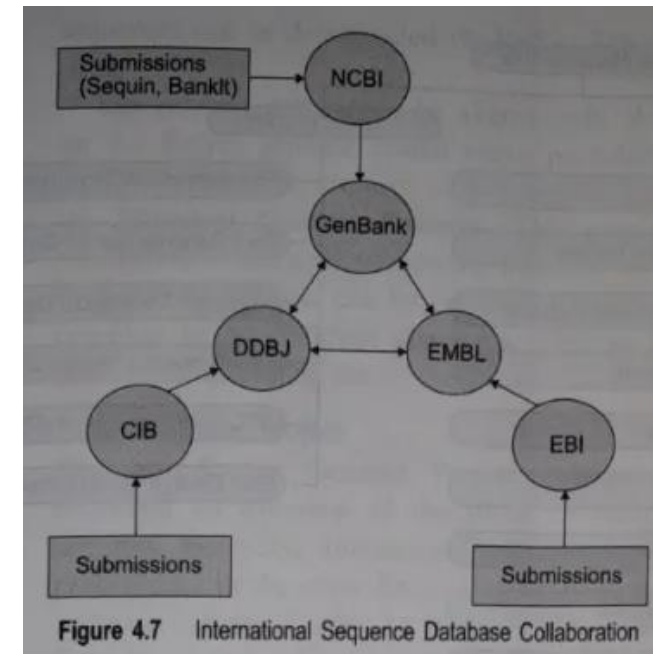


# **Primary Resource Institutes**

**Shatakshi Kulkarni**

# Introduction

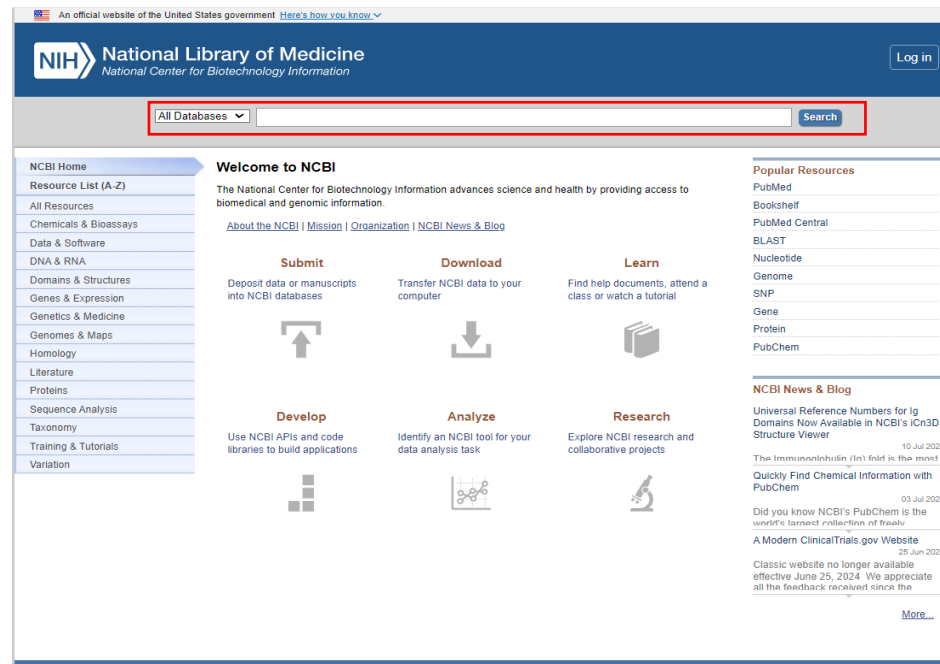
- ❑ Primary resource institutes in bioinformatics are key organizations that provide foundational data, tools, and resources for the global bioinformatics community.
- ❑ These institutes play a crucial role in collecting, curating, and disseminating biological data, as well as developing software and databases to facilitate research.
- ❑ International Nucleotide Sequence Database collaboration (INSDC)



# NCBI/National Center for Biotechnology Information

- ❑ <https://www.ncbi.nlm.nih.gov/>
- ❑ Resource institute for biochemical and genetic information and bioinformatics tools

Resources



Tools & Resources

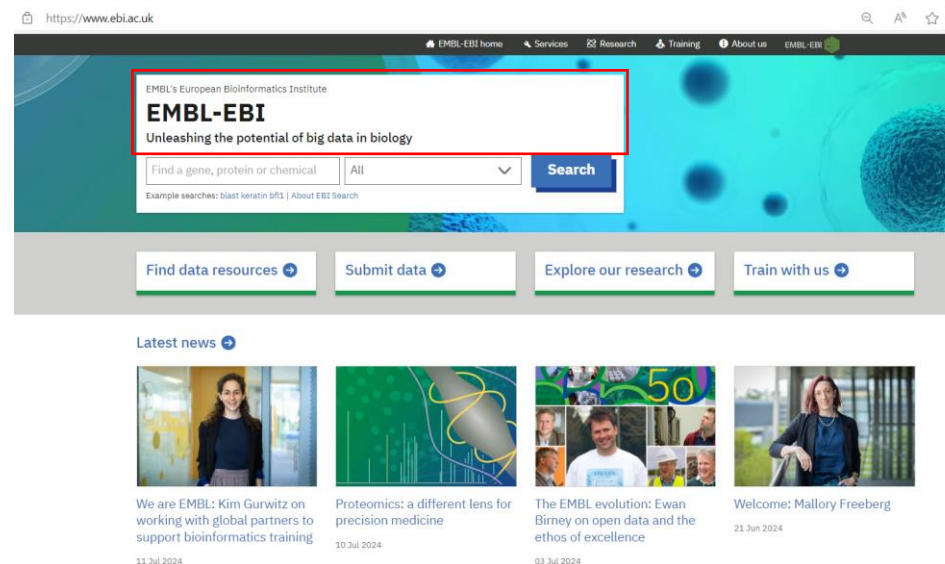
# NCBI

## □ Key Resources:

- **GenBank:** A comprehensive database of nucleotide sequences.
- **PubMed:** A searchable database of biomedical literature.
- **BLAST:** A tool for comparing an input sequence against a database of sequences.

# EMBL/European Molecular Biology Laboratory

- ❑ [EMBL-EBI homepage | EMBL-EBI](https://www.ebi.ac.uk)
- ❑ Established in 1980 and maintained by EBI/European Bioinformatics Institute
- ❑ Aims to collect and present nucleotide sequence and annotation with comprehensive global coverage
- ❑ Key goal of EMBL is to build, maintain and prepare biological databases and other computational services to support data deposition and data analysis.
- ❑ It is a huge warehouse of biological data and bio-software.
- ❑ 1<sup>st</sup> completed genomes from viruses and organelles were deposited into the EMBL database.



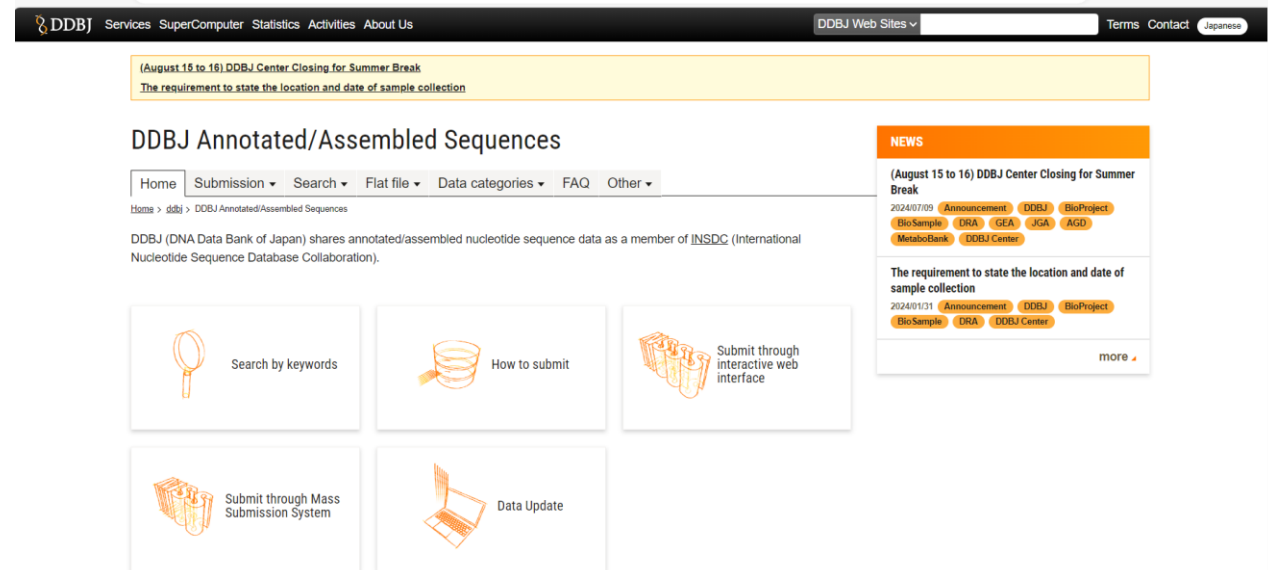
# EMBL

## □ Key Resources:

- **ENA (European Nucleotide Archive):** Repository for nucleotide sequence data.
- **UniProt:** Comprehensive resource for protein sequence and functional information.
- **Ensembl:** A genome browser for vertebrate genomes.
- **ArrayExpress:** Gene expression database

# DDBJ/DNA Data Bank of Japan

- ❑ Collects nucleotide sequences i.e., DNA, RNA
- ❑ Established in 1986, at the National Institute of Genetics (NIG), Shizuoka, Japan
- ❑ In collaboration with EMBL and NCBI
- ❑ Getentry and SRS are the retrieval systems
- ❑ GTOP/Genomes to Protein structure and functions is also available in DDBJ which can help in 3D prediction of structure, functional prediction, homology modeling
- ❑ [DDBJ Annotated/Assembled Sequences \(nig.ac.jp\)](https://nig.ac.jp)



# DDBJ

## □ Key Resources:

- **DDBJ:** Primary database for nucleotide sequences, supporting a wide range of organisms and research projects.