

Intended Users:	Information Professionals	Researchers
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NIH Comparative Genomics Resource

Description: The NIH Comparative Genomics Resource (CGR) maximizes the impact of research on eukaryotic (non-bacterial, non-viral organisms such as animals, plants, and fungi) lifeforms and their genomic data. CGR facilitates reliable comparative genomics analyses, including the study of structure, function, evolution, and mapping of eukaryotic genomes. Researchers can compare characteristics of sequenced genomes across different species. Comparative genomics provides insight into evolution and how species change over time, how genes control biological functions, and how gene variants in a single species may contribute to disease. CGR facilitates this through community collaboration and an NCBI Toolkit of interconnected and interoperable data and tools.

Popular uses:

Information Professionals	Researchers
• Include CGR tools in subject guides for biology, chemistry, and genetic resources. • Curate FAIR, detailed metadata for genomic research data. • Give feedback on the usability and usefulness of CGR tools by reaching out to the NCBI Helpdesk. • Promote CGR as a multi-faceted resource for facilitating diverse types of comparative genomics research.	• Download comprehensive genomic data including gene, transcript, protein sequences, and metadata. • Visualize and compare eukaryotic genomes assemblies and annotations. • Use tools to improve the quality of your genome assemblies prior to GenBank submission. • Share curated data with NCBI to expand and enhance genomic related content. • Give feedback on the usability and usefulness of CGR tools by reaching out to the NCBI Helpdesk.

Key Points:

1. Connect researchers to data sources, tools for analysis and visualization, and tools for improving the quality of genome assemblies and associated data to enhance comparative genomics research.
2. Contribute to improvement of the NCBI Toolkit by offering feedback and exploring opportunities to connect community curated genome-related content.

Considerations:

1. Encourage researchers to get involved with CGR and offer feedback about what support they need for comparative genomics analyses.

Teaching Example:

1. Have learners describe a research question that involves more than one species and identify which CGR tool or resource they would use to compare genes, genomes, or biological traits across those species.
2. Have learners describe a research project that requires genomic data from one or more species and identify how they would use CGR resources to discover, access, and download the data needed for their analysis.

Real-life Examples:

1. A biomedical researcher studying cancer resistance compares genes in mammals to identify genetic differences that may contribute to disease resistance. They ask where to find reliable cross-species genomic data. The librarian points them to CGR tools that connect genome sequences, gene annotations, and comparative analysis resources in one place.

2. A computational biologist is studying gene evolution across hundreds of vertebrate species and asks the librarian how to do so programmatically. The librarian suggests CGR resources to discover and access genome datasets and metadata from multiple organisms.
3. A genome sequencing team asks a librarian for resources to help evaluate the quality of a newly assembled genome. The librarian suggests CGR-supported quality-control tools that can identify contamination and improve genome annotations before the data are shared or submitted to NCBI.

CGR tools:

Data resources	Tools to analyze, visualize, and compare genomic sequences.	Improve data quality and prepare for submission
Explore and Download Taxonomy, Genes, Genomes and Proteins Data - NCBI Datasets: web and command-line tools Proteins - Protein Family Models - Conserved Domains - SPARCLE	Compare genomic sequences - Basic Local Alignment Search Tool (BLAST) - BLAST ClusteredNR Database Visualize - Comparative Genome Viewer - Multiple Comparative Genome Viewer - Genome Data Viewer	Contamination Screening - Foreign Contamination Screening (FCS) Annotation - Eukaryotic Annotation Pipeline (EGAPx)

More Information:

[NCBI GitHub](#)

[NCBI News and Blog](#)

[CURATED- data curation for librarians](#)

[CGR FAQs](#)

[Comparative Genomics Fact Sheet](#)

[Ten Quick Tips for using CGR article](#)