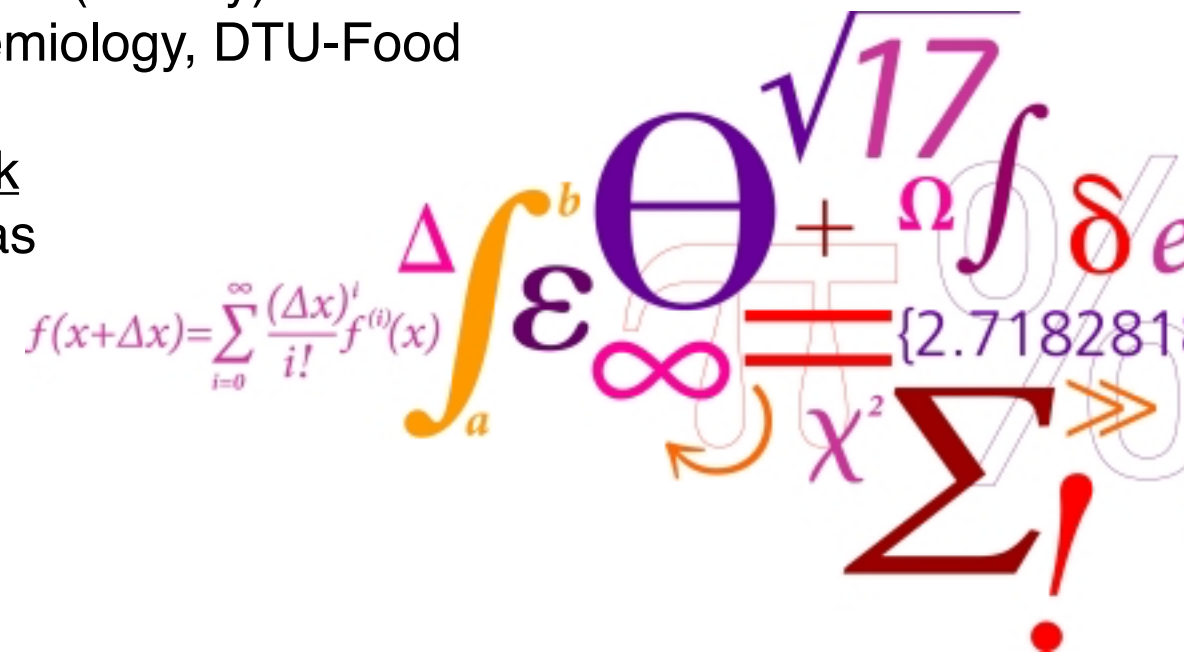


Sharing raw sequence data to ENA

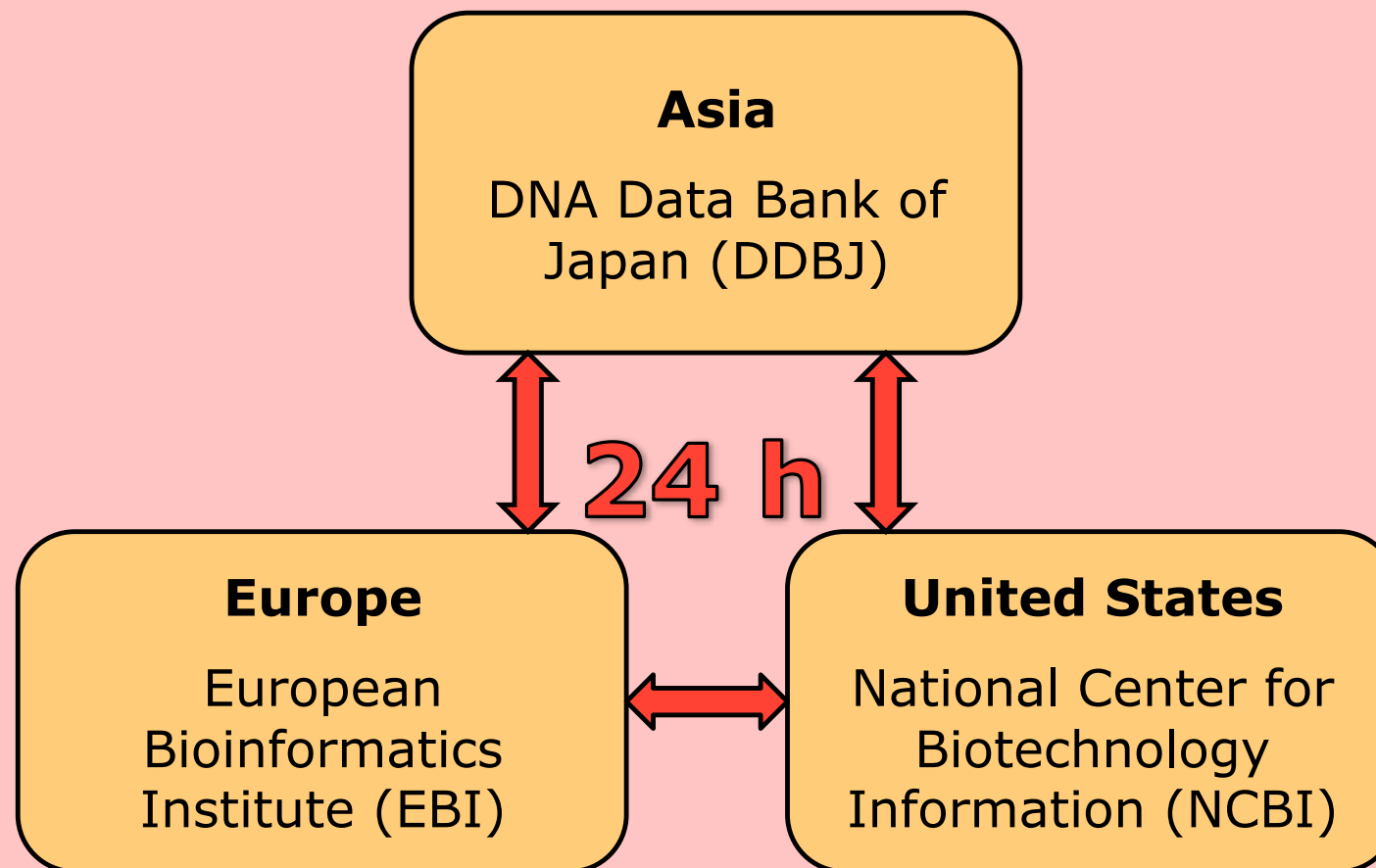
Pimlapas Leekitcharoenphon (Shinny)
Research Group of Genomic Epidemiology, DTU-Food

pile@food.dtu.dk
 @ShinnyPimlapas



Data storage & Access

International Nucleotide Sequence Database Collaboration (INSDC)



Data storage & Access

European Bioinformatics Institute (EBI)

EMBL-EBI
<http://www.ebi.ac.uk/ena>
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About us



Examples: [BN000065](#), [histone](#)

[Advanced](#)
[Sequence](#)

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European Nucleotide Archive

The European Nucleotide Archive (ENA) provides a comprehensive record of the world's nucleotide sequencing information, covering raw sequencing data, sequence assembly information and functional annotation. [More about ENA](#)

Access to ENA data is provided through the browser, through search tools, large scale file download and through the API.

Text Search

Examples: [BN000065](#), [histone](#)

[Advanced search](#)

Sequence Search

Enter or paste a nucleotide sequence or accession number

[Advanced search](#)

Popular

- [Submit and update](#)
- [Sequence submissions](#)
- [Genome assembly submissions](#)
- [Submitting environmental sequences](#)
- [Citing ENA data](#)
- [Rest URLs for data retrieval](#)
- [Rest URLs to search ENA](#)

Latest ENA News

24 Sep 2014: [ENA Release 121](#)
Release 121 of ENA's assembled/annotated sequences now available.

20 Aug 2014: [Read data through Globus GridFTP](#)
Read data can now be downloaded using [Globus GridFTP](#) through [ebi#ena](#) Globus Online public endpoint.

18 Aug 2014: [Changes to SRA XML 1.5](#)
Small changes to Experiment XML, Analysis XML, EGA Dataset XML, EGA DAC XMLs were deployed on 11th of August 2014.

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NEWS AND ANNOUNCEMENTS

CRAM toolkit 0.7 released
7 Mar 2012
CRAM toolkit 0.7 has been released. More information with download, installation and usage instructions are available [here](#).

The future of sequence archiving
2 Mar 2012
Future of sequence archiving and the role of data compression is explored in a [new paper](#) from EBI to be published in [Gigascience](#).

EBI Home » ENA Home »

European Nucleotide Archive

The European Nucleotide Archive (ENA) provides a comprehensive record of the world's nucleotide sequencing information, covering raw sequencing data, sequence assembly information and functional annotation ... [more](#)

Access to ENA data is provided through the browser, through search tools, large scale file download and through the API.

Text search

Enter search query, for example: BN000065

Search

Sequence Search

Enter or paste a nucleotide sequence or accession number

Search

[Advanced Search](#)

ENA

European Nucleotide Archive

www.ebi.ac.uk/ena/

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EBI Search

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X

🔍

Examples: [VAV_HUMAN](#) , [tpi1](#) , [Sulston ...](#)
[Build Query](#)

[Feedback](#)

EMBL-EBI to be HTTPS by default from 1st October

On the 1st October the majority of services hosted on www.ebi.ac.uk will be served over HTTPS by default. Services that are becoming HTTPS by default will automatically redirect users accessing the site on insecure HTTP URLs to secure HTTPS URLs.

Users of EMBL-EBI services may wish to update links, bookmarks or API clients to use the HTTPS URLs.

Search results for *PRJEB22091*

Showing **15** results out of **129** in All results

Filter your results

Source

All results (129)

[Nucleotide sequences](#) (129)

Nucleotide sequences (129 results)

[PRJEB22091](#)

Danmap 2016

Related data ▾

Source: Study
ID: PRJEB22091

Navigation Read Files Portal Attributes

Bulk Download Files ⚠ (Please use Firefox to launch the bulk downloader app.)

Download: 1 - 127 of 127 results in TEXT

Select columns

Showing results 1 - 10 of 127 results

Study accession	Sample accession	Secondary sample accession	Experiment accession	Run accession	Tax ID	Scientific name	Instrument model	Library layout	FASTQ files (FTP)	FASTQ files (Galaxy)	Submitted files (FTP)	Submitted files (Galaxy)	NCBI SRA file (FTP)	NCBI SRA file (Galaxy)	CRAM Index files (FTP)	CRAM Index files (Galaxy)
PRJEB22091	SAMEA104205896	ERS1864914	ERX2148098	ERR2091304	562	Escherichia coli	Illumina MiSeq	PAIRED	File 1 File 2	File 1 File 2	Fastq file 1 Fastq file 2	Fastq file 1 Fastq file 2	File 1	File 1		
PRJEB22091	SAMEA104205897	ERS1864915	ERX2148099	ERR2091305	562	Escherichia coli	Illumina MiSeq	PAIRED	File 1 File 2	File 1 File 2	Fastq file 1 Fastq file 2	Fastq file 1 Fastq file 2	File 1	File 1		
PRJEB22091	SAMEA104205898	ERS1864916	ERX2148100	ERR2091306	562	Escherichia coli	Illumina MiSeq	PAIRED	File 1 File 2	File 1 File 2	Fastq file 1 Fastq file 2	Fastq file 1 Fastq file 2	File 1	File 1		
PRJEB22091	SAMEA104205899	ERS1864917	ERX2148101	ERR2091307	562	Escherichia coli	Illumina MiSeq	PAIRED	File 1 File 2	File 1 File 2	Fastq file 1 Fastq file 2	Fastq file 1 Fastq file 2	File 1	File 1		
PRJEB22091	SAMEA104205900	ERS1864918	ERX2148102	ERR2091308	562	Escherichia coli	Illumina MiSeq	PAIRED	File 1 File 2	File 1 File 2	Fastq file 1 Fastq file 2	Fastq file 1 Fastq file 2	File 1	File 1		
PRJEB22091	SAMEA104205901	ERS1864919	ERX2148103	ERR2091309	562	Escherichia coli	Illumina MiSeq	PAIRED	File 1 File 2	File 1 File 2	Fastq file 1 Fastq file 2	Fastq file 1 Fastq file 2	File 1	File 1		
PRJEB22091	SAMEA104205902	ERS1864920	ERX2148104	ERR2091310	562	Escherichia coli	Illumina MiSeq	PAIRED	File 1 File 2	File 1 File 2	Fastq file 1 Fastq file 2	Fastq file 1 Fastq file 2	File 1	File 1		
PRJEB22091	SAMEA104205903	ERS1864921	ERX2148105	ERR2091311	562	Escherichia coli	Illumina MiSeq	PAIRED	File 1 File 2	File 1 File 2	Fastq file 1 Fastq file 2	Fastq file 1 Fastq file 2	File 1	File 1		

Submitting data in ENA

- Manual and automated
- Use Webin (interactive web submission system) for new sequencing projects, assembled sequences and annotation
- For other types of data, different channels are available (e.g. datasubs@ebi.ac.uk, FTP, RESTful web-based service)
- www.ebi.ac.uk/ena/about/submit_and_update

Submitting data in ENA

- 1) Install a program to connect to FTP
- <https://filezilla-project.org>

The screenshot shows the FileZilla website homepage. At the top, the FileZilla logo is displayed with the tagline 'The free FTP solution'. Below the logo, there is a navigation menu on the left with links to Home, FileZilla (Features, Screenshots, Download, Documentation, FileZilla Pro), FileZilla Server (Download), Community (Forum, Project page, Wiki), General (FAQ, Support, Contact, License, Privacy Policy, Trademark Policy), Development (Source code, Nightly builds, Translations, Version history, Changelog, Issue tracker), and Other projects (libfilezilla, Octochess). A sidebar on the right contains logos for sponsors: WINCHER, INTERNETVING, NDC, and WHUK. The main content area features a 'Promotion' banner for FileZilla Pro, described as 'The Best FTP Solution', with a 'GET IN NOW >' button. Below the banner is an 'Overview' section welcoming users to the homepage and explaining that FileZilla is free software distributed under the GNU General Public License. It also mentions that FileZilla Pro offers additional protocol support for WebDAV, Amazon S3, Backblaze B2, Dropbox, Microsoft OneDrive, Google Drive, Microsoft Azure Blob and File Storage, and Google Cloud Storage. The 'Quick download links' section provides buttons for 'Download FileZilla Client' (All platforms) and 'Download FileZilla Server' (Windows only). A 'News' section lists recent releases: FileZilla Client 3.44.2 released (2019-08-15), FileZilla Client 3.44.1 released (2019-08-09), and FileZilla Client 3.44.0 released (2019-08-09). Each release includes a list of bugfixes and minor changes. At the bottom right, there is an advertisement for Carbon, a BuySellAds member, with the text 'Reach developers effortlessly through this ad banner with Carbon.'

FileZilla The free FTP solution

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Sponsors:

- WINCHER
- INTERNETVING
- NDC
- WHUK

Promotion:

FileZilla® Pro
The Best FTP Solution

GET IN NOW >

Overview

Welcome to the homepage of FileZilla®, the free FTP solution. The *FileZilla Client* not only supports FTP, but also FTP over TLS (FTPS) and SFTP. It is open source software distributed free of charge under the terms of the GNU General Public License.

We are also offering *FileZilla Pro*, with additional protocol support for WebDAV, Amazon S3, Backblaze B2, Dropbox, Microsoft OneDrive, Google Drive, Microsoft Azure Blob and File Storage, and Google Cloud Storage.

Last but not least, *FileZilla Server* is a free open source FTP and FTPS Server.

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

Download FileZilla Client
All platforms

Download FileZilla Server
Windows only

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

News

2019-08-15 - FileZilla Client 3.44.2 released

Bugfixes and minor changes:

- MSW: Fixed a crash if using predefined sites through fzdefaults.xml
- Fixes to protocol selection glitches in the Site Manager
- Increase maximum length of response lines when using FTP

2019-08-09 - FileZilla Client 3.44.1 released

Bugfixes and minor changes:

- Fixed a regression introduced in 3.44.0-rc1 breaking support for insecure servers

2019-08-09 - FileZilla Client 3.44.0 released

Bugfixes and minor changes:

- Fixed export in context menu of Site Manager to handle multiple selected items

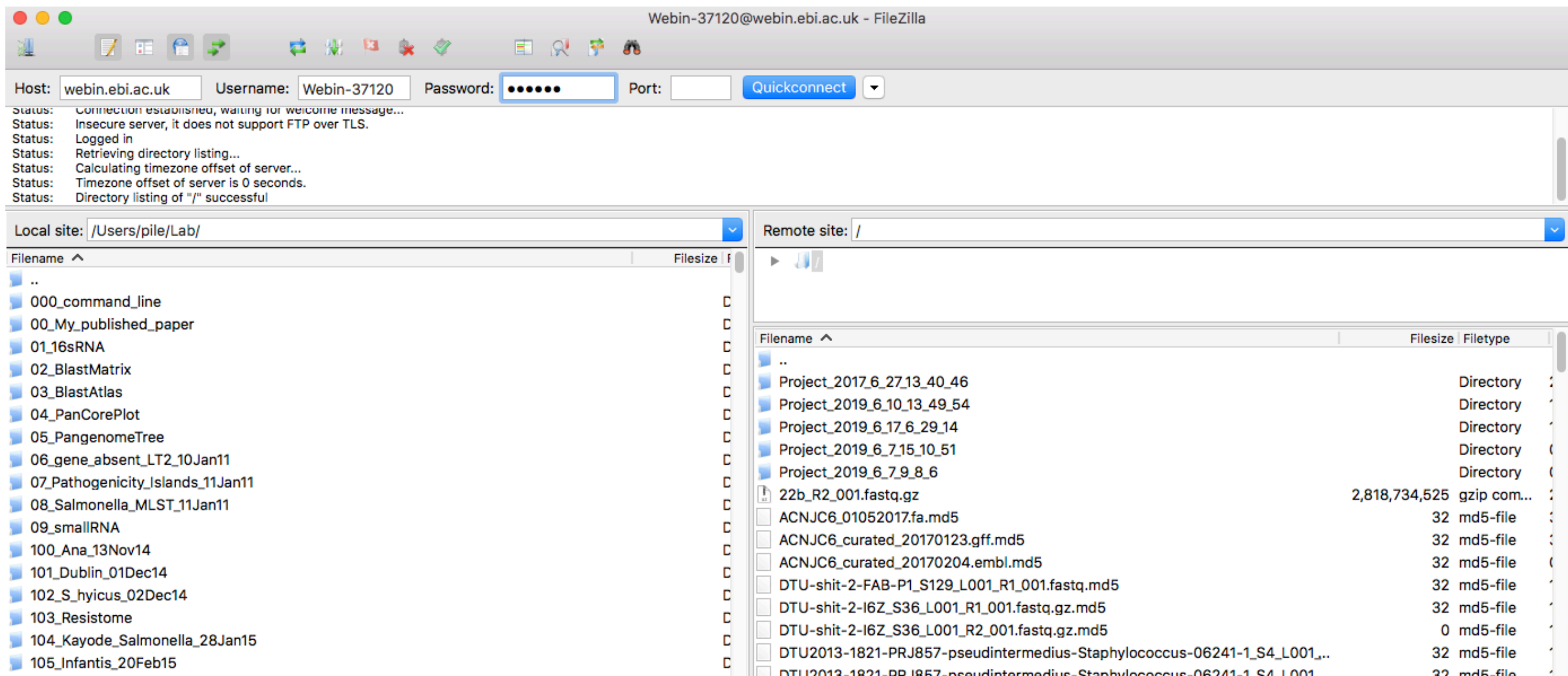
2019-07-29 - FileZilla refocuses on security after participation in EU bug bounty program

Advertisement:

Carbon
BuySellAds

Reach developers effortlessly through this ad banner with Carbon.

- 2) Connect to FTP
- Host: webin.ebi.ac.uk
- Username: Your own Webin ID
- Password: Your own password for your ENA account. Then click 'Connect'



- 3) Transfer the genome files to ENA FTP

Webin-37120@webin.ebi.ac.uk - FileZilla

Host: webin.ebi.ac.uk Username: Webin-37120 Password: Port: Quickconnect

Status: Resolving address of webin.ebi.ac.uk
 Status: Connecting to 193.62.192.11:21...
 Status: Connection established, waiting for welcome message...
 Error: Connection closed by server
 Error: Could not connect to server
 Status: Disconnected from server
 Status: Delaying connection for 5 seconds due to previously failed connection attempt...

Local site: /Users/pile/Lab/ Remote site: /

Filename	Filesize	File
..		Dire
000_command_line		Dire
00_My_published_paper		Dire
01_16sRNA		Dire
02_BlastMatrix		Dire
03_BlastAtlas		Dire
04_PanCorePlot		Dire
05_PangenomeTree		Dire
06_gene_absent_LT2_10Jan11		Dire
07_Pathogenicity_Islands_11Jan11		Dire
08_Salmonella_MLST_11Jan11		Dire
09_smallRNA		Dire
100_Ana_13Nov14		Dire
101_Dublin_01Dec14		Dire
102_S_hyicus_02Dec14		Dire
103_Resistome		Dire
104_Kayode_Salmonella_28Jan15		Dire
105_Infantis_20Feb15		Dire
106_source_attribution		Dire

22 files and 381 directories. Total size: 97,370,680 bytes

Filename	Filesize	Filetype	La
..			
Project_2017_6_27_13_40_46		Directory	28,
Project_2019_6_10_13_49_54		Directory	11/
Project_2019_6_17_6_29_14		Directory	17/
Project_2019_6_7_15_10_51		Directory	07/
Project_2019_6_7_9_8_6		Directory	07/
22b_R2_001.fastq.gz	2,818,734,525	gzip com...	23,
ACNJC6_01052017.fa.md5	32	md5-file	30,
ACNJC6_curated_20170123.gff.md5	32	md5-file	30,
ACNJC6_curated_20170204.embl.md5	32	md5-file	04,
DTU-shit-2-FAB-P1_S129_L001_R1_001.fastq.md5	32	md5-file	19/
DTU-shit-2-I6Z_S36_L001_R1_001.fastq.gz.md5	32	md5-file	19/
DTU-shit-2-I6Z_S36_L001_R2_001.fastq.gz.md5	0	md5-file	19/
DTU2013-1821-PRJ857-pseudintermedius-Staphylococcus-06241-1_S4_L001_...	32	md5-file	13/
DTU2013-1821-PRJ857-pseudintermedius-Staphylococcus-06241-1_S4_L001_...	32	md5-file	13/

151 files and 5 directories. Total size: 60,712,631,420 bytes

Server/Local file	Direction	Remote file
Webin-37120@webin.ebi.ac.uk		
/Users/pile/Meetings/175_EURL_September2018/presentation/Exercise_3/Fastq_files/Ecoli_036_R1.fq.gz	-->>	/Ecoli_036_R1.fq.gz
00:00:00 elapsed --:--:-- left		
/Users/pile/Meetings/175_EURL_September2018/presentation/Exercise_3/Fastq_files/Ecoli_036_R2.fq.gz	-->>	/Ecoli_036_R2.fq.gz
00:00:20 elapsed 02:38:46 left 9.5% 8,233,328 bytes (8.0 KiB/s)		

Submitting data in ENA

- 4) log in ENA with your own webin account
- <https://www.ebi.ac.uk/ena/submit/sra/#home>

The screenshot shows the ENA submission interface. At the top, there's a navigation bar with 'EMBL-EBI' and links for 'Services', 'Research', 'Training', and 'About us'. Below this is the ENA logo and the text 'European Nucleotide Archive'. A secondary navigation bar includes links for 'ENA Home', 'Search & Browse', 'Submit & Update', 'About ENA', 'Contact', and 'FAQ'. On the right, there's a 'Contact Helpdesk' link with a green checkmark icon.

The main content area is titled 'Welcome to the Webin submission service.' and contains the following text:

You can use this service to submit sequence reads, genome assemblies, targeted assembled and annotated sequences and to register studies (projects) and samples. To submit human data requiring controlled access please use [EGA Webin](#). To register umbrella studies, used to group together sequencing studies, please contact datasubs@ebi.ac.uk.

New to Webin? Please register using the button below.


Below the text, there are two buttons: '★ Register' and '↻ Reset Password'.

Underneath these buttons is a 'Login' section with two input fields: '* Username:' and '* Password:'. A blue information icon is next to the username field. Below the password field is a 'Login >' button.


At the bottom of the page, there's a dark grey footer with the Elixir logo and the text 'This service is part of the ELIXIR infrastructure'.

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Welcome to the Webin submission service.

You can use this service to submit [sequence reads](#), [genome assemblies](#), [targeted assembled and annotated sequences](#) and to register [studies \(projects\)](#) and [samples](#). To register umbrella studies, used to group together sequencing studies, please contact datasubs@ebi.ac.uk.

[Help about submitting read data](#)


▶ My account details

 This service is part of the ELIXIR infrastructure
[Learn more >](#)

- 5) click 'New Submission' and add 'Center Name'. Then click 'Next'

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Finish

You can use this service to submit [sequence reads](#), [genome assemblies](#), [targeted assembled and annotated sequences](#) and to register [studies \(projects\)](#) and [samples](#). To register umbrella studies, used to group together sequencing studies, please contact datasubs@ebi.ac.uk.

Please select the type of submission you would like to make:

☒ **Submit sequence reads and experiments**

We recommend that Fastq, BAM, and CRAM read files are submitted using [Webin-CLI](#).

When using this interface instead of [Webin-CLI](#), raw sequences must be [uploaded](#) in one of the supported [data formats](#) before they can be submitted. All data submitted in a single submission will be associated with the same study. Data for different studies must be submitted in separate submissions. The study and the sequenced samples can be either pre-registered or registered during the submission process. Please note that each individual study and sample should be registered only once. In addition, you will be asked to provide information about the sequencing libraries and instruments. Please quote the study accession number (ERP*) when citing data submitted to ENA.

Read [here](#) for more information on how submit your raw reads to ENA.

☐ Register study (project)
☐ Taxonomy Check/Request
☐ Register samples
☐ Submit genome assemblies
☐ Submit other assembled and annotated sequences [formerly EMBL-Bank]


The first step of your submission is to [upload data files](#). Data files can be uploaded using FTP or Aspera, or using the [Webin File Uploader](#). If you have already uploaded your data files into your Webin upload area please proceed directly to the next step. Please note that unsubmitted files that are older than 2 months will be deleted as explained in our [Fair Use Policy](#).


Specify the name of the center you are submitting for.

Centre Name: (*)


Next >>

- 6) Click 'Create a new study'


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
[Start](#)  [Study](#) [Sample](#) [Run](#) [Finish](#)

Select an existing study or [Create a new study](#)

Search by: Accession / Unique name: 

Show: ☒ accession ☐ unique name [Reset](#)


	Primary Accession	Secondary Accession	Title	Submission Date	Status
<input type="radio"/>	PRJEB33587	ERP116393	Whole genome sequencing of non-typhoidal Salmonellae serovars isolated from humans and poultry in Ma [...]	19-Jul-2019	Public
<input type="radio"/>	PRJEB33169	ERP115939	EFSA_EURL-AR_Confirmatory_Testing_2017	24-Jun-2019	Confidential
<input type="radio"/>	PRJEB32144	ERP114785	Formalin-fixed paraffin-embedded (FFPE) ring trial	12-Apr-2019	Public
<input type="radio"/>	PRJEB32083	ERP114714	Bacterial alpha diversity trajectories and immune-microbial associations of the gut, oral, and nasal [...]	08-Apr-2019	Confidential
<input type="radio"/>	PRJEB31650	ERP114226	Metagenomic assessment of the effect of sample processing on different microbiomes	11-Mar-2019	Public
<input type="radio"/>	PRJEB30991	ERP113496	The ESBL/AmpC resistance pool in Escherichia coli in pigs and pig farmers Vietnam	28-Jan-2019	Confidential
<input type="radio"/>	PRJEB30894	ERP113384	The gut, oral, and nasal microbiota in pediatric allogeneic HSCT and microbial marker candidates for [...]	21-Jan-2019	Confidential
<input type="radio"/>	PRJEB30892	ERP113382	Food Metagenomic ring trial - smoked salmon spiked with a microbial mock community	21-Jan-2019	Confidential
<input type="radio"/>	PRJEB30604	ERP113078	Genomic of Vibrio Cholera from Tanzania	07-Jan-2019	Confidential
<input type="radio"/>	PRJEB27955	ERP110095	Comamonas testosteroni	27-Jul-2018	Public

1-10 of 67   Number of rows


[Previous](#) [Next](#)

- 7) Set release date, provide title, and abstract


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[Select an existing study](#) or Create a new study

You can use this page to submit a new study into the European Nucleotide Archive (ENA).

Please answer the questions below. Mandatory fields are denoted by (*).

If you need to create umbrella studies to group several studies together, please contact us at datasubs@ebi.ac.uk. You can then link your umbrella study by using the 'Studies' report tab, click on the 'Edit' button of the study you want to edit and use the 'Edit ENA links' tab.

Please specify the release date of your study:
This is when your study will be made public.

30-Nov-2019

Please provide a short name for the study:

Please provide a short descriptive title for the study: (*)

E.coli

Please provide an abstract to describe the study in detail: (*)

E.coli

Please provide attributes to add a deeper description of the study:

Tag	FieldType
<div>Add</div>	

Please provide PubMed IDs of publications you want to associate with the study:
(numeric value)

PubMed IDs
<div>Add</div>

For genome assembly projects only: In this study, will you provide functional genome annotation? (*)
PLEASE ANSWER WITH YES IF YOU HAVE ANNOTATION: Locus tag prefixes are only associated to studies providing functional genome annotation.


☐ Yes
☒ No

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- 8) 'Select Checklist'

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Start building your submission


 We use checklists to help provide required information in a standard format.
You will be guided through the following steps:

- Selecting a checklist
- Selecting optional fields in addition to mandatory ones
- Entering your data directly into this application

Alternatively, after selecting the checklist and fields you will be able to download a template spreadsheet. You can then enter your data in the spreadsheet and upload it.

Select Checklist >

Upload a submission completed using a template spreadsheet

 If you have downloaded and filled a template spreadsheet please upload it using the **Submit Completed Spreadsheet** button.
Please note that only spreadsheets in tab-delimited text format are supported (with either .tsv or .txt extensions). If you edited the spreadsheet in Microsoft Excel (or equivalent) please save the spreadsheet as Text (Tab delimited). To do this please see [these instructions](#).

Submit Completed Spreadsheet

- 9) Select 'Pathogens Checklists' and then select 'ENA GMI_MDK:1.1'

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Start **>>** **Study** **>>** **Sample** **>>** **Run** **>>** **Finish**

Please select the most appropriate checklist from the list below then click the **Next >>** button.

+ Environmental Checklists
This group currently includes Genomic Standards Consortium (GSC) MixS sample checklists

+ Marine Checklists
This group currently includes Micro B3 and Tara Oceans sample checklists

- Pathogens Checklists
This group currently includes several prokaryote and virus pathogen sample checklists

☒ **ENA Global Microbial Identifier reporting standard checklist GMI_MDM:1.1**
Minimum Data for Matching (MDM). A checklist for reporting metadata of pathogen samples for the Global Microbial Identifier (GMI) reporting system. More about GMI can be found here <http://www.g-m-i.org/>

☐ **COMPARE-ECDC-EFSA pilot food-associated reporting standard**
A checklist for reporting metadata of food-borne pathogen samples for the COMPARE-ECDC-EFSA reporting system.

☐ **COMPARE-ECDC-EFSA pilot human-associated reporting standard**
A checklist for reporting metadata of human-associated pathogen samples for the COMPARE-ECDC-EFSA reporting system.

ENA parasite sample checklist

☐ Minimum information about parasite samples. A checklist for reporting metadata of parasite samples associated with molecular data. This standard was developed by the COMPARE platform and can be used for submission of sample metadata derived from protozoan parasites (e.g. Cryptosporidium) and also multicellular eukaryotic parasites (e.g. Platyhelminthes and Nematoda).

☐ **ENA prokaryotic pathogen minimal sample checklist**
Minimum information required for a prokaryotic pathogen sample

ENA virus pathogen reporting standard checklist

☐ Minimum information about a virus pathogen. A checklist for reporting metadata of virus pathogen samples associated with genomic data. This minimum metadata standard was developed by the COMPARE platform for submission of virus surveillance and outbreak data (such as Ebola) as well as virus isolate information.

ENA Influenza virus reporting standard checklist

☐ Minimum information about an Influenza virus sample. A checklist for reporting metadata of Influenza virus samples associated with genomic data. This minimum metadata standard supports submission of avian, human and mammalian surveillance data as well as serology and virus isolate information (where available). The ENA Influenza sample checklist is based on standards in use at the Influenza Research Database.

+ Other Checklists

<< Previous **Skip >>** **Next >>**

- 10) You have an option to download metadata as excel template or you just click 'Next' to fill out metadata via website

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Start >> Study >> **Sample** >> Run >> Finish

Please select any additional optional fields. Mandatory and recommended fields are selected by default. You may add any of the optional fields. You may also add custom fields.

Filter fields...
Add your own custom f + Add

- + Human surveillance data
- + Collection event information
- + sample collection
- + Organism characteristics
- + host disorder
- + host description
- + General collection event information
- + Host association
- + Pointer to physical material

14 of 46 fields selected


+ Expand - Collapse

When you have selected the fields click the **Next >>** button to begin entering your data. Alternatively, download a template spreadsheet using the **Download Template Spreadsheet** button. Once you have filled the spreadsheet please restart the submission process and upload the spreadsheet using the **Upload Completed Spreadsheet** button.



Download Template Spreadsheet


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- 11) Add 'title', search 'Escherichia coli' (you have to wait until the system give you organism name to choose), add 'collected_by', add 'collection date'

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 Please complete any fields that you would like to apply to all samples. This will act as a template for all samples.


Template Basic Details

Unique Name Prefix:



* Title:  



Description:

Organism Details

 If your organism is not found please go [here](#) and email datasubs@ebi.ac.uk with the required details listed on the page in order for us to request a taxon Id for your organism.



Search:



* Tax Id:  

* Scientific Name:  

Common Name:

Collection event information

* collected_by:  

* collection date:  

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- 12) Add 'country', 'latitude', 'longitude', 'environmental_sample', host health state', 'host scientific name', 'host associated' and 'isolate'

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Please complete any fields that you would like to apply to all samples. This will act as a template for all samples.

* geographic location (country and/or sea):

* geographic location (latitude): DD

* geographic location (longitude): DD

sample collection

* environmental_sample:

host description

* host health state:

* host scientific name:

Host association

* Is the sequenced pathogen host associated?:

Intraspecies information

* isolate:

serovar:

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- 13) add number of sample. In this case, it is only 1 sample to add (click '+Add')

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Home


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Please add samples to the submission. Multiple samples can be created by increasing the number by the add button


+ Add


1

samples

☒

1





1-1 of 1

Please submit by clicking the **Submit** Button. Alternatively, download your data as a spreadsheet using the **Download Spreadsheet** button. Once you have filled the spreadsheet please restart the submission process and upload the spreadsheet using the **Upload Completed Spreadsheet** button.

Download Spreadsheet

There are no samples to submit

Previous Sample

Next Sample

Basic Details

* Unique Name: 1

* Title: Ecoli

Description:

Organism Details

If your organism is not found please go [here](#) and email datasubs@ebi.ac.uk with the required details listed on the page in order for us to request a taxon Id for your organism.

Search:

* Tax Id: 562

* Scientific Name: Escherichia coli

Common Name:

Collection event information

* collected_by: DTU

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- 14) Add 'Unique Name' for the submitted sample. In this case, try to add 'Ecoli_001'

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Please add samples to the submission. Multiple samples can be created by increasing the number by the add button

+ Add 1 samples

☒ Ecoli_001

1-1 of 1

Please submit by clicking the **Submit** Button. Alternatively, download your data as a spreadsheet using the **Download Spreadsheet** button. Once you have filled the spreadsheet please restart the submission process and upload the spreadsheet using the **Upload Completed Spreadsheet** button.

Download Spreadsheet

There are no samples to submit

< Previous Sample
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Basic Details

* Unique Name:

* Title:

Description:

Organism Details

If your organism is not found please go [here](#) and email datasubs@ebi.ac.uk with the required details listed on the page in order for us to request a taxon Id for your organism.

Search:

* Tax Id:

* Scientific Name:

Common Name:

Collection event information

* collected_by:

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- 15) Click type of submitted files. In this case is 'Two Fastq files (Paired)'

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Please provide library, instrument and data file details by uploading a spreadsheet or by editing the table below.

Please select the file format. If you have files of different types please submit them in separate submissions.

☐ CRAM
☐ BAM
☐ SFF
☐ One Fastq file (Single)

☒ **Two Fastq files (Paired)**

Two fastq files containing *paired reads* are submitted for each run. All technical sequences including adaptor sequences, linker sequences and barcode sequences must be removed from the reads before submission. *The first reads must be in the first Fastq file and the second reads must be in the second Fastq file ordered in the same order as in the first file.*

☐ Complete Genomics
☐ PacBio HDF5
☐ Oxford Nanopore

Mandatory fields are denoted by (*).

▼ Download Template Spreadsheet
▲ Upload Completed Spreadsheet
▼ Download Spreadsheet

	[Sample reference suggestions] ⓘ	Sample reference (*) ⓘ	Instrument Model (*) ⓘ	Library Name ⓘ	Library Source (*) ⓘ	Library Selection (*) ⓘ	Library Strategy (*) ⓘ	Des
✗								
✚								

- 16) Add required metadata (*)

Download Template Spreadsheet
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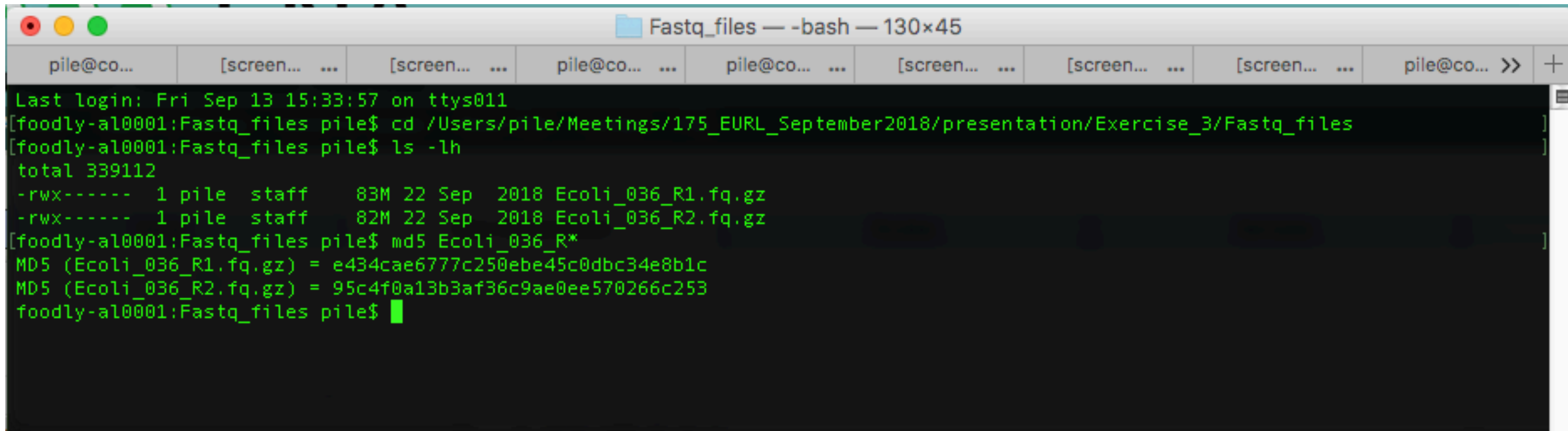
[Sample reference suggestions] ⓘ	Sample reference (*) ⓘ	Instrument Model (*) ⓘ	Library Name ⓘ	Library Source (*) ⓘ	Library Selection (*) ⓘ	Library Strategy (*) ⓘ	Des
✖	Ecoli_001	Ecoli_001	Illumina MiSeq		GENOMIC	RANDOM	WGS
+							

Mandatory fields are denoted by (*).

Library Strategy (*) ⓘ	Design description ⓘ	Library construction protocol ⓘ	Insert Size (*) ⓘ	First File Name (*) ⓘ	First MD5 checksum ⓘ	Second File Name (*) ⓘ	Second MD5 checksum ⓘ
			300	Ecoli_036_R1.fq.gz		Ecoli_036_R2.fq.gz	

Disable Edit mode

- 17) MD5 checksum is also required



```
Fastq_files — -bash — 130x45
pile@co... [screen... ... [screen... ... pile@co... ... pile@co... ... [screen... ... [screen... ... [screen... ... pile@co... >> +
Last login: Fri Sep 13 15:33:57 on ttys011
[foodly-al0001:Fastq_files pile$ cd /Users/pile/Meetings/175_EURL_September2018/presentation/Exercise_3/Fastq_files
[foodly-al0001:Fastq_files pile$ ls -lh
total 339112
-rwx----- 1 pile staff 83M 22 Sep 2018 Ecoli_036_R1.fq.gz
-rwx----- 1 pile staff 82M 22 Sep 2018 Ecoli_036_R2.fq.gz
[foodly-al0001:Fastq_files pile$ md5 Ecoli_036_R*
MD5 (Ecoli_036_R1.fq.gz) = e434cae6777c250ebe45c0dbc34e8b1c
MD5 (Ecoli_036_R2.fq.gz) = 95c4f0a13b3af36c9ae0ee570266c253
foodly-al0001:Fastq_files pile$
```

- 18) The last step is to click 'Submit'. If something goes wrong, the system will give you error message.

Mandatory fields are denoted by (*).

Strategy (*)	Design description	Library construction protocol	Insert Size (*)	First File Name (*)	First MD5 checksum	Second File Name (*)	Second MD5 checksum
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="300"/>	<input type="text" value="Ecoli_036_R1.fq.gz"/>	<input type="text" value="e434cae6777c250ebe45c"/>	<input type="text" value="Ecoli_036_R2.fq.gz"/>	<input type="text" value="95c4f0a13b3af36c9ae0e"/>

Disable Edit mode

<< Previous Submit