

Resource Summary Report

Generated by NIF on Aug 7, 2026

NCBI Genome Survey Sequences Database

RRID:SCR_002146

Type: Tool

Proper Citation

NCBI Genome Survey Sequences Database (RRID:SCR_002146)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/genbank/dbgss/>

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Description: Database of unannotated short single-read primarily genomic sequences from GenBank including random survey sequences clone-end sequences and exon-trapped sequences. The GSS division of GenBank is similar to the EST division, with the exception that most of the sequences are genomic in origin, rather than cDNA (mRNA). It should be noted that two classes (exon trapped products and gene trapped products) may be derived via a cDNA intermediate. Care should be taken when analyzing sequences from either of these classes, as a splicing event could have occurred and the sequence represented in the record may be interrupted when compared to genomic sequence. The GSS division contains (but is not limited to) the following types of data: * random single pass read genome survey sequences. * cosmid/BAC/YAC end sequences * exon trapped genomic sequences * Alu PCR sequences * transposon-tagged sequences Although dbGSS sequences are incorporated into the GSS Division of GenBank, annotation in dbGSS is more comprehensive and includes detailed information about the contributors, experimental conditions, and genetic map locations.

Abbreviations: GSS

Synonyms: Entrez GSS, NCBI dbGSS, dbGSS

Resource Type: database, data or information resource

Keywords: gene sequencing, database, exon trapped, gene trapped, genomic sequences in origin, gold standard

Availability: Free, Freely available

Resource Name: NCBI Genome Survey Sequences Database

Resource ID: SCR_002146

Alternate IDs: SCR_015063, nif-0000-20938, r3d100010783

Old URLs: <http://www.ncbi.nlm.nih.gov/sites/entrez?db=nucgss>,
<http://www.ncbi.nlm.nih.gov/dbGSS/>

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260807T042536+0000

Ratings and Alerts

No rating or validation information has been found for NCBI Genome Survey Sequences Database.

No alerts have been found for NCBI Genome Survey Sequences Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

H??ser D, et al. (2010) Integration preferences of wildtype AAV-2 for consensus rep-binding sites at numerous loci in the human genome. PLoS pathogens, 6(7), e1000985.

McClellan PE, et al. (2010) Synteny mapping between common bean and soybean reveals extensive blocks of shared loci. BMC genomics, 11, 184.