

# Resource Summary Report

Generated by [dkNET](#) on Sep 20, 2026

## Comparative Vertebrate Sequencing

RRID:SCR\_008213

Type: Tool

---

### Proper Citation

Comparative Vertebrate Sequencing (RRID:SCR\_008213)

---

### Resource Information

**URL:** [http://www.nisc.nih.gov/projects/comp\\_seq.html](http://www.nisc.nih.gov/projects/comp_seq.html)

**Proper Citation:** Comparative Vertebrate Sequencing (RRID:SCR\_008213)

**Description:** Generates data for use in developing and refining computational tools for comparing genomic sequence from multiple species. The NISC Comparative Sequencing Program's goal is to establish a data resource consisting of sequences for the same set of targeted genomic regions derived from multiple animal species. The broader program includes plans for a diverse set of analytical studies using the generated sequence and the publication of a series of papers describing the results of those analysis in peer-reviewed journals in a timely fashion. Experimentally, this project involves the shotgun sequencing of mapped BAC clones. For each BAC, an assembly is first performed when a sufficient number of sequence reads have been generated to provide full shotgun coverage of the clone. At that time, the assembled sequence is submitted to the HTGS division of GenBank. Subsequent refinements of the sequence, including the generation of higher-accuracy finished sequence, results in the updating of the sequence record in GenBank. By immediately submitting our BAC-derived sequences to GenBank, it makes their data available as a public service to allow colleagues to speed up their research, consistent with the now well-established routine of sequencing centers participating in the Human Genome Project. However, at the same time, it has made considerable investment in acquiring these mapping and sequence data, including sizable efforts of graduate students, postdoctoral fellows, and other trainees. Furthermore, in most cases, large data sets involving multiple BAC sequences from multiple species must first be generated, often taking many months to accumulate, before the planned analysis can be performed and the resulting papers written and submitted for publication.

**Synonyms:** Comparative Vertebrate Sequencing

**Resource Type:** data or information resource, database

**Keywords:** accuracy, animal, bac, clone, comparative, computational, genome, genomic, human, map, mapping, model organisms and comparative genomics databases,

sequence, specie, tool

**Resource Name:** Comparative Vertebrate Sequencing

**Resource ID:** SCR\_008213

**Alternate IDs:** nif-0000-21291

**Record Creation Time:** 20220129T080246+0000

**Record Last Update:** 20260919T195716+0000

---

## Ratings and Alerts

No rating or validation information has been found for Comparative Vertebrate Sequencing.

No alerts have been found for Comparative Vertebrate Sequencing.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We have not found any literature mentions for this resource.