

Methoden der Hochdurchsatzsequenzierung

Vorlesung 02

Sommersemester 2021

Index of /

Name	Last modified	Size
1000genomes/	2021-04-25 22:48	-
ReferenceSamples/	2021-04-05 17:33	-
SampleData/	2021-04-25 22:48	-
asn1-converters/	2011-09-01 18:05	-
bigwig/	2021-04-25 22:48	-
bioproject/	2021-04-25 22:48	-
biosample/	2021-04-25 22:48	-
blast/	2021-04-25 22:48	-
cgap/	2004-09-13 11:14	-
cn3d/	2014-10-03 10:22	-
dbgap/	2021-04-25 22:48	-
diffexpIR-notebook/	2017-09-21 12:38	-
entrez/	2013-07-18 18:49	-
epigenomics/	2021-04-25 22:48	-
eqtl/	2017-09-19 15:34	-
fa2htgs/	2006-08-04 17:02	-
genbank/	2021-04-25 22:48	-
gene/	2021-04-25 22:48	-
genomes/	2021-04-25 22:48	-
geo/	2021-04-26 01:11	-
giab/	2021-04-25 22:48	-
hapmap/	2011-09-20 10:18	-
hmm/	2021-04-25 22:48	-
mmdb/	2019-03-22 11:50	-
ncbi-asn1/	2021-04-25 22:48	-
nist-imsa/	2017-05-10 14:47	-
osiris/	2021-02-10 17:01	-
pathogen/	2021-04-25 22:48	-
pub/	2021-03-18 09:29	-
pubchem/	2021-04-25 22:48	-
pubmed/	2021-04-12 11:33	-
rapt/	2021-04-25 22:48	-
refsam/	2021-04-05 17:33	-
refseq/	2021-04-25 22:48	-
repository/	2021-04-25 22:48	-
seqc/	2021-04-25 22:48	-
sequin/	2021-01-26 17:04	-
sky-cgh/	2016-06-23 15:20	-
snp/	2021-04-25 22:48	-
sra/	2021-04-25 22:48	-
tech-reports/	2004-09-29 08:49	-
toolbox/	2013-07-25 14:03	-
tpa/	2020-09-23 10:42	-
variation/	2016-08-09 10:36	-
1.xml	2009-02-20 11:45	40K
100GB	2017-05-11 21:04	100G
10GB	2017-05-11 21:04	10G
1GB	2017-05-11 21:04	1.0G
50GB	2017-05-11 21:04	50G
5GB	2017-05-11 21:04	5.0G
README.ftp	2017-05-10 14:47	2.0K
favicon.ico	2017-05-10 14:48	3.2K
robots.txt	2017-05-10 14:47	26

- NCBI FTP-Server: <https://ftp.ncbi.nih.gov/>

- Liste verfügbarer Vertebratengenome:
https://ftp.ncbi.nih.gov/genomes/refseq/vertebrate_mammalian/

Index of /genomes/refseq/vertebrate_mammalian

Name	Last modified	Size
Parent Directory		-
Acinonyx_jubatus/	2021-04-25 15:02	-
Ailuropoda_melanoleuca/	2021-04-25 15:02	-
Aotus_nancymae/	2021-04-25 15:02	-
Artibeus_jamaicensis/	2021-04-25 14:52	-
Arvicantis_niloticus/	2021-04-25 14:53	-
Arvicola_amphibius/	2021-04-25 14:55	-
Balaenoptera_acutorostrata/	2021-04-25 14:53	-
Balaenoptera_musculus/	2021-04-25 14:52	-
Bison_bison/	2021-04-25 14:53	-
Bos_indicus/	2021-04-25 14:52	-
Bos_indicus_x_Bos_taurus/	2021-04-25 14:52	-
Bos_mutus/	2021-04-25 14:53	-
Bos_taurus/	2021-04-25 15:02	-
Bubalus_bubalis/	2021-04-25 15:02	-
Callithrix_jacchus/	2021-04-25 15:02	-
Callorhinus_ursinus/	2021-04-25 14:52	-
Camelus_bactrianus/	2021-04-25 14:52	-
Camelus_dromedarius/	2021-04-25 15:02	-
Camelus_ferus/	2021-04-25 15:02	-
Canis_lupus_dingo/	2021-04-25 15:02	-
Canis_lupus_familiaris/	2021-04-25 15:02	-
Capra_hircus/	2021-04-25 15:02	-
Carlito_syricta/	2021-04-25 14:59	-
Castor_canadensis/	2021-04-25 14:53	-
Cavia_porcellus/	2021-04-25 14:52	-
Cebus_imitator/	2021-04-25 15:02	-
Ceratotherium_simum/	2021-04-25 14:53	-
Cercopithecus_atys/	2021-04-25 14:52	-
Chinchilla_lanigera/	2021-04-25 14:52	-
Chlorocebus_sabaeus/	2021-04-25 15:02	-
Choloepus_didactylus/	2021-04-25 14:52	-
Chrysochloris_asiatica/	2021-04-25 14:53	-
Colobus_angolensis/	2021-04-25 14:53	-
Condylura_cristata/	2021-04-25 14:53	-
Cricetulus_griseus/	2021-04-25 15:02	-
Dasypus_novemcinctus/	2021-04-25 14:52	-
Delphinapterus_leucas/	2021-04-25 15:02	-
Desmodus_rotundus/	2021-04-25 14:52	-
Dipodomys_ordii/	2021-04-25 14:52	-
Echinops_telfairi/	2021-04-25 15:02	-
Elephantulus_edwardii/	2021-04-25 14:52	-
Enhydra_lutris/	2021-04-25 14:53	-
Eptesicus_fuscus/	2021-04-25 14:52	-
Equus_asinus/	2021-04-25 15:02	-
Equus_caballus/	2021-04-25 14:52	-
Equus_przewalskii/	2021-04-25 14:52	-
Erinaceus_europaeus/	2021-04-25 14:52	-
Eumetopias_jubatus/	2021-04-25 14:52	-
Felis_catus/	2021-04-25 15:02	-
Fukomys_damarensis/	2021-04-25 15:03	-
Galeopterus_variegatus/	2021-04-25 14:54	-
Globecephala_melas/	2021-04-25 14:52	-
Gorilla_gorilla/	2021-04-25 15:02	-
Grammomys_surdaster/	2021-04-25 14:54	-
Halichoerus_grypus/	2021-04-25 14:52	-
Heterocephalus_glaber/	2021-04-25 15:02	-
Hipposideros_armiger/	2021-04-25 14:53	-
Homo_sapiens/	2021-04-25 15:02	-
Hyaena_hyaena/	2021-04-25 14:53	-
Hylobates_moloch/	2021-04-25 15:02	-
Ictidomys_tridaceloneatus/	2021-04-25 15:02	-
Jaculus_jaculus/	2021-04-25 14:53	-
Lagenorhynchus_obliquidens/	2021-04-25 14:53	-
Leptonychotes_weddellii/	2021-04-25 14:52	-
Lipotes_vexillifer/	2021-04-25 14:53	-
Lontra_canadensis/	2021-04-25 14:53	-
Loxodonta_africana/	2021-04-25 14:52	-
Lynx_canadensis/	2021-04-25 15:02	-
Macaca_fascicularis/	2021-04-25 14:52	-
Macaca_mulatta/	2021-04-25 15:02	-
Macaca_nemestrina/	2021-04-25 14:52	-
Mandrillus_leucophaeus/	2021-04-25 14:52	-
Manis_javanica/	2021-04-25 15:02	-
Manis_pentadactyla/	2021-04-25 14:53	-
Marmota_flaviventris/	2021-04-25 15:02	-
Marmota_marmota/	2021-04-25 15:02	-
Mastomys_coucha/	2021-04-25 14:52	-
Meriones_unguiculatus/	2021-04-25 14:52	-
Mesocricetus_auratus/	2021-04-25 15:02	-

General feature format

From Wikipedia, the free encyclopedia

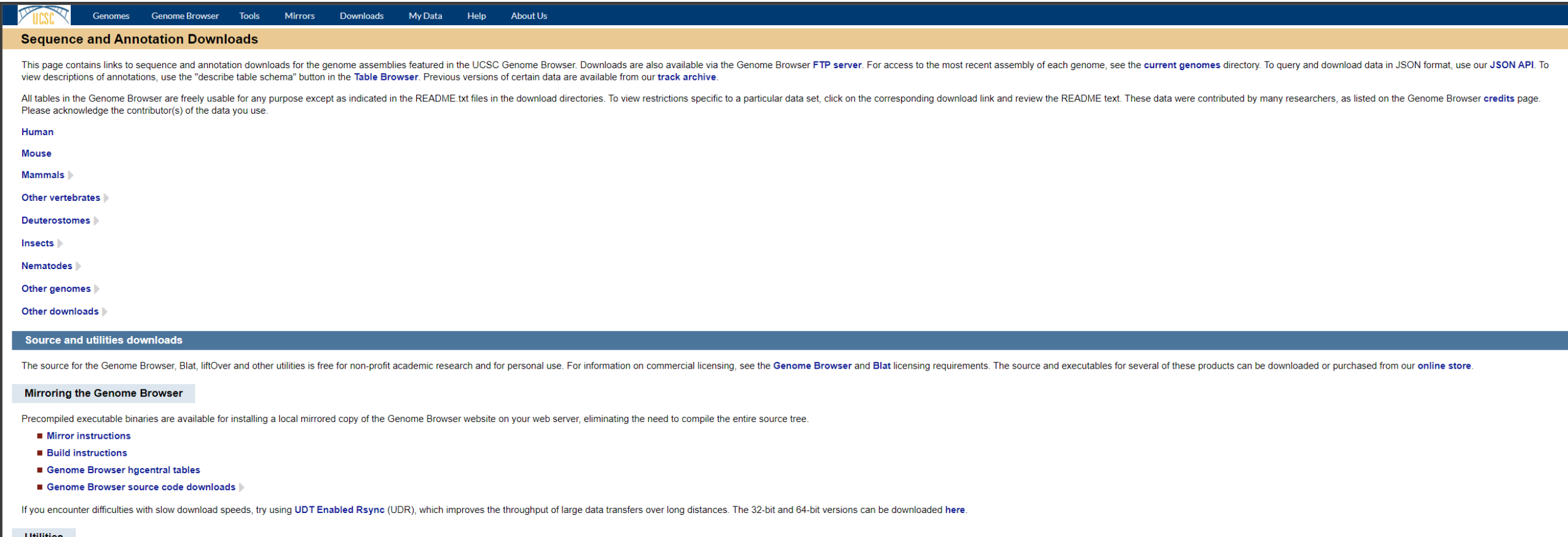
In [bioinformatics](#), the **general feature format** (**gene-finding format**, **generic feature format**, **GFF**) is a [file format](#) used for describing [genes](#) and other features of [DNA](#), [RNA](#) and [protein](#) sequences. ""block other devise order""

Contents [hide]	
1	GFF Versions
2	GFF general structure
2.1	The 8th field: phase of CDS features
2.2	Meta Directives
3	GFF software
3.1	Servers
3.2	Clients
3.3	Validation
4	See also
5	References

General feature format	
Filename extensions	<code>.gff</code>
Internet media type	<code>text/gff3</code>
Developed by	Sanger Centre (v2), Sequence Ontology Project (v3)
Type of format	Bioinformatics
Extended from	Tab-separated values
Open format?	yes
Website	github.com/The-Sequence-Ontology/Specifications/blob/master/gff3.md

https://en.wikipedia.org/wiki/General_feature_format

- Aktuelle Version des humanen Genoms vom UCSC Genome Browser:
<https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/>
- Weitere aktuelle Genome von Modellorganismen vom UCSC Genome Browser:
<https://hgdownload.soe.ucsc.edu/downloads.html>



The screenshot shows the UCSC Genome Browser website. At the top is a navigation bar with the UCSC logo and links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Help, and About Us. Below this is a yellow header for 'Sequence and Annotation Downloads'. The main content area contains a paragraph about downloading genome assemblies, followed by a list of organism categories: Human, Mouse, Mammals, Other vertebrates, Deuterostomes, Insects, Nematodes, Other genomes, and Other downloads. Below this is a blue header for 'Source and utilities downloads', followed by a paragraph about the source code and a section for 'Mirroring the Genome Browser' with a list of links for mirror and build instructions, hgcentral tables, and source code downloads. At the bottom, there is a note about using UDT Enabled Rsync (UDR) for better download speeds.

Sequence and Annotation Downloads

This page contains links to sequence and annotation downloads for the genome assemblies featured in the UCSC Genome Browser. Downloads are also available via the Genome Browser **FTP server**. For access to the most recent assembly of each genome, see the **current genomes** directory. To query and download data in JSON format, use our **JSON API**. To view descriptions of annotations, use the "describe table schema" button in the **Table Browser**. Previous versions of certain data are available from our **track archive**.

All tables in the Genome Browser are freely usable for any purpose except as indicated in the README.txt files in the download directories. To view restrictions specific to a particular data set, click on the corresponding download link and review the README text. These data were contributed by many researchers, as listed on the Genome Browser **credits** page. Please acknowledge the contributor(s) of the data you use.

- [Human](#)
- [Mouse](#)
- [Mammals](#) ▶
- [Other vertebrates](#) ▶
- [Deuterostomes](#) ▶
- [Insects](#) ▶
- [Nematodes](#) ▶
- [Other genomes](#) ▶
- [Other downloads](#) ▶

Source and utilities downloads

The source for the Genome Browser, Blat, liftOver and other utilities is free for non-profit academic research and for personal use. For information on commercial licensing, see the **Genome Browser** and **Blat** licensing requirements. The source and executables for several of these products can be downloaded or purchased from our **online store**.

Mirroring the Genome Browser

Precompiled executable binaries are available for installing a local mirrored copy of the Genome Browser website on your web server, eliminating the need to compile the entire source tree.

- [Mirror instructions](#)
- [Build instructions](#)
- [Genome Browser hgcentral tables](#)
- [Genome Browser source code downloads](#) ▶

If you encounter difficulties with slow download speeds, try using **UDT Enabled Rsync** (UDR), which improves the throughput of large data transfers over long distances. The 32-bit and 64-bit versions can be downloaded [here](#).

Utilities

Sequenziertechnologien

- Sanger Sequencing: <https://www.youtube.com/watch?v=KTstRrDTmWI>
- Illumina Sequencing: <https://www.youtube.com/watch?v=fCd6B5HRaZ8>
- Maxam-Gilbert Sequencing: https://www.youtube.com/watch?v=_B5Dj8PL4E0
- SMRT Sequencing: <https://www.youtube.com/watch?v=v8p4ph2MAvI>
- Nanopore Sequencing: <https://www.youtube.com/watch?v=E9-Rm5AoZGw>
- Roche 454 Sequencing: <https://www.youtube.com/watch?v=KzdWZ5ryBIA>