

Resource Summary Report

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High Throughput Genomic Sequences Division

RRID:SCR_002150

Type: Tool

Proper Citation

High Throughput Genomic Sequences Division (RRID:SCR_002150)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/HTGS/>

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Description: Database of high-throughput genome sequences from large-scale genome sequencing centers, including unfinished and finished sequences. It was created to accommodate a growing need to make unfinished genomic sequence data rapidly available to the scientific community in a coordinated effort among the International Nucleotide Sequence databases, DDBJ, EMBL, and GenBank. Sequences are prepared for submission by using NCBI's software tools Sequin or tbl2asn. Each center has an FTP directory into which new or updated sequence files are placed. Sequence data in this division are available for BLAST homology searches against either the htgs database or the month database, which includes all new submissions for the prior month. Unfinished HTG sequences containing contigs greater than 2 kb are assigned an accession number and deposited in the HTG division. A typical HTG record might consist of all the first-pass sequence data generated from a single cosmid, BAC, YAC, or P1 clone, which together make up more than 2 kb and contain one or more gaps. A single accession number is assigned to this collection of sequences, and each record includes a clear indication of the status (phase 1 or 2) plus a prominent warning that the sequence data are unfinished and may contain errors. The accession number does not change as sequence records are updated; only the most recent version of a HTG record remains in GenBank.

Abbreviations: HTG Sequences, HTG Division

Synonyms: HTG GenBank Division, HTG database, NCBI High-Throughput Genomic Sequences, HTG Sequence, High-Throughput Genomic Sequences

Resource Type: storage service resource, data repository, service resource, database, data or information resource

Defining Citation: [PMID:9331365](#)

Keywords: gap, gene, accession, arabidopsis, bac, biological, c. elegans, clone, contig, cosmid, dna, genomic, high-throughput, homology, homo sapiens, invertebrate, nematode, nucleotide, p1, plant, primate, sequence, structure, taxonomy, yac, genome, sequence, nucleotide sequence, dna sequence, nucleotide, dna, gold standard

Availability: Free, Freely available

Resource Name: High Throughput Genomic Sequences Division

Resource ID: SCR_002150

Alternate IDs: nif-0000-20943

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260805T044034+0000

Ratings and Alerts

No rating or validation information has been found for High Throughput Genomic Sequences Division.

No alerts have been found for High Throughput Genomic Sequences Division.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Dennis MY, et al. (2012) Evolution of human-specific neural SRGAP2 genes by incomplete segmental duplication. Cell, 149(4), 912.

Capelle V, et al. (2010) QTLs and candidate genes for desiccation and abscisic acid content in maize kernels. BMC plant biology, 10, 2.

Fields RR, et al. (2002) Usher syndrome type III: revised genomic structure of the USH3 gene and identification of novel mutations. American journal of human genetics, 71(3), 607.

Lichter-Konecki U, et al. (2001) Genetic and physical mapping of the locus for autosomal dominant renal Fanconi syndrome, on chromosome 15q15.3. American journal of human genetics, 68(1), 264.

Joensuu T, et al. (2001) Mutations in a novel gene with transmembrane domains underlie Usher syndrome type 3. American journal of human genetics, 69(4), 673.