BingGuang. In Czech Journal of Genetics and Plant Breeding. 2021 57(3):102-112. Language: English. DOI: 10.17221/8/2021-CJGPB Full Text from CABI: Click here for CABI electronic resource , Database: CAB Abstracts
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Subjects: quantitative trait loci; single nucleotide polymorphism; genes; genetic markers; backcrossing; biochemical markers; gene mapping; genetic distance; genomes; quantitative traits; tobacco; genetic polymorphism; DNA sequencing; pedigree; agronomic characteristics; biological markers; genetic sequencing; Nicotiana tabacum; Nicotiana
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4. Comparison of ONT and CCS sequencing technologies on the polyploid genome of a medicinal plant showed that high

Genome-wide association study of body conformation traits by whole genome sequencing in Dazu black goats.

Language: English

Authors: Gu BoWen, author
Sun RuiFan, author
Fang XingQiang, author
Zhang JiPan, author
Zhao ZhongQuan, author
Huang DeLi, author
Zhao YuanPing, author
Zhao YongJu, author

Source: Animals 23 February 2022 12(5).

Address: College of Animal Science and Technology, Southwest University, Chongqing 400715,

Publisher Information: Basel, Switzerland : MDPI AG

Publication Date: 2022

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Subject Terms: body measurements
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Keywords: DNA sequences; nucleotide sequence analysis; nucleotide **sequencing**;

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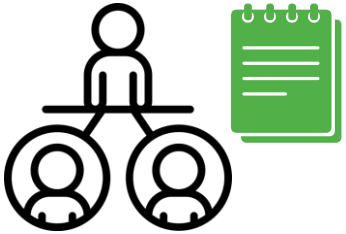
Genome-Wide Association Study of Body Conformation Traits by Whole Genome Sequencing in Dazu Black Goats

Bowen Gu [1,2,3], Ruifan Sun [1,2,3], Xingqiang Fang [1,2,3], Jipan Zhang [1,2,3], Zhongquan Zhao [1,2,3], Deli Huang [4], Yuanping Zhao [5] and Yongju Zhao [1,2,3,*]

1 College of Animal Science and Technology, Southwest University, Chongqing 400715, China; gubw04@163.com (B.G.); sunruifan111@163.com (R.S.); 15881044561@163.com (X.F.); jpanzhang@live.com (J.Z.); zhaozhongquan@swu.edu.cn (Z.Z.)
2 Chongqing Key Laboratory of Herbivore Science, Chongqing 400715, China

Faculty Opinions

Faculty Opinions



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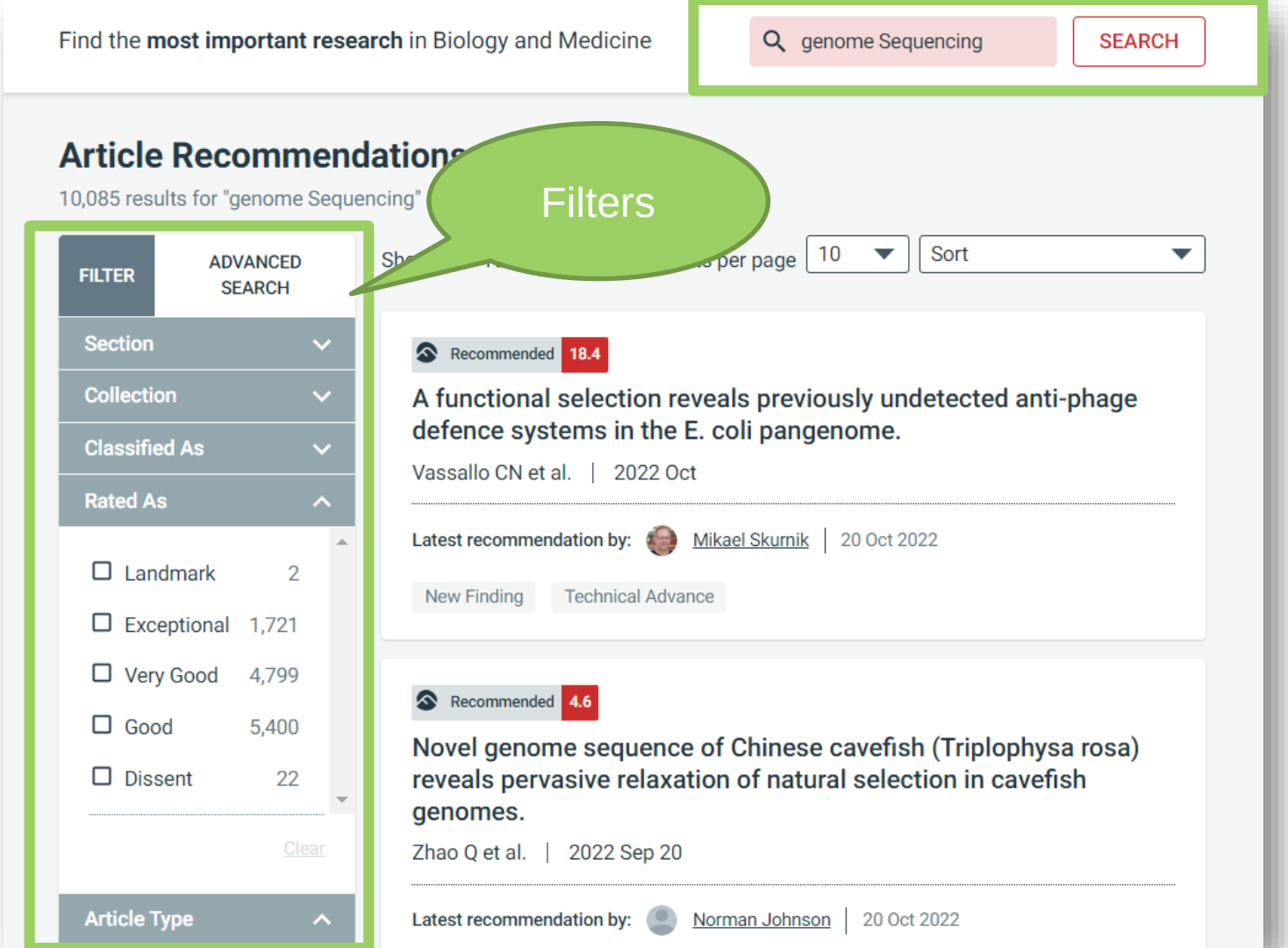
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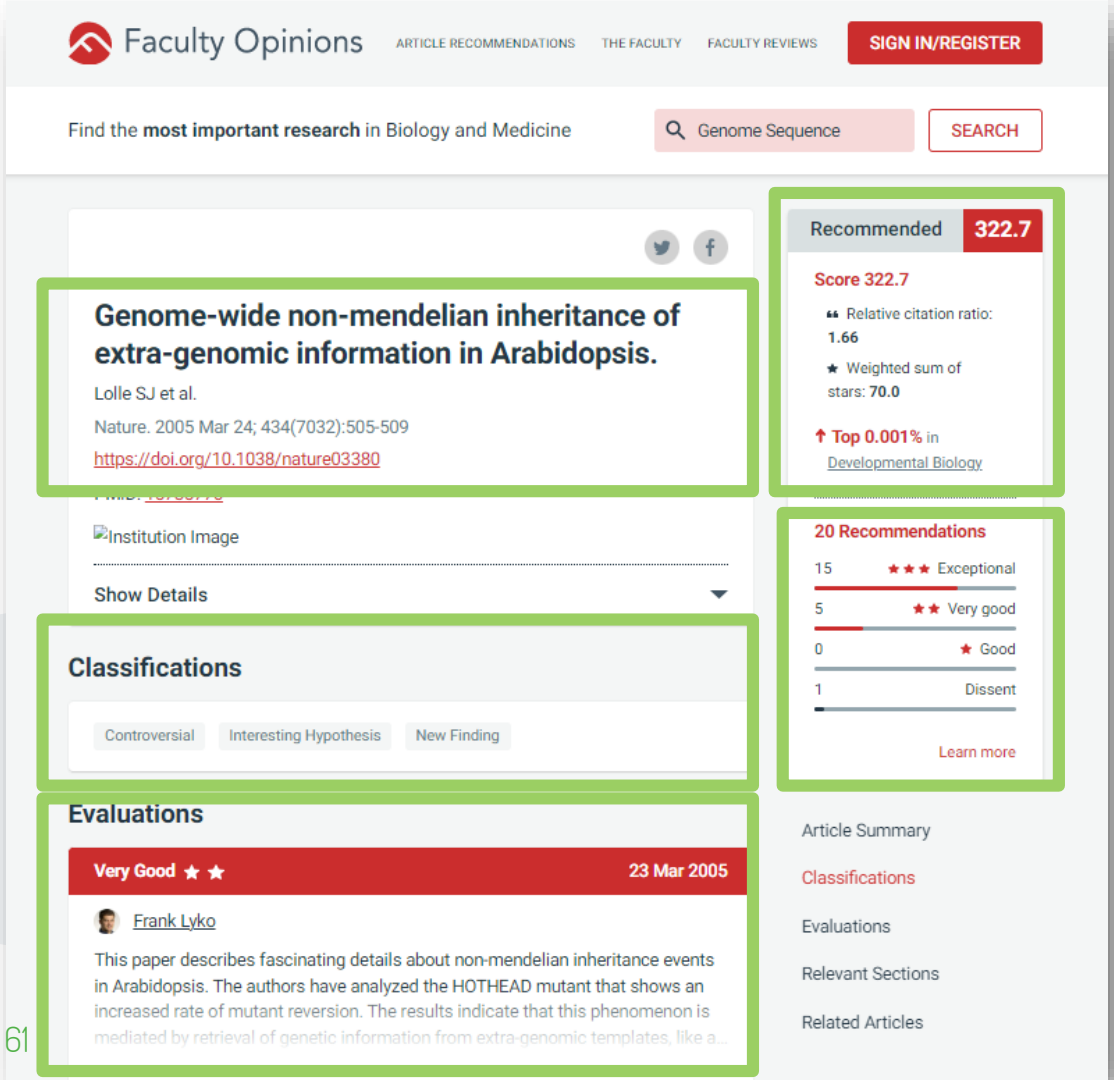

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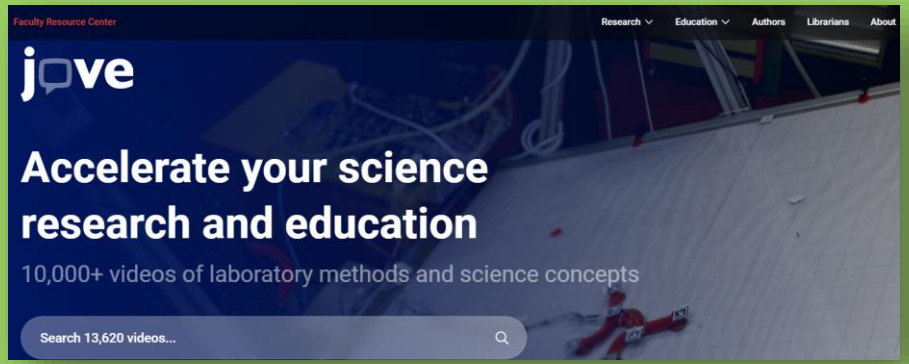

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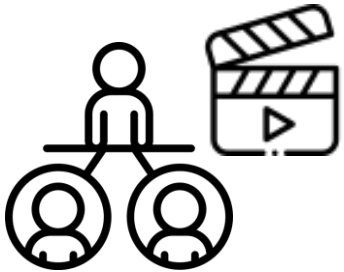

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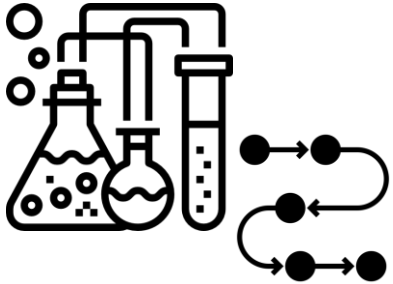

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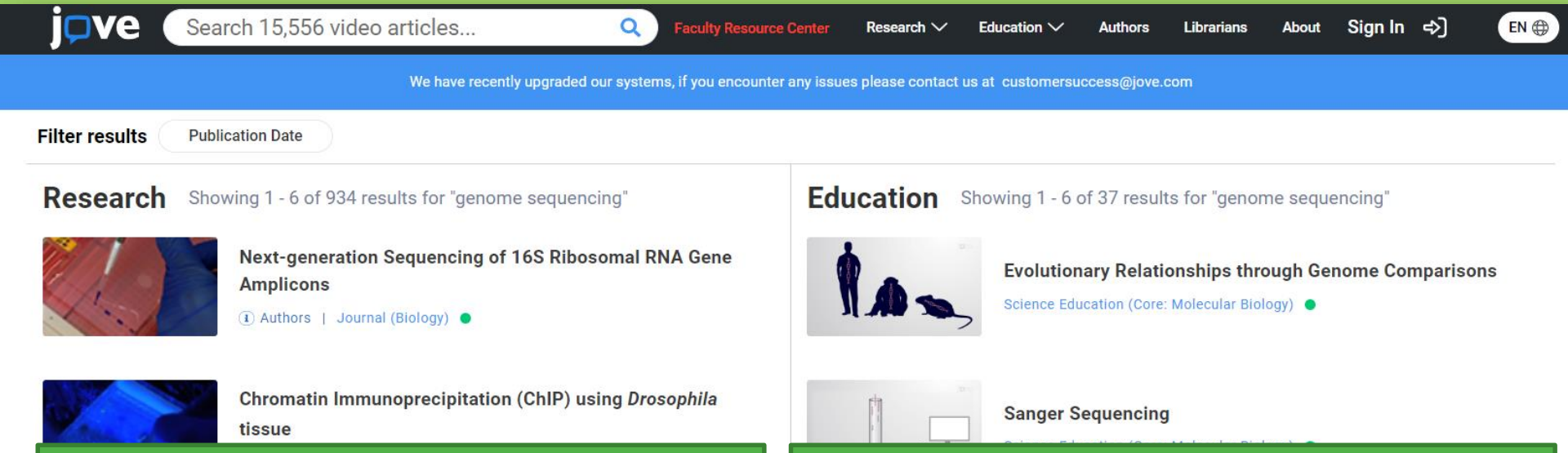

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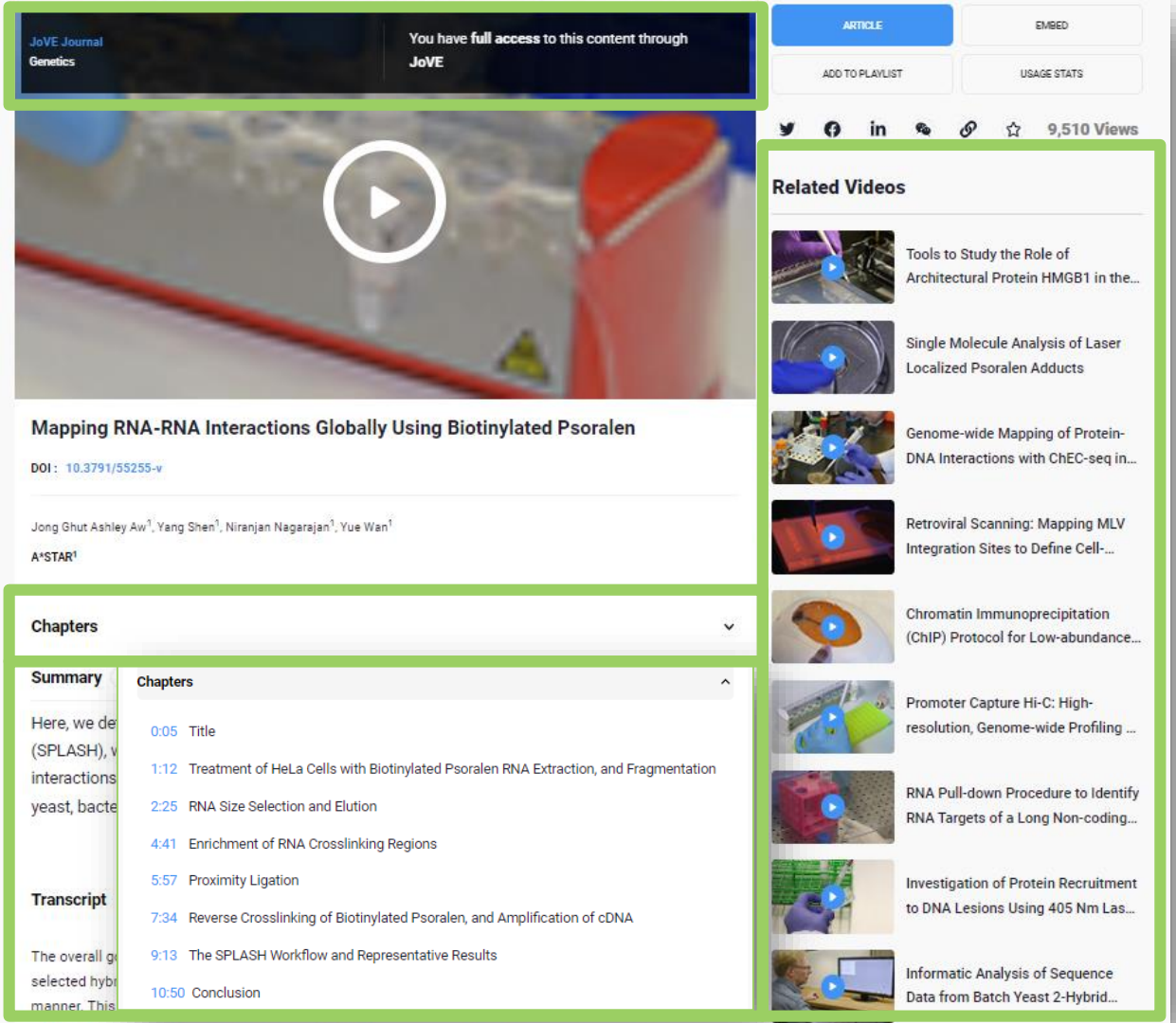
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Mapping RNA-RNA Interactions Globally Using Biotinylated Psoralen

Published: May 24th, 2017 DOI: 10.3791/55255

Jong Ghut Ashley Aw[1], Yang Shen[1], Niranjan Nagarajan[1], Yue Wan[1]

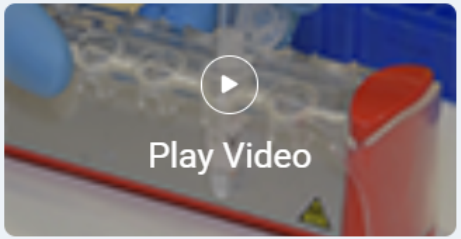
A*STAR[1]

Summary

Here, we detail the method of Sequencing of Psoralen crosslinked, Ligated, and Selected Hybrids (SPLASH), which enables genome-wide mapping of intramolecular and intermolecular RNA-RNA interactions *in vivo*. SPLASH can be applied to study RNA interactomes of organisms including yeast, bacteria and humans.

Abstract

Knowing how RNAs interact with themselves and with others is key to understanding RNA based gene regulation in the cell. While examples of RNA-RNA interactions such as microRNA-mRNA interactions have been shown to regulate gene expression, the full extent to which RNA interactions occur in the cell is still unknown. Previous methods to study RNA interactions have primarily focused on subsets of RNAs that are interacting with a particular protein or RNA species. Here, we detail a method named Sequencing of Psoralen crosslinked, Ligated, and Selected Hybrids (SPLASH) that allows genome-wide capture of RNA interactions *in vivo* in an unbiased manner. SPLASH utilizes *in vivo* crosslinking, proximity ligation, and high



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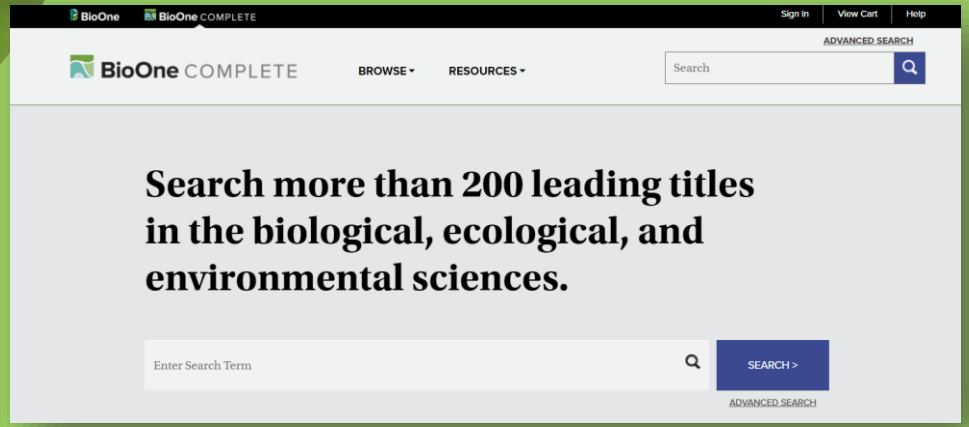
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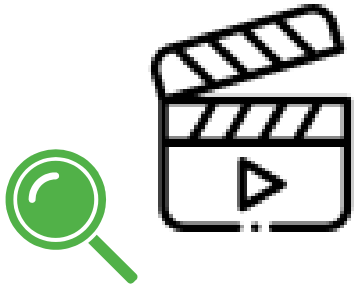

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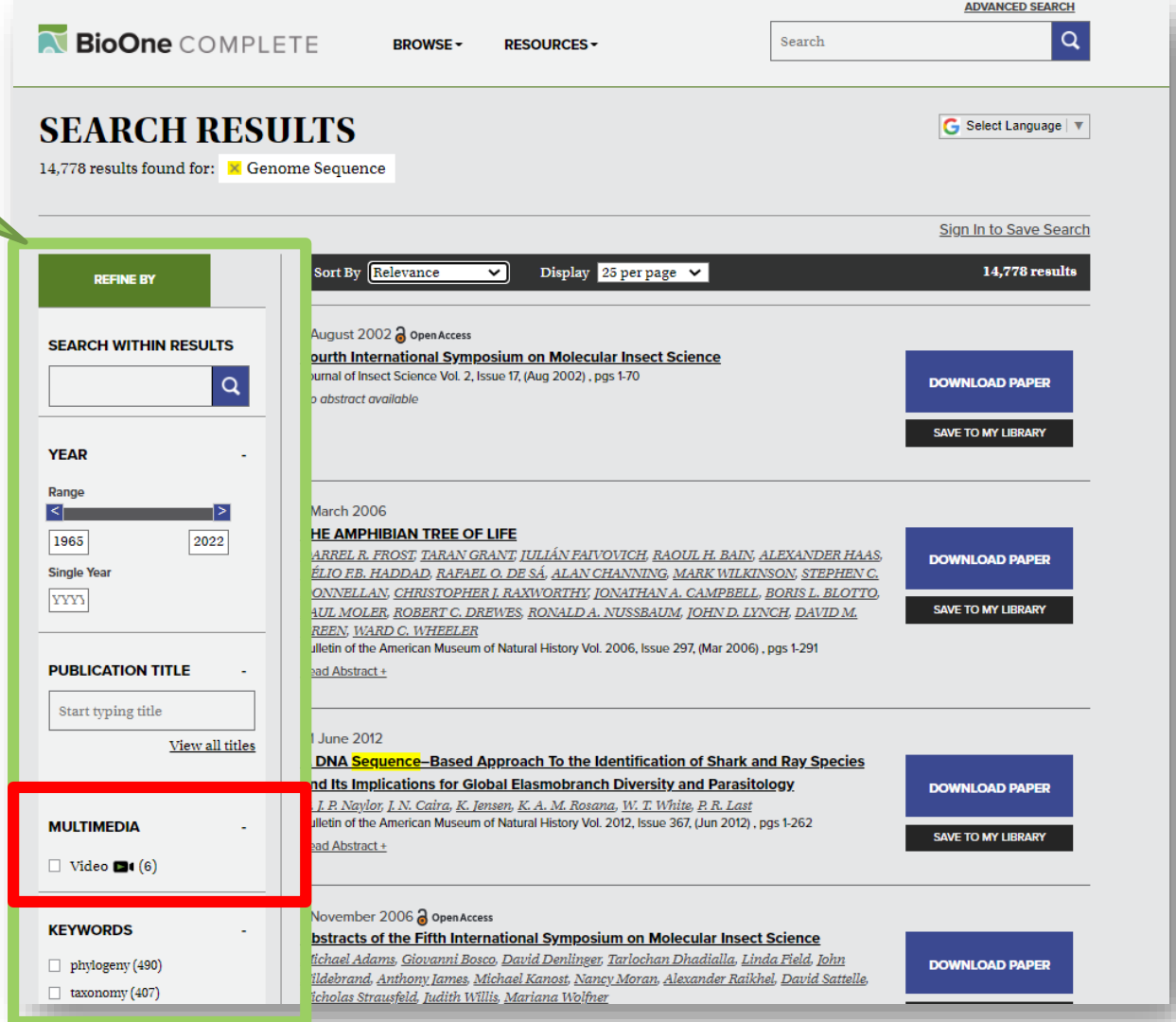
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Kazunori Tachibana, *Masaaki Matsumoto*, *Aiko Minowa*, *Ryusaku Deguchi*

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Zoological Science, 37(3):263-270 (2020). https://doi.org/10.2108/zs190122

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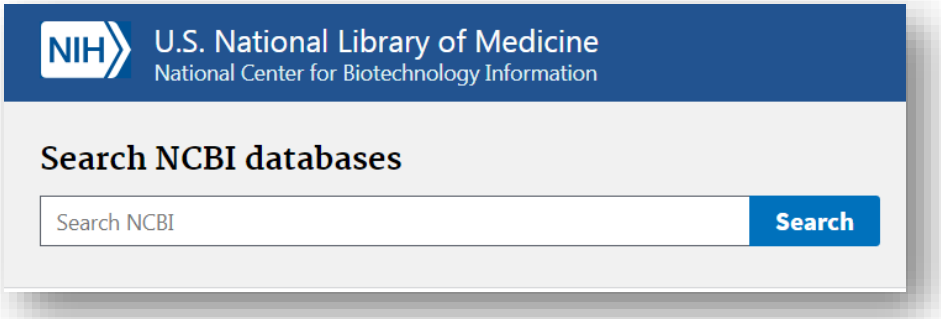

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Protein sequences, 3-D structures, and tools for the study of functional protein domains and active sites

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- **Nucleotide** — DNA and RNA sequences
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Heritable DNA variations, associations with human pathologies, and clinical diagnostics and treatments

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- **dbVar** — Genome structural variation studies
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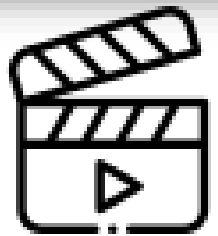

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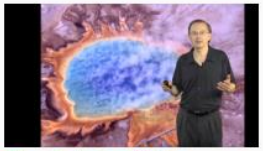

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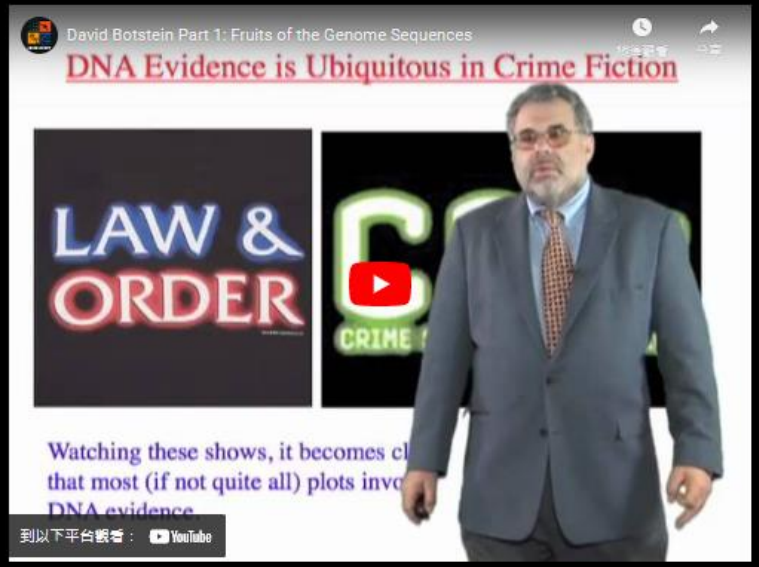

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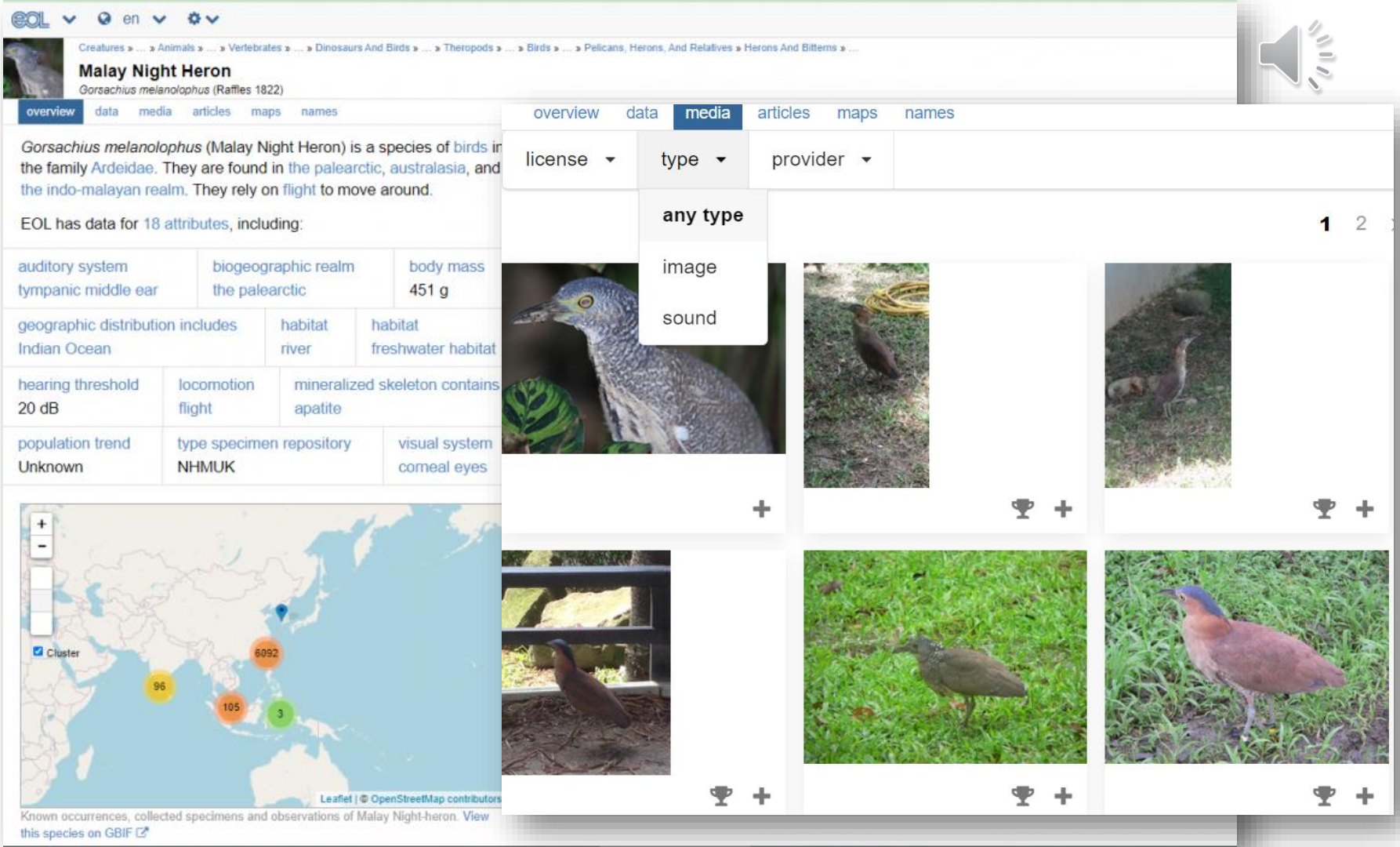
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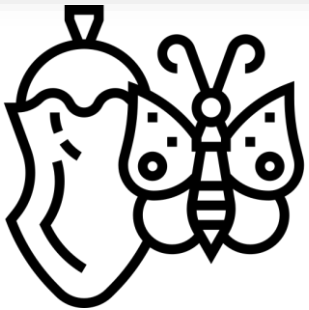

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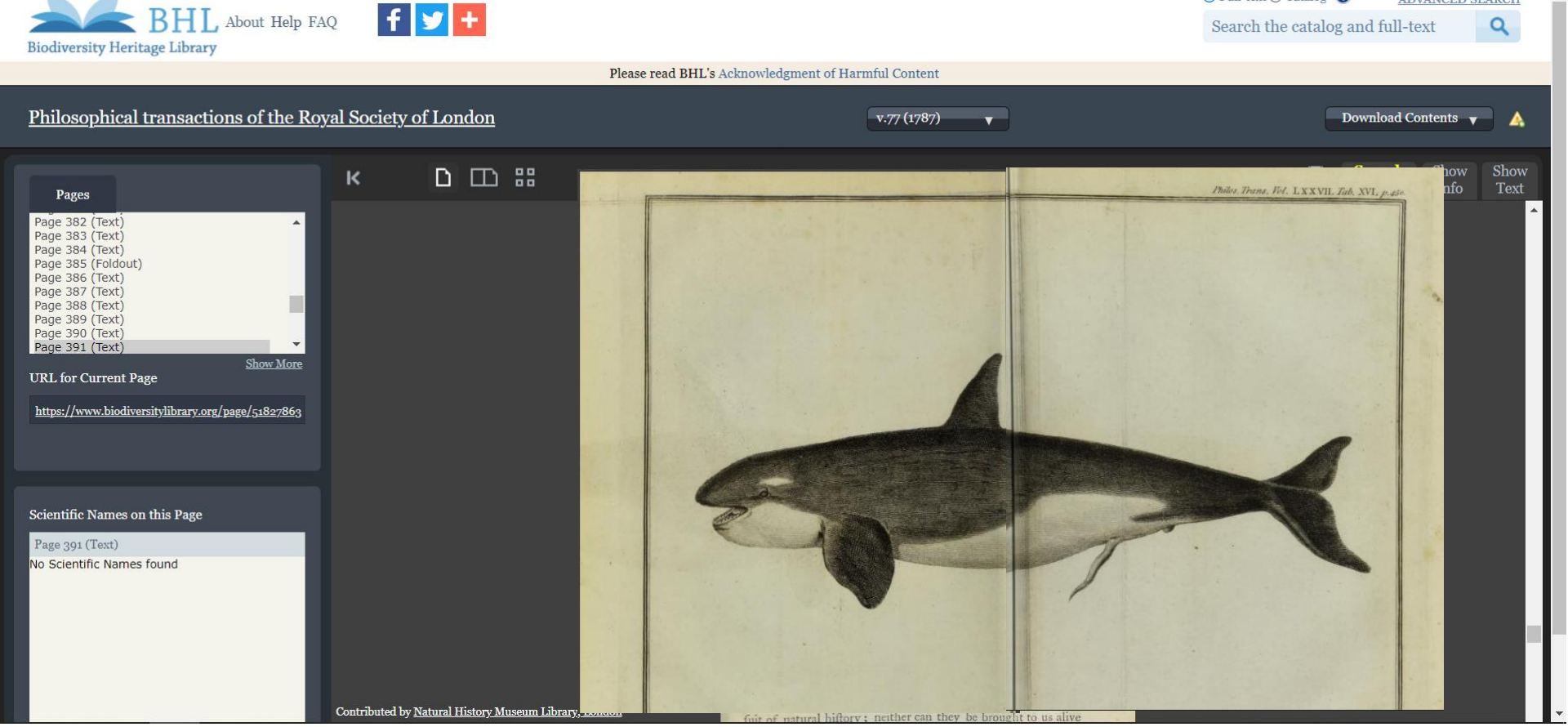

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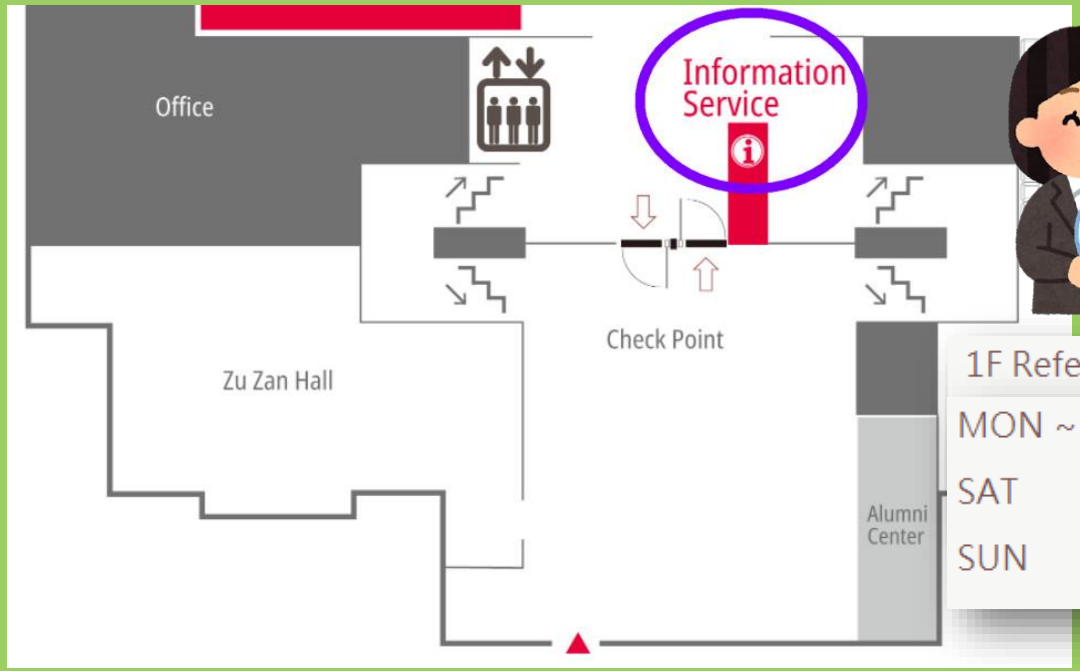

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