

Data sharing case study – genome sequence

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The Bermuda principles



- Primary Genomic Sequence Should be Rapidly Released
- Sequence assemblies should be released as soon as possible; in some centres, assemblies of greater than 1 Kb would be released automatically on a daily basis.
- Finished annotated sequence should be submitted immediately to the public databases.

Patenting of genes

Patenting of genes

(Slip Opinion)

OCTOBER TERM, 2012

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Syllabus

NOTE: Where it is feasible, a syllabus (headnote) will be released, as is being done in connection with this case, at the time the opinion is issued. The syllabus constitutes no part of the opinion of the Court but has been prepared by the Reporter of Decisions for the convenience of the reader. See *United States v. Detroit Timber & Lumber Co.*, 200 U. S. 321, 337.

SUPREME COURT OF THE UNITED STATES

Syllabus

ASSOCIATION FOR MOLECULAR PATHOLOGY ET AL.
v. MYRIAD GENETICS, INC., ET AL.

CERTIORARI TO THE UNITED STATES COURT OF APPEALS FOR
THE FEDERAL CIRCUIT

No. 12–398. Argued April 15, 2013—Decided June 13, 2013

- Held: A naturally occurring DNA segment is a product of nature and not patent eligible merely because it has been isolated, but cDNA is patent eligible because it is not naturally occurring.

Data sharing - funders

Final NIH Policy for Data Management and Sharing

Notice Number:

NOT-OD-21-013

Key Dates

Release Date:

October 29, 2020

Effective Date:

January 25, 2023

- The final DMS Policy states that “[s]hared scientific data should be made accessible as soon as possible, and no later than the time of an associated publication, or the end of the award/support period, whichever comes first.”

Data sharing – research community



The screenshot shows the top section of the GenBank website. At the top left is the NIH logo and the text "National Library of Medicine" and "National Center for Biotechnology Information". Below this is a search bar with "GenBank" on the left, a dropdown menu set to "Nucleotide", and an empty search input field. Under the search bar is a horizontal navigation bar with links: "GenBank", "Submit", "Genomes", "WGS", "Metagenomes", "TPA", "TSA", "INSDC", and "Documentation". Below the navigation bar is a section titled "How to submit data to GenBank". The text in this section states: "The most important source of new data for GenBank® is direct submissions from scientists. GenBank depends on its contributors to help keep the database as comprehensive, current, and accurate as possible. NCBI provides timely and accurate processing and biological review of new entries and updates to existing entries, and is ready to assist authors who have new data to submit."

- GenBank will, upon request, withhold release of new submissions for a specified period of time. However, if the accession number or sequence data appears in print or online prior to the specified date, your sequence will be released. In order to prevent the delay in the appearance of published sequence data, we urge authors to inform us of the appearance of the published data.

Data sharing - journals

- PLoS Biology

All data and related metadata underlying reported findings should be deposited in appropriate public data repositories, unless already provided as part of a submitted article. Repositories may be either subject-specific repositories that accept specific types of structured data, or cross-disciplinary generalist repositories that accept multiple data types.

Thank you!