Nucleotide Databases

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Introduction

❑ Nucleotide databases are specialized repositories that store nucleotide sequences from DNA and RNA.

❑ **Applications:**

- Comparative genomics and evolutionary studies.
- Gene and genome annotation.
- Identifying and characterizing genes and regulatory elements.
- Studying genetic variation and its implications for health and disease.

Primary Nucleotide Databases

Primary Databases

- Primary databases contain raw, unprocessed data directly submitted by researchers.
- These databases typically store original experimental results without additional interpretation or significant processing. E.g., raw nucleotide sequences, raw proteomics data.
- They provide access to unprocessed nucleotide sequences along with associated metadata, such as the source organism and experimental conditions.
- Researchers can submit their nucleotide sequences along with metadata through various submission tools provided by these databases.
- Users can search for sequences based on various criteria such as gene name, organism, or sequence similarity.
- These databases offer advanced search tools and interfaces for data retrieval.
- **Primary nucleotide databases:**

A. GenBank

B. ENA

C. ARSA

GenBank

- GenBank (R) is a comprehensive database that contains publicly available nucleotide sequences for more than 240 000 named organisms, obtained primarily through submissions from individual laboratories and batch submissions from large-scale sequencing projects.
- Submissions made using web based BankIt or Sequin programs.
- GenBank is accessible through NCBI's retrieval system, Entrez.
- Key divisions in GenBank:

a. WGS: Major portion of database consists of whole genome sequencing i.e., complete genetic material of an organism

b. EST/Expressed sequence tags: About 16% of the sequences in GenBank are of human origin and 13% of all sequences are human ESTs. ESTs are short sub-sequences of cDNA sequences which helps to understand the gene expression in specific tissues.

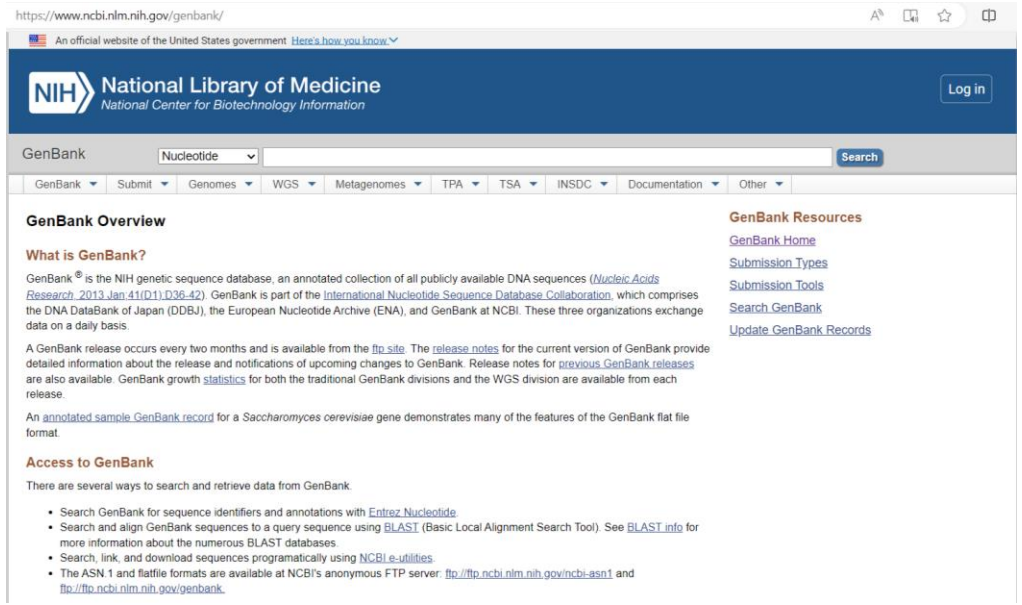
c. High Throughput Genomic (HTG): contains sequences generated from large-scale genomic projects through sequencing technologies. HTG supports genome assembly, mapping and annotation of these sequences.

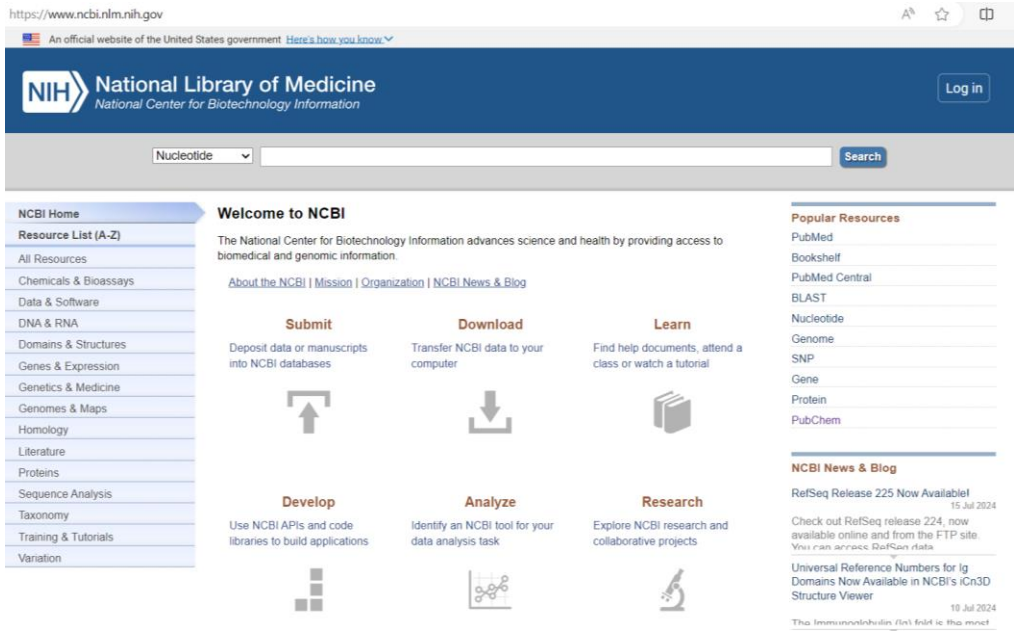
d. ENV: The ENV division contains sequences obtained from environmental samples, which can include sequences from microbial communities in various environments (e.g., soil, water, human gut). These sequences are used in metagenomics data.

e. PRI/Primates, ROD/Rodents, BCT/bacteria, MAM/Other mammals, etc.

GenBank Homepage

- GenBank Overview (nih.gov) or National Center for Biotechnology Information (nih.gov) and choose nucleotide



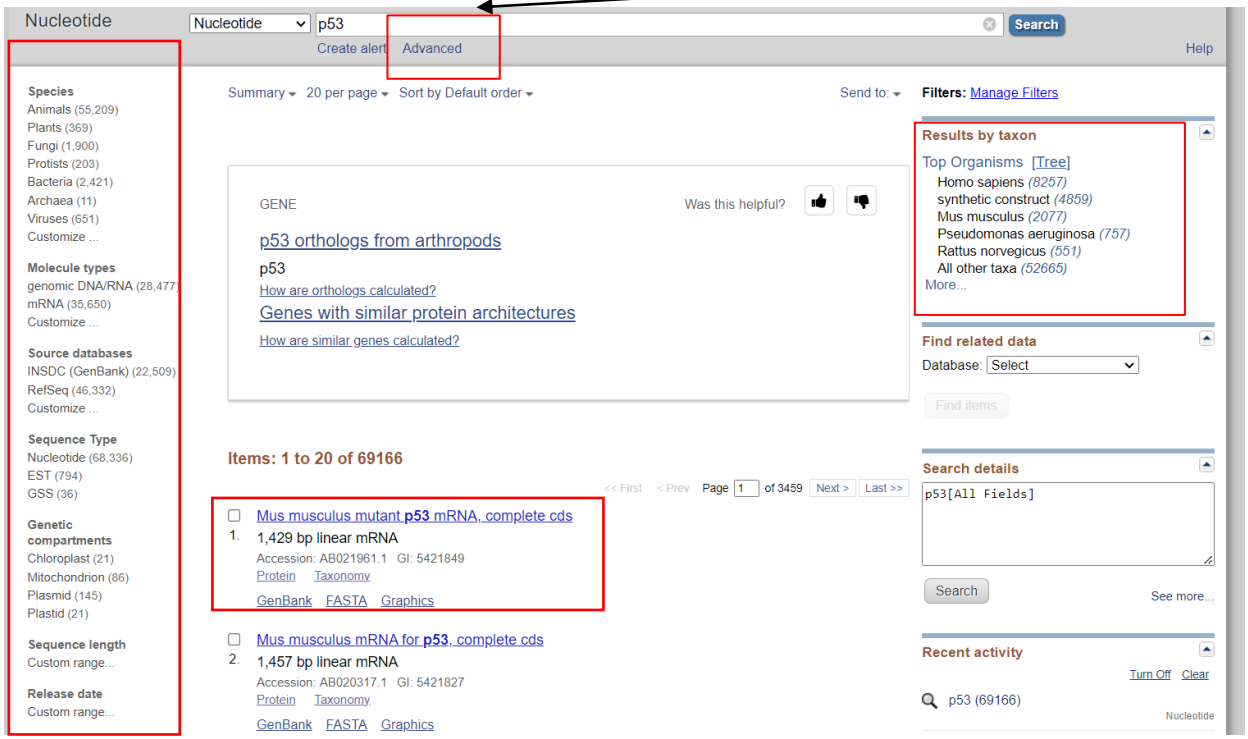


GenBank Query Search

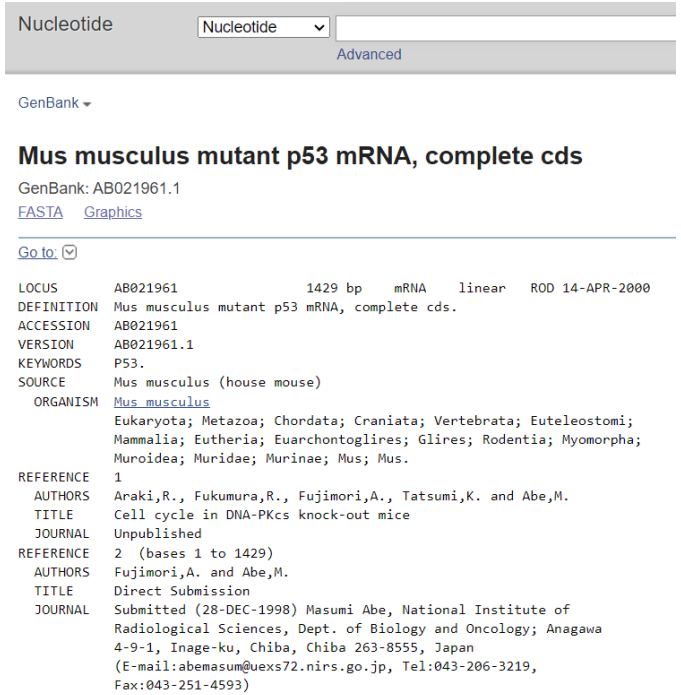
- Organism, name, no. of nucleotides and accession number (unique identifier of a sequence)

Advanced Filtered Search

Filter



GenBank Flat file

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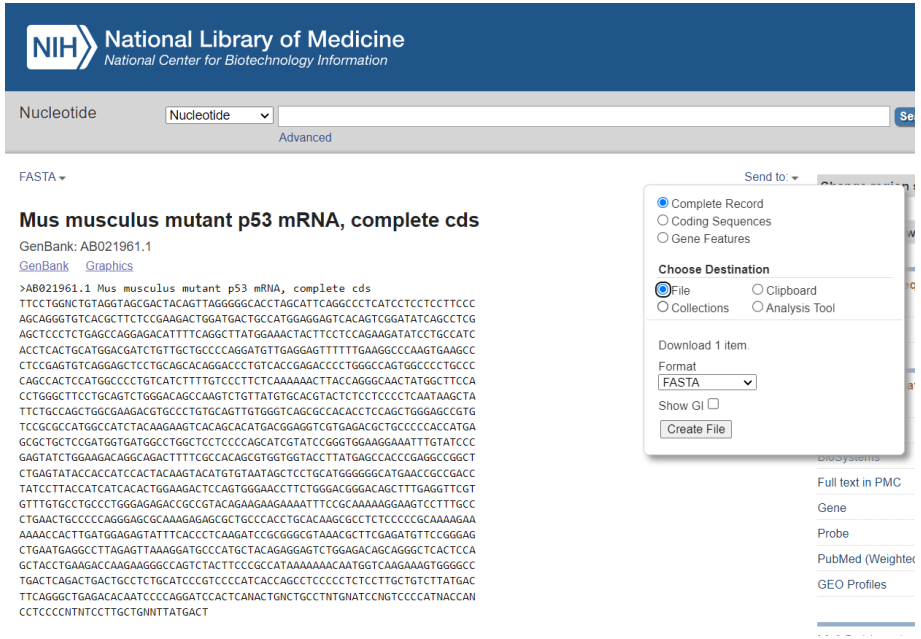
FASTA

- FASTA format: Nucleotides and Amino acids presented using single letter codes



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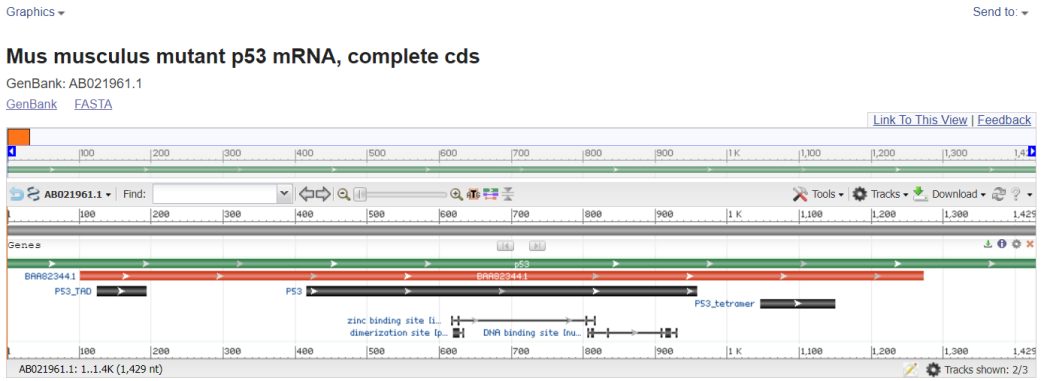


Graphics View

GenBank Flat file

- **Locus:** Accession number, no. of nucleotides/base pairs, type of molecule, topology, division and date of submission
- **Definition:** Source/organism, name of gene
- **Features:** genes and gene products along with regions of biological significance with their locations. These can include regions of the sequence that code for proteins and RNA molecules, as well as a number of other features. Introns, exons can also be included.
  - Source

    /organism: Will specify the organism from which sequence is derived.

    /mol_type: indicates molecular type of sequence

    /db_xref: Cross-reference to taxonomy database
  - Gene:

    /gene specifies gene symbol

GenBank Flat file

❑ **Features (Con):**

- mRNA: Describes the locations of exons that are joined together to form the mature mRNA transcript.

  /gene provides gene associated with mRNA

  /product Specifies the product of this mRNA

- CDS: Coding sequence responsible for coding for a protein. /translation provides the protein that gene sequence is coding for.

- Variation:

  /note Describes the nature of the variation. E.g., amino acid substitution

  /replace Specifies the nucleotide change responsible for the variation.

GenBank Flat file

❑ **Features (Con):**

Locations in Feature section:

- 1...1429

Complete feature (Whole sequence)

- <1..>695

The < symbol indicates partial on the 5' end.

The > symbol indicates partial on the 3' end.

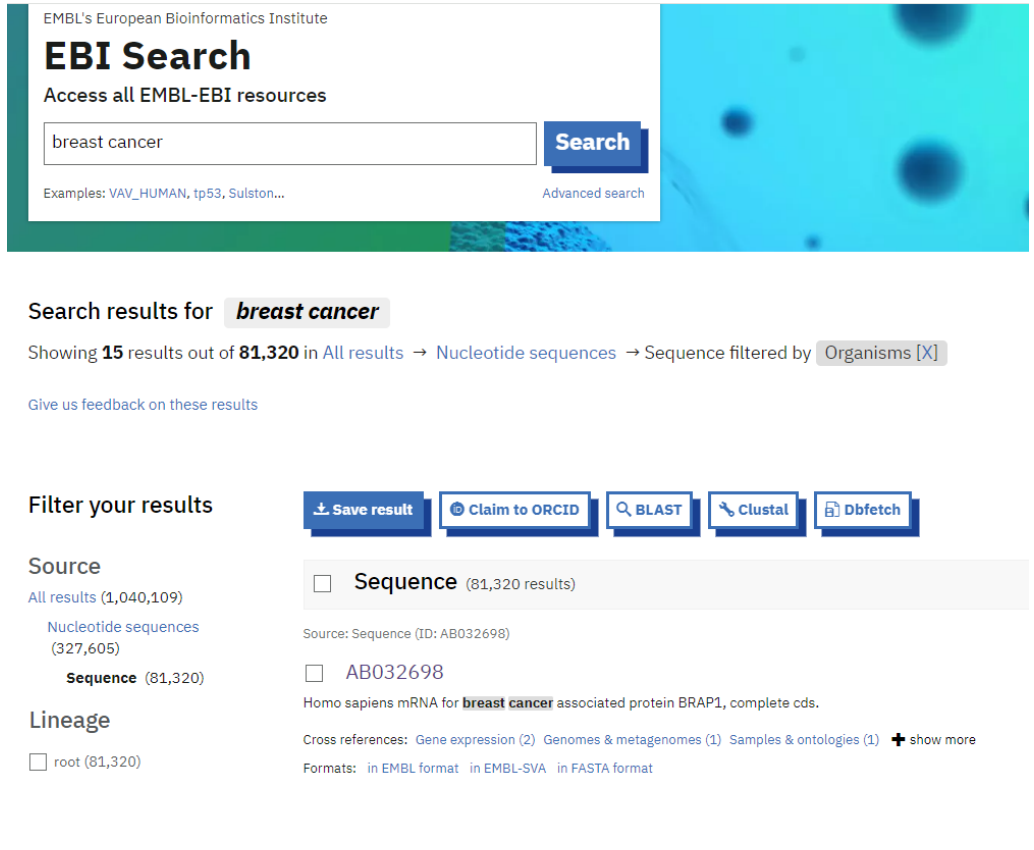
❑ **Origin:** nucleotide sequence of the gene

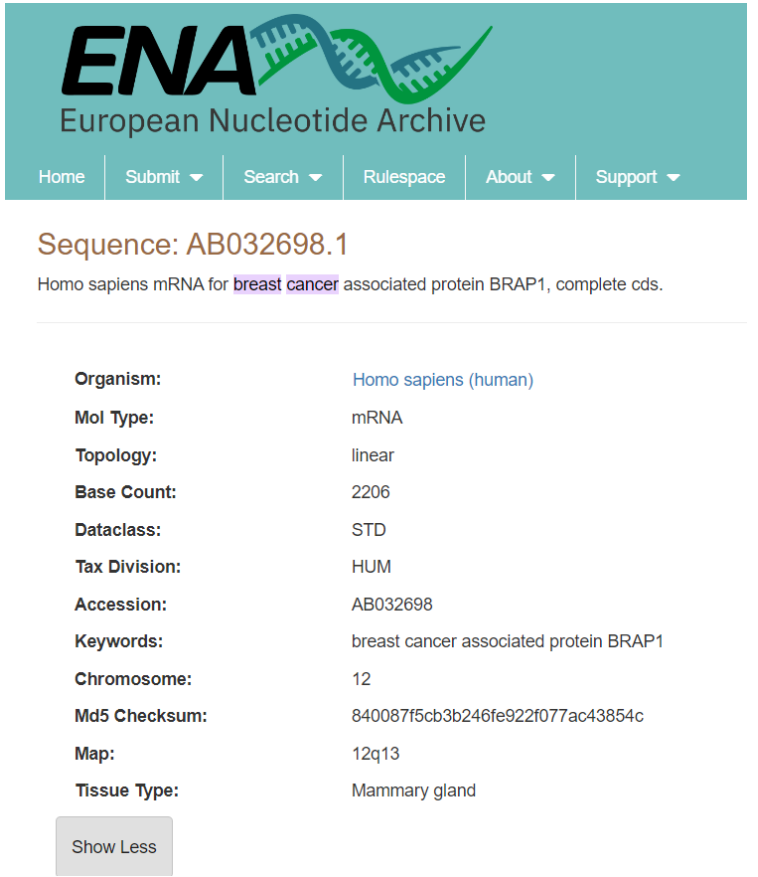
ENA/European Nucleotide Archive

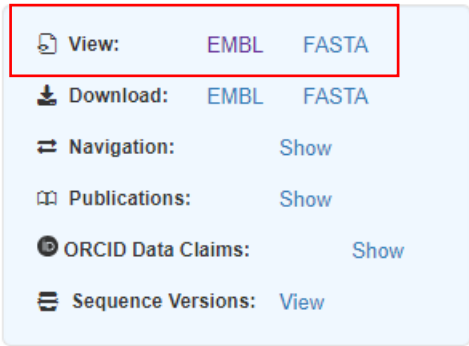
- https://www.ebi.ac.uk/ and choose nucleotide sequences (Filter Sequences)
- A comprehensive repository that provides access to primary nucleotide sequences
- Accepts data in various formats, including FASTQ for raw reads, FASTA for sequences, and XML for metadata
- ENA data is cross-referenced with other major biological databases, including GenBank, DDBJ, UniProt, and the Protein Data Bank (PDB)
- Data can be used to further perform analyses such as alignment, variant calling, or functional annotation
- Widely used by researchers for accessing reference genomes, comparative genomics, and evolutionary studies
- Flat file contains a ladder of information and total nucleotide count

ENA

Can Filter the search according to ENA (Sequences) and organisms







ENA Flat File

Accession No., Topology, Genomic type, Organism, Total nucleotide bases

Date created & updated

Description

Taxonomy (Organism source)

Reference No., Reference Author Reference Title Reference Literature

Cross-references

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DT   07-OCT-2008 (Rel. 97, Last updated, Version 3)
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XX
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XX
OS   Homo sapiens (human)
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OC   Homo.
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RL   Submitted (22-SEP-1999) to the INSDC.
RL   Yoshio Miki, The Cancer Institute, Japanese Foundation for Cancer Research,
RL   Dept. of Molecular Diagnosis; 1-37-1, Kami-ikebukuro, Toshimaku, Tokyo
RL   170-8455, Japan (E-mail:yosmiki@ims.u-tokyo.ac.jp, Tel:81-3-5394-4035,
RL   Fax:81-3-5394-4035)
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ENA Flat File

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Cross References

AA sequence (Protein) coded by CDS

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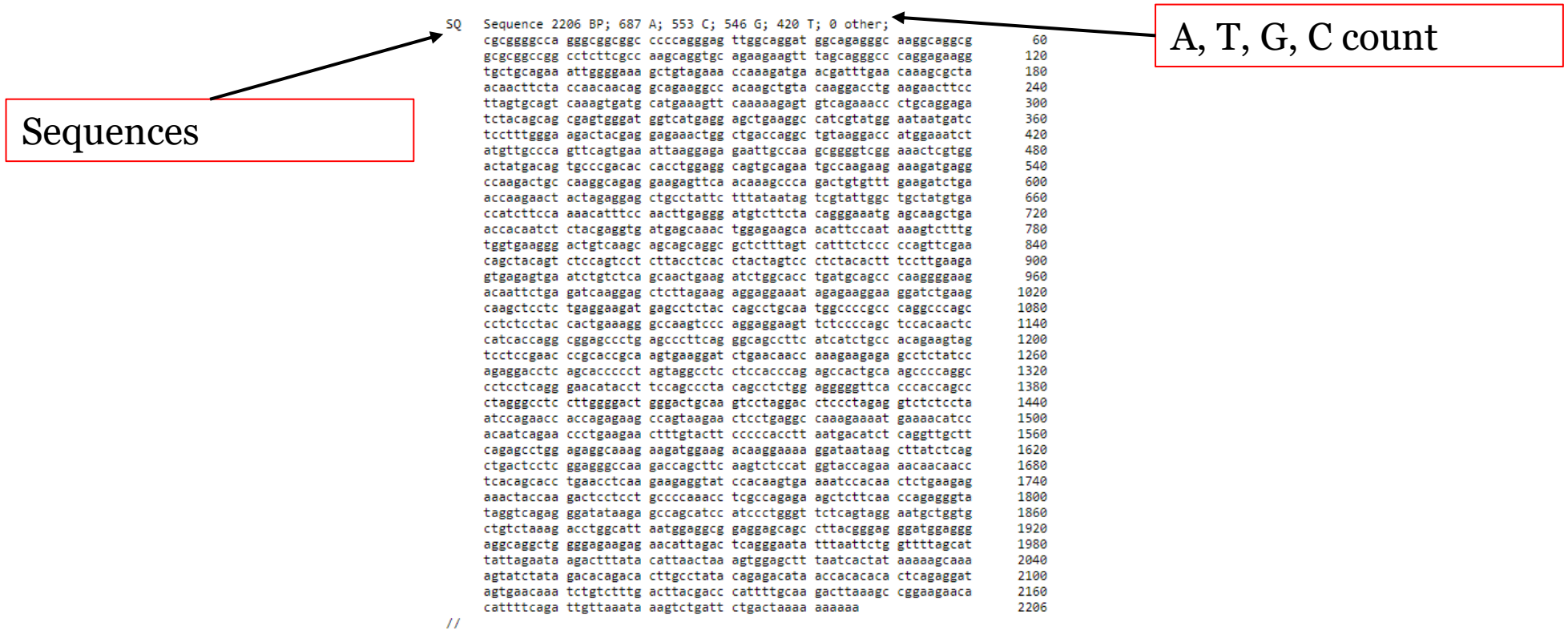


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ARSA

- ARSA | DDBJ | Quick Search (nig.ac.jp)
- Primary nucleotide sequence database stored in DDBJ databases
- ARSA supports the use of Boolean operators (AND, OR, NOT) to refine search queries.
- FASTA, Flatfile can be downloaded
- DDBJ collaborates with GenBank and ENA to ensure that nucleotide sequence data is shared and updated across all three databases.
- Sequence records in DDBJ are cross-referenced with related entries in other biological databases, enhancing data interoperability.
- Flat file provides total nucleotide count, detailed information about variation

ARSA

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  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 62)
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            PA   Keio University
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