## **Resource Summary Report**

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# **Genomic Standards Consortium**

RRID:SCR\_006273 Type: Tool

### **Proper Citation**

Genomic Standards Consortium (RRID:SCR\_006273)

### **Resource Information**

#### URL: http://gensc.org/

Proper Citation: Genomic Standards Consortium (RRID:SCR\_006273)

**Description:** An open-membership International community to promote mechanisms that standardize the description of genomes and the exchange and integration of genomic data. Community-driven standards have the best chance of success if developed within the auspices of international working groups. Participants in the GSC include biologists, computer scientists, those building genomic databases and conducting large-scale comparative genomic analyses, and those with experience of building community-based standards. The mission of the GSC is to work with the wider community towards: \* the implementation of new genomic standards \* methods of capturing and exchanging metadata \* harmonization of metadata collection and analysis efforts across the wider genomics community

#### Abbreviations: GSC

**Resource Type:** data or information resource, standard specification, knowledge environment, narrative resource, international standard specification

Keywords: genome, genomics, standards

**Funding:** National Institute for Environmental eScience ; NERC NE/3521773/1

Resource Name: Genomic Standards Consortium

Resource ID: SCR\_006273

Alternate IDs: nlx\_151884, OMICS\_01780

**Old URLs:** http://gensc.org/gc\_wiki/index.php/Main\_Page

**Record Creation Time:** 20220129T080235+0000

Record Last Update: 20250521T061102+0000

### **Ratings and Alerts**

No rating or validation information has been found for Genomic Standards Consortium.

No alerts have been found for Genomic Standards Consortium.

### Data and Source Information

Source: <u>SciCrunch Registry</u>

### **Usage and Citation Metrics**

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Kimotho RN, et al. (2024) Unraveling plant-microbe interactions: can integrated omics approaches offer concrete answers? Journal of experimental botany, 75(5), 1289.

Kopczynski D, et al. (2024) The lipidomics reporting checklist a framework for transparency of lipidomic experiments and repurposing resource data. Journal of lipid research, 65(9), 100621.

Ritsch M, et al. (2023) Navigating the Landscape: A Comprehensive Review of Current Virus Databases. Viruses, 15(9).

Bernasconi A, et al. (2021) A review on viral data sources and search systems for perspective mitigation of COVID-19. Briefings in bioinformatics, 22(2), 664.

Schriml LM, et al. (2020) COVID-19 pandemic reveals the peril of ignoring metadata standards. Scientific data, 7(1), 188.

Dheilly NM, et al. (2019) Parasite microbiome project: Grand challenges. PLoS pathogens, 15(10), e1008028.

Goh KM, et al. (2019) Current Status and Potential Applications of Underexplored Prokaryotes. Microorganisms, 7(10).

Harrison PW, et al. (2019) The European Nucleotide Archive in 2018. Nucleic acids research, 47(D1), D84.

Roux S, et al. (2019) Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature biotechnology, 37(1), 29.

Harper L, et al. (2018) AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database : the journal of biological databases and curation, 2018.

Klemetsen T, et al. (2018) The MAR databases: development and implementation of databases specific for marine metagenomics. Nucleic acids research, 46(D1), D692.

Reiser L, et al. (2018) FAIR: A Call to Make Published Data More Findable, Accessible, Interoperable, and Reusable. Molecular plant, 11(9), 1105.

Ellenberg J, et al. (2018) A call for public archives for biological image data. Nature methods, 15(11), 849.

Fujiyoshi S, et al. (2017) Transmission of Airborne Bacteria across Built Environments and Its Measurement Standards: A Review. Frontiers in microbiology, 8, 2336.

Bowers RM, et al. (2017) Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature biotechnology, 35(8), 725.

Vallenet D, et al. (2017) MicroScope in 2017: an expanding and evolving integrated resource for community expertise of microbial genomes. Nucleic acids research, 45(D1), D517.

Kaput J, et al. (2017) Propelling the paradigm shift from reductionism to systems nutrition. Genes & nutrition, 12, 3.

Mitchell A, et al. (2016) EBI metagenomics in 2016--an expanding and evolving resource for the analysis and archiving of metagenomic data. Nucleic acids research, 44(D1), D595.

Mineta K, et al. (2016) Databases of the marine metagenomics. Gene, 576(2 Pt 1), 724.

Pafilis E, et al. (2016) EXTRACT: interactive extraction of environment metadata and term suggestion for metagenomic sample annotation. Database : the journal of biological databases and curation, 2016.