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| **Intended Users:** | **Information Professionals** | **Researchers** |

# [NIH Comparative Genomics Resource](https://www.ncbi.nlm.nih.gov/comparative-genomics-resource/)

**Description:** The NIH Comparative Genomics Resource (CGR) is a multiyear project intended to maximize 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. Its development is led by the National Center for Biotechnology Information.

## Popular uses of this product:

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| **Information Professionals** | **Researchers** |
| * Include CGR 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 (yellow feedback button). * 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. * Request NCBI evaluation of your human, mouse, or rat genome assemblies for accuracy, completeness, and correctness. * Share curated data with NCBI to expand and enhance genomic related content. * Give feedback on the usability and usefulness of CGR (yellow feedback button). |

## 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 briefly describe their current research project and identify at least one tool that would help them at their current research stage.
2. Have learners explore the website and name two to three ways to get involved with CGR (yellow feedback button on CGR website or direct feedback on a resource in the NCBI Toolkit, email [cgr@nlm.nih.gov](mailto:cgr@nlm.nih.gov), sign up for [mailing list](https://public.govdelivery.com/accounts/USNLMOCPL/subscriber/new?topic_id=USNLMOCPL_50)).

**Real-life Examples:**

1. A genomics researcher is studying rat genomes. They use CGR to find data quality improvement tools and uses them to remove contaminants before submitting the data to NCBI.
2. A researcher asks a librarian about ways to submit their newly assembled genome to GenBank. The librarian suggests CGR as a resource to enhance data quality and illustrate the ways the researcher’s genome may be accessed for re-use after submission.

## CGR tools:

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| [**Data resources**](https://www.ncbi.nlm.nih.gov/comparative-genomics-resource/data-resources/) | [**Tools to analyze, visualize, and compare genomic sequences.**](https://www.ncbi.nlm.nih.gov/comparative-genomics-resource/analysis-tools/) | [**Improve data quality and prepare for submission**](https://www.ncbi.nlm.nih.gov/comparative-genomics-resource/data-quality-tools/) |
| **Download Genome and Gene Data Packages**   * NCBI Datasets: web and command-line tools   **Explore Taxonomy, Genes, Genomes and Proteins**   * Gene * NCBI Orthologs * NCBI Taxonomy   **Proteins**   * Protein Family Models * Conserved Domains * SPARCLE | **Compare genomic sequences**   * Basic Local Alignment Search Tool (BLAST) * BLAST ClusteredNR Database   **Visualize**   * Comparative Genome Viewer * Genome Data Viewer * Multiple Sequence Alignment Viewer | **Contamination Screening**   * Foreign Contamination Screening   **Quality Control**   * Assembly QC Service   **Annotation (Coming Soon!)**   * Eukaryotic Annotation Pipeline |

## More Information:

[NCBI Github](https://github.com/ncbi) [CURATED- data curation for librarians](https://datacurationnetwork.org/outputs/workflows/) [Comparative Genomics Fact Sheet](https://www.genome.gov/about-genomics/fact-sheets/Comparative-Genomics-Fact-Sheet#:~:text=Comparative%20genomics%20is%20a%20field,regions%20of%20similarity%20and%20difference.)

[NCBI News and Blog](https://ncbiinsights.ncbi.nlm.nih.gov/) [CGR FAQs](https://www.ncbi.nlm.nih.gov/comparative-genomics-resource/faqs/)