NCBI ftp server

for microbial genomes

ftp – file transfer protocol

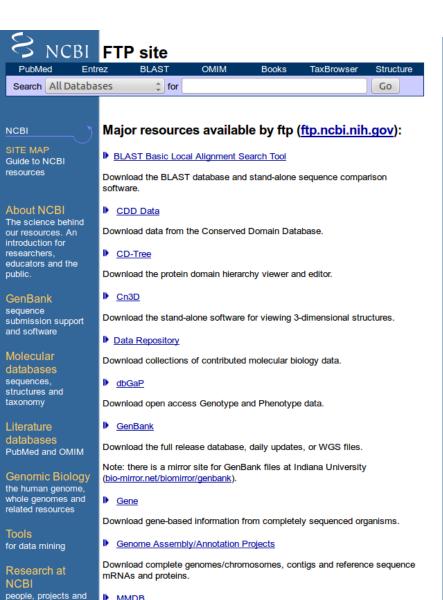
Made to transfer files from one computer to another

modern web browsers support protocol



http: hypertext transfer protocol WWW build by hyperlinks

http://www.ncbi.nlm.nih.gov/Ftp/



Download NCBI's structure database.

seminars

people, projects and seminars

Software engineering tools, R&D and databases

Education teaching resources and on-line tutorials

Contact information how to reach us

▶ MMDB

Download NCBI's structure database.

NCBI Toolbox

Download the NCBI software tools for building bioinformatics resources.

PubChem

Download the database of chemical structures of small organic molecules and information on their biological activities.

RefSeq

Download the curated RefSeq full release or daily updates.

Sequin

Download the stand-alone GenBank sequence submission software.

dbSNP

Download the database of short genetic variations.

Taxonomy

Download data files from the Taxonomy database.

UniGene

Download data files from the UniGene datasets of non-redundant gene-oriented clusters.

▶ UniSTS

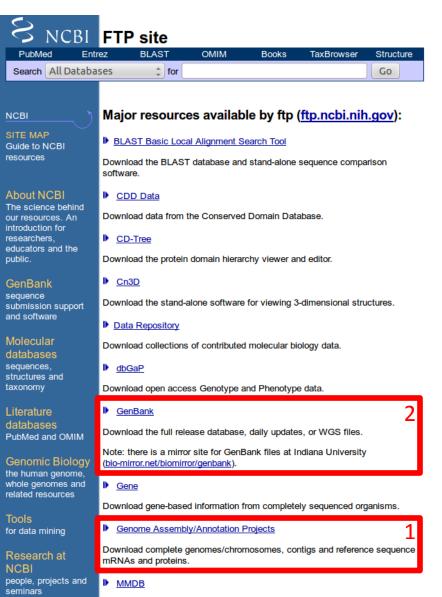
Download data files from the UniSTS resource of sequence tagged sites.

Information on <u>how to uncompress</u> *.gz and *.Z files is also available.

Disclaimer Privacy statement

Revised: January 13, 2009.

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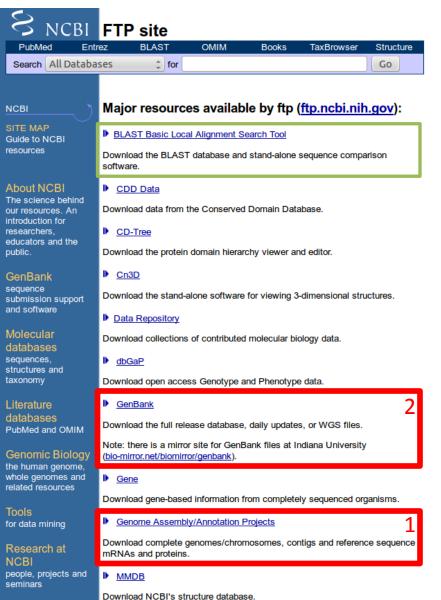
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Information on how to uncompress *.gz and *.Z files is also

available

Revised: January 13, 2009.

Privacy statement

Disclaimer

Genome Assembly/Annotation Projects **RefSeq**



Up to higher level directory		
op to higher teret directory		
Name	Size	Last Modified
ASSEMBLY_REPORTS		18.10.2012 02:51:00
Acyrthosiphon_pisum		15.03.2012 00:00:00
Aedes_aegypti		21.09.2010 00:00:00
Ailuropoda_melanoleuca		06.09.2012 20:24:00
Amphimedon_queenslandica		15.03.2012 00:00:00
Anolis_carolinensis		15.03.2012 00:00:0
Anopheles_gambiae		14.01.2008 00:00:0
Apis_florea		13.04.2012 00:00:0
Apis_mellifera		14.06.2011 00:00:0
Arabidopsis_lyrata		11.05.2011 00:00:0
Arabidopsis_thaliana		30.09.2008 00:00:0
■ BACENDS		13.05.2010 00:00:0
Bacteria		18.10.2012 10:42:00
Bacteria_DRAFT		10.10.2012 16:14:00
Bombus_impatiens		15.03.2012 00:00:0
Bombus_terrestris		15.03.2012 00:00:0
Bos_taurus		07.03.2012 00:00:0
Brachypodium_distachyon		15.03.2012 00:00:0
Branchiostoma_floridae		26.01.2010 00:00:0
Brugia_malayi		26.09.2007 00:00:00
CLONEEND		21.12.2006 00:00:00
CLUSTERS		30.11.2010 00:00:00
Caenorhabditis_elegans		10.10.2008 00:00:00
Callithrix_jacchus		12.07.2012 21:11:00
Canis_familiaris		10.02.2012 00:00:00
Canis_lupus_familiaris		15.03.2012 00:00:0
Cavia_porcellus		15.03.2012 00:00:00
Chloroplasts		01.06.2011 00:00:00

FileZilla



More comfort with special ftp clients, like FileZilla (GPL)

http://filezilla-project.org/



Overview

Home FileZilla

> Features Screenshots

Download Documentation

Download General

Contact

Forum Project page

FileZilla Server

Development

Source code

Nightly builds Translations

Version history Changelog

Issue tracker

Welcome to the homepage of FileZilla, the free FTP solution. Both a client and a server are available. FileZilla is open source software distributed free of charge under the terms of the GNU General Public License

Support is available through our forums, the wiki and the bug and feature request trackers.

In addition, you will find documentation on how to compile FileZilla and nightly builds for multiple platforms in the development section.

Quick download links



Pick the client if you want to transfer files. Get the server if you want to make files available for others.

- ♦ News

Bugfixes and minor changes:

- Fix parsing of IP address filters ending with :0 or equivalent substringss.
- Allow speed limits larger than 64 MiB/s.
- Show more verbose error messages if transfer connection cannot be established.
- ♦ 2012-01-08 FileZilla Client 3.5.3 released

New features:

Octrl+Shift+O can be used to toggle between modification time and filesize based directory comparison

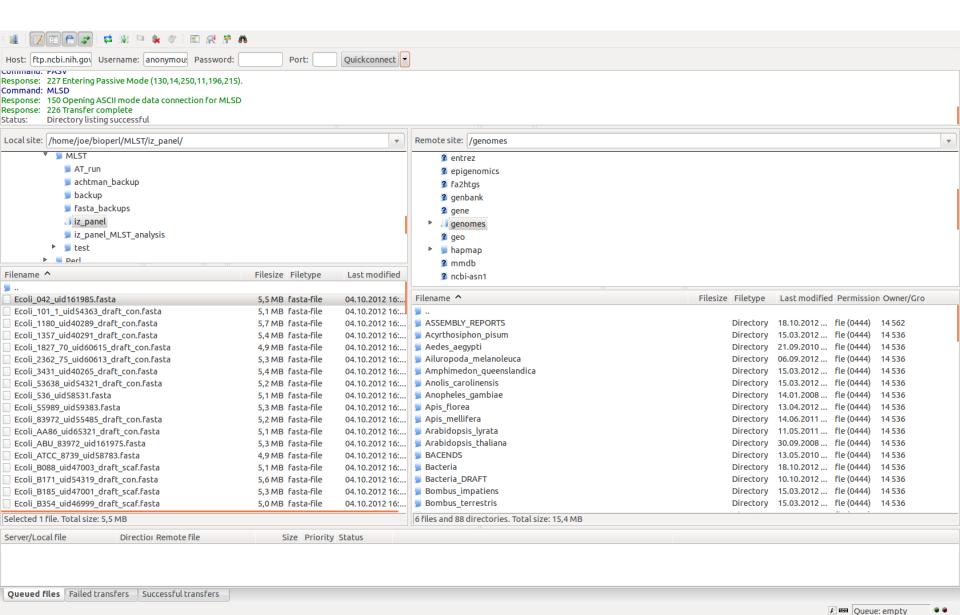
Bugfixes and minor changes:



H O S Y

ftp://ftp.ncbi.nih.gov/genomes/

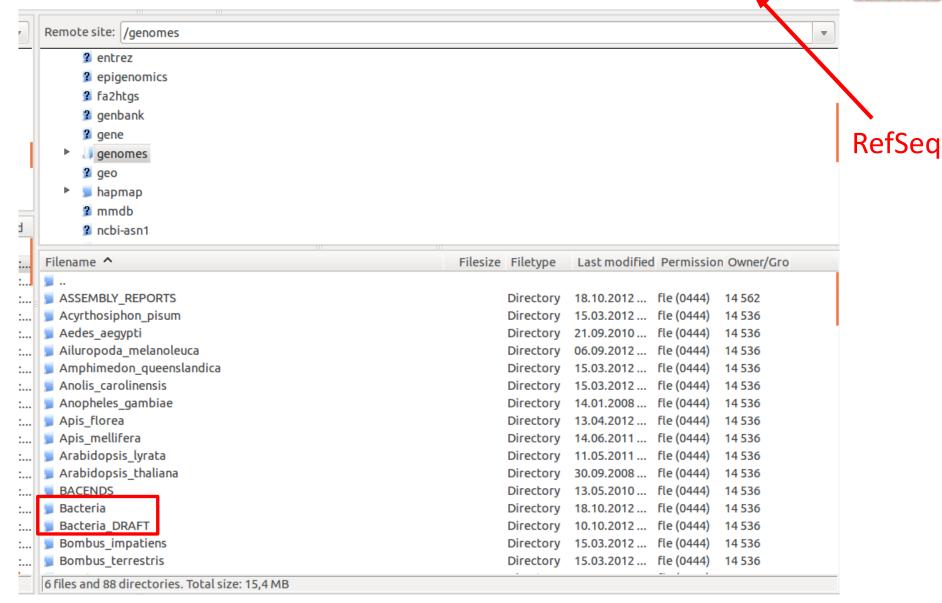




1. RefSeq

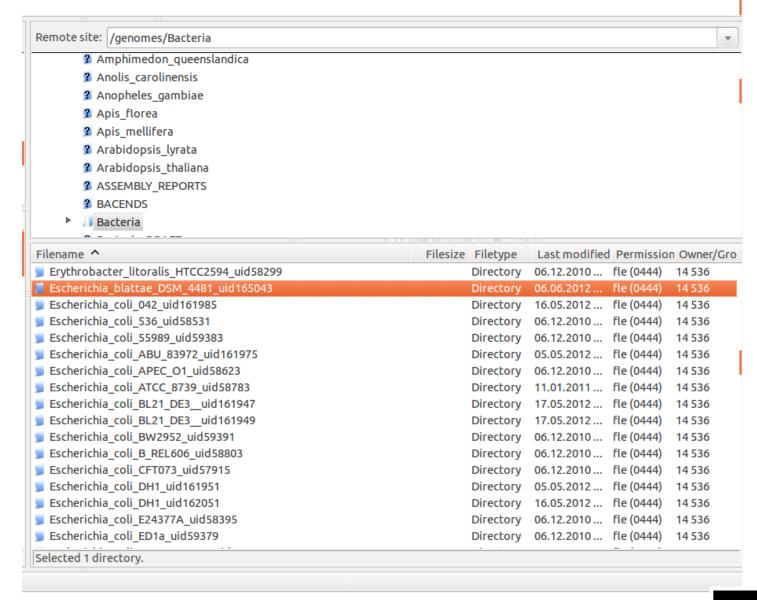
1. ftp://ftp.ncbi.nih.gov/genomes/





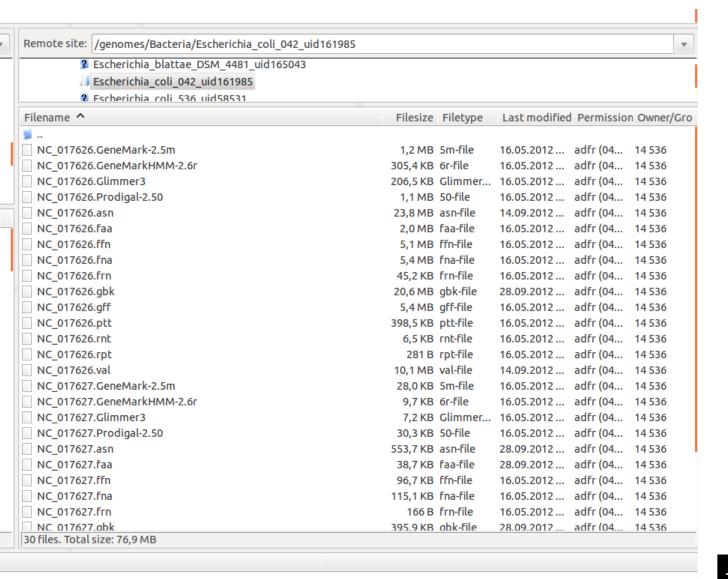
1. ftp://ftp.ncbi.nih.gov/genomes/Bacteria





1. ftp://ftp.ncbi.nih.gov/genomes/**Bacteria**/ Escherichia_coli_042_uid161985

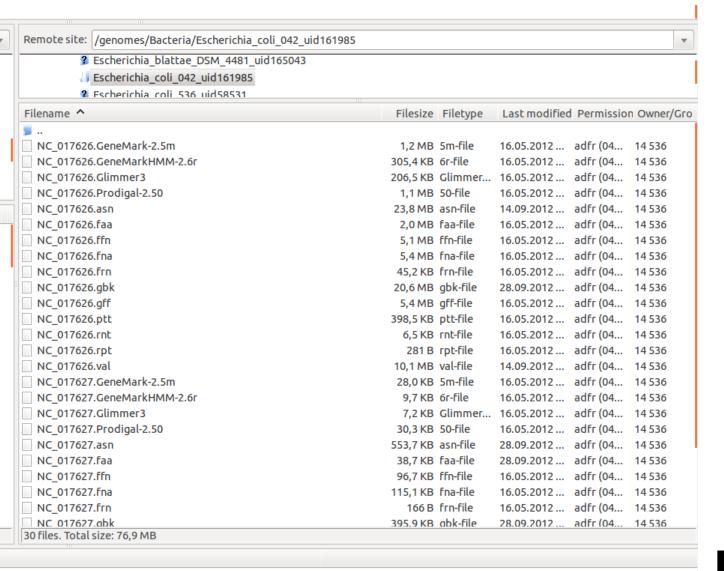




Multiple replicons

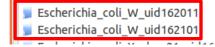
1. ftp://ftp.ncbi.nih.gov/genomes/**Bacteria**/ Escherichia_coli_042_uid161985





Multiple replicons

Multiple Project ids (uid)



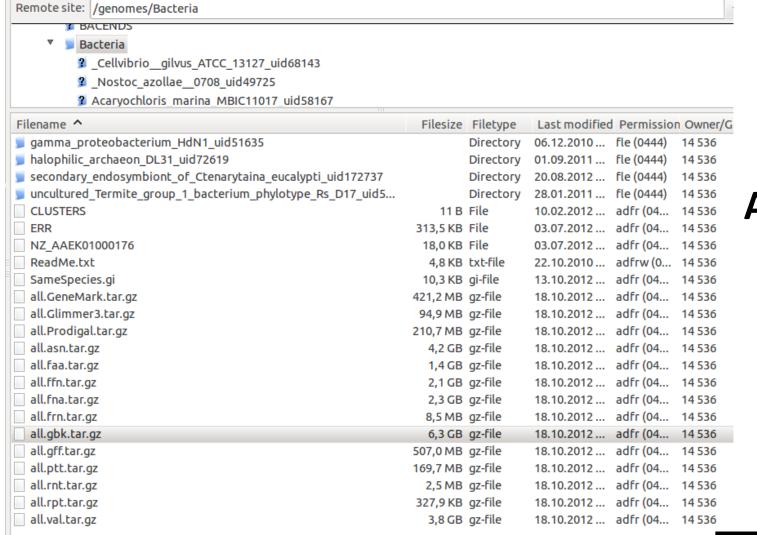
- Complete Genomes -

File formats

- *.asn: replicon in asn.1 format
- *.faa: aa sequences of all CDS, multi-fasta
- *.ffn: nt sequences of all CDS, multi-fasta
- *.fna: replicon sequence, fasta
- *.frn: nt sequences of all RNA genes, multi-fasta
- *.gbk: replicon in genbank format
- *GeneMark*/Glimmer3/Prodigal: Genemark ab initio ORF finding results
- *.gff: CDS/genes in GFF3 format (genome feature file)
- *.ptt: CDS in ptt format (protein table file)
- *.rnt: RNA genes table file
- *.rpt: report file on features (e.g. acc#, GI, taxid, CDS count, gene count ...)
- *.val: binary asn.1 format

1. ftp://ftp.ncbi.nih.gov/genomes/Bacteria





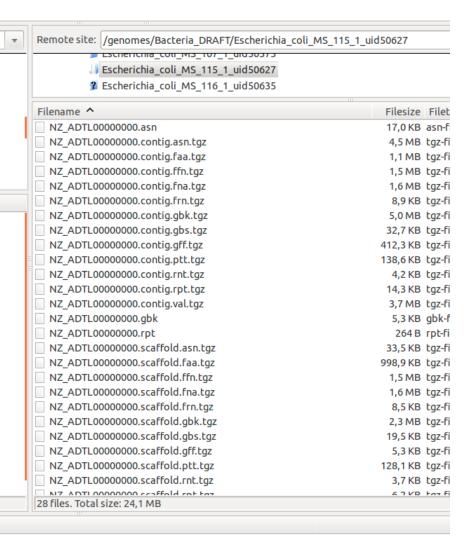
Selected 1 file. Total size: 6.3 GB

All Bacteria tarballs

- Complete Genomes -

1. ftp://ftp.ncbi.nih.gov/genomes/**Bacteria_DRAFT**/ Escherichia_coli_MS_115_1_uid50627



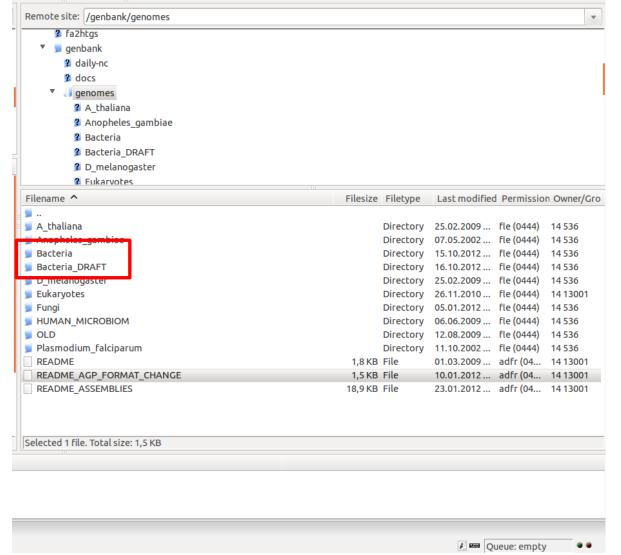


- Draft bacteria contain contigs or contigs + scaffolds
- Contigs/scaffolds packed in zipped tarballs
- Unzipped files are the master record
- Of course plasmids and chromosomes are mixed
- Annotation either in scaffolds or contigs!!!

2. Genbank

International Nucleotide Sequence Database Collaboration (INSDC) NCBI, EMBL, DDBJ 2. ftp://ftp.ncbi.nih.gov/genbank/

genomes/





Same folder organisation as RefSeq, but no 'all' tarballs!

RefSeq - Genbank numbers

Database	Bacteria	Bacteria_DRAFT	HUMAN_MICROBIOM/Bacteria
RefSeq	2105	1879	682
Genbank	2174	4026	899

wget (- curl)

Non-interactive network downloader

GNU Wget 1.11.4 Red Hat modified, a non-interactive network retriever. Usage: wget [OPTION]... [URL]... Mandatory arguments to long options are mandatory for short options too. Startup: -V, --version display the version of Wget and exit. -h, --help print this help. -b, --background go to background after startup. -e, --execute=COMMAND execute a `.wgetrc'-style command. Logging and input file: log messages to FILE. -o, --output-file=FILE -a, --append-output=FILE append messages to FILE. -d, --debug print lots of debugging information. guiet (no output). -- guiet -v, --verbose be verbose (this is the default). -nv, --no-verbose turn off verboseness, without being quiet. -i, --input-file=FILE download URLs found in FILE. -F, --force-html treat input file as HTML. -B, --base=URL prepends URL to relative links in -F -i file. Download: --tries=NUMBER set number of retries to NUMBER (0 unlimits). --retry-connrefused retry even if connection is refused. --output-document=FILE write documents to FILE. -nc, --no-clobber skip downloads that would download to existing files. -c, --continue resume getting a partially-downloaded file. select progress gauge type. --progress=TYPE don't re-retrieve files unless newer than --timestamping local. -S, --server-response print server response. --spider don't download anything. -T, --timeout=SECONDS set all timeout values to SECONDS. --dns-timeout=SECS set the DNS lookup timeout to SECS. --connect-timeout=SECS set the connect timeout to SECS. --read-timeout=SECS set the read timeout to SECS. -w, --wait=SECONDS wait SECONDS between retrievals. wait 1..SECONDS between retries of a retrieval --waitretry=SECONDS --random-wait wait from 0...2*WAIT secs between retrievals. --no-proxy explicitly turn off proxy. -Q, --quota=NUMBER set retrieval quota to NUMBER. --hind-address=ADDRESS bind to ADDRESS (hostname or IP) on local host. --limit-rate=RATE limit download rate to RATE. --no-dns-cache disable caching DNS lookups. restrict chars in file names to ones 05 allows. --restrict-file-names=0S --ignore-case ignore case when matching files/directories. -4, --inet4-only connect only to IPv4 addresses. -6, --inet6-only connect only to IPv6 addresses. --prefer-family=FAMILY connect first to addresses of specified family, one of IPv6, IPv4, or none. --user=USER set both ftp and http user to USER. --password=PASS set both ftp and http password to PASS. Directories: -nd, --no-directories don't create directories. -x, --force-directories force creation of directories. -nH, --no-host-directories don't create host directories. --protocol-directories use protocol name in directories. -P, --directory-prefix=PREFIX save files to PREFIX/... ignore NUMBER remote directory components. --cut-dirs=NUMBER HTTP options: --http-user=USER set http user to USER. --http-password=PASS set http password to PASS. --no-cache disallow server-cached data.

save HTML documents with `.html' extension.

-E. --html-extension

wget

E.g. get all RefSeq E. coli genbanks and fastas:

URLs

RefSeq

- ftp://ftp.ncbi.nih.gov/genomes/Bacteria/
- ftp://ftp.ncbi.nih.gov/genomes/Bacteria_DRAFT/
- ftp://ftp.ncbi.nih.gov/genomes/Fungi/
- ftp://ftp.ncbi.nih.gov/genomes/Fungi_DRAFT/ Currently empty
- ftp://ftp.ncbi.nih.gov/genomes/Plasmids/
- ftp://ftp.ncbi.nih.gov/genomes/Viruses/
- ftp://ftp.ncbi.nih.gov/genomes/HUMAN_MICROBIOM/
- ftp://ftp.ncbi.nlm.nih.gov/genomes/GENOME_REPORTS/prokaryotes.txt

Genbank

- ftp://ftp.ncbi.nih.gov/genbank/genomes/Bacteria/
- ftp://ftp.ncbi.nih.gov/genbank/genomes/Bacteria_DRAFT/
- ftp://ftp.ncbi.nih.gov/genbank/genomes/HUMAN_MICROBIOM/
- ftp://ftp.ncbi.nih.gov/genbank/genomes/Fungi

#Organism/Name

BioProject Accession

BioProject ID

Group

SubGroup

Size (Mb)

GC%

Chromosomes/RefSeq

Chromosomes/INSDC

Plasmids/RefSeq

Plasmids/INSDC

WGS

Scaffolds

Genes

Proteins

Release Date

Modify Date

Status

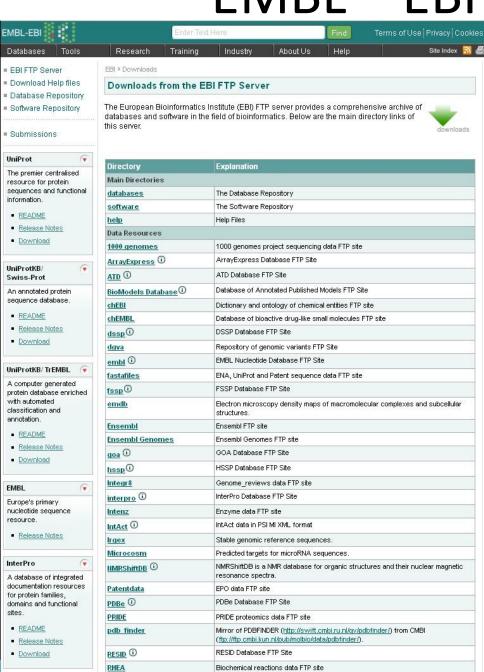
Center

Overview

ftp://ftp.ncbi.nlm.nih.gov/genomes/ GENOME_REPORTS/prokaryotes.txt

#Organism/Name	BioProject Acc∈ BioProject I	D Group	SubGroup	Size (Mb)	GC%	Chromosomes/RefSe	q Chromosomes/IN	ISDC P
Escherichia coli O157:H7 str. FRIK966	PRJNA55561 5556	1 Proteobacteria	Gammaproteobacteria	537.691	50	-	-	-
Escherichia coli O157:H7 str. FRIK2000	PRJNA55943 5594	3 Proteobacteria	Gammaproteobacteria	540.869	50	-		- 2
Escherichia coli str. K-12 substr. MG1655	PRJNA57779 5777	9 Proteobacteria	Gammaproteobacteria	463.968	51	NC_000913.2	U00096.2	-
Escherichia coli O157:H7 str. Sakai	PRJNA57781 5778	1 Proteobacteria	Gammaproteobacteria	559.448	####	NC_002695.1	BA000007.2	N
Escherichia coli O157:H7 str. EDL933	PRJNA57831 5783	1 Proteobacteria	Gammaproteobacteria	562.052	####	NC_002655.2	AE005174.2	N
Escherichia coli CFT073	PRJNA57915 5791	5 Proteobacteria	Gammaproteobacteria	523.143	51	NC_004431.1	AE014075.1	42
Escherichia coli HS	PRJNA58393 5839	3 Proteobacteria	Gammaproteobacteria	464.354	51	NC_009800.1	CP000802.1	-

EMBL – EBI ftp server



http://www.ebi.ac.uk/FTP/

 Use for faster downloads, e.g. whole 'nr' database

ftp://ftp.ebi.ac.uk/pub/databases/