

EMBL-EBI workshop: Tools for functional genomics data

Annotare: “your” web-form submission tool

Laura Huerta, PhD

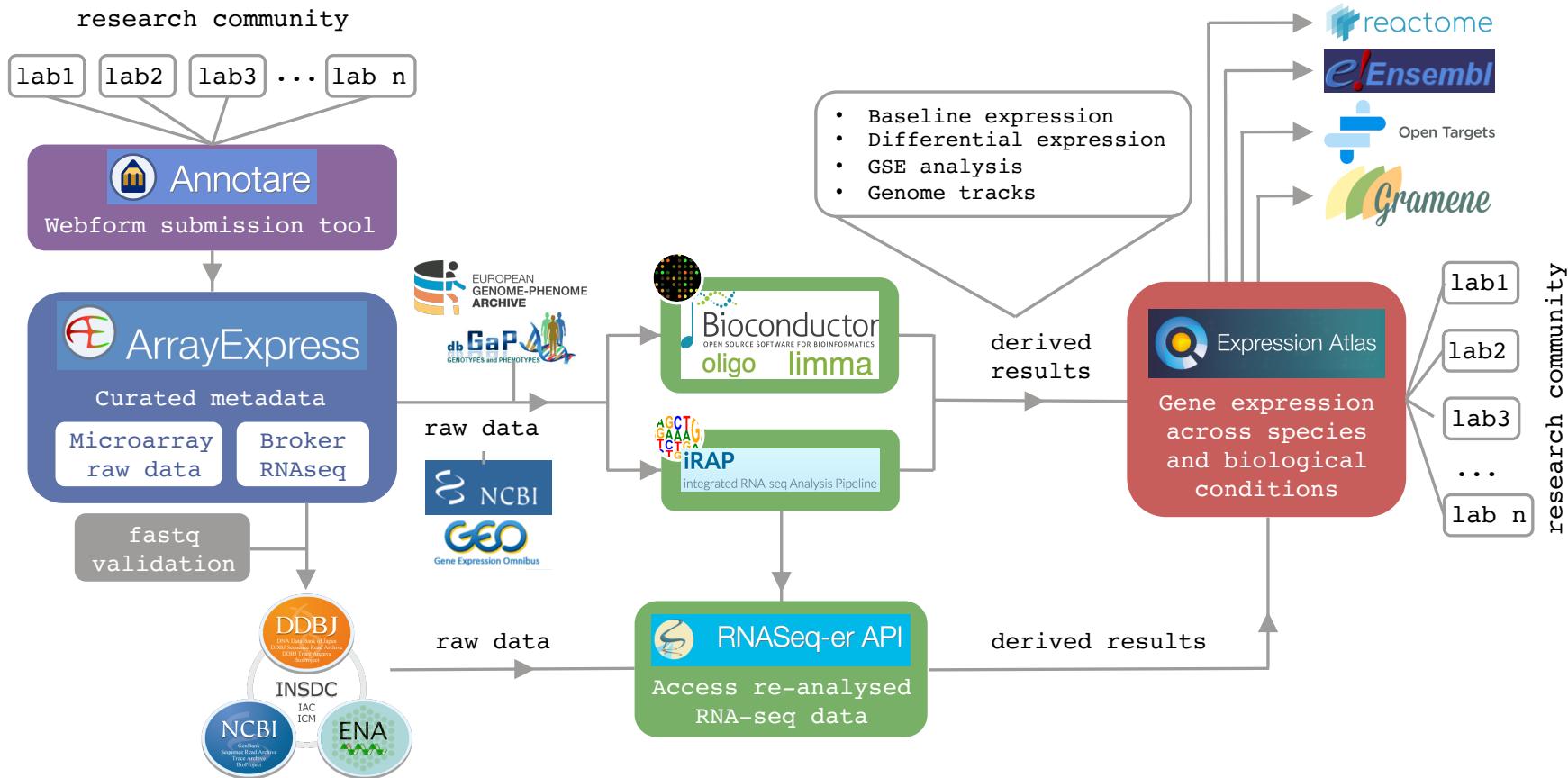
Senior Scientific Curator

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24 May 2018



Functional genomics resources at EMBL-EBI



Outline of the session

- ✓ What is Annotare?
 - ✓ Getting started
 - ✓ Describe your experiment
 - ✓ Sample attributes
 - ✓ Microarray experiment
 - ✓ Sequencing experiment
 - ✓ Upload files and assign to samples

- ✓ Data submission with Annotare
 - ✓ Hands-on exercise



What is Annotare?

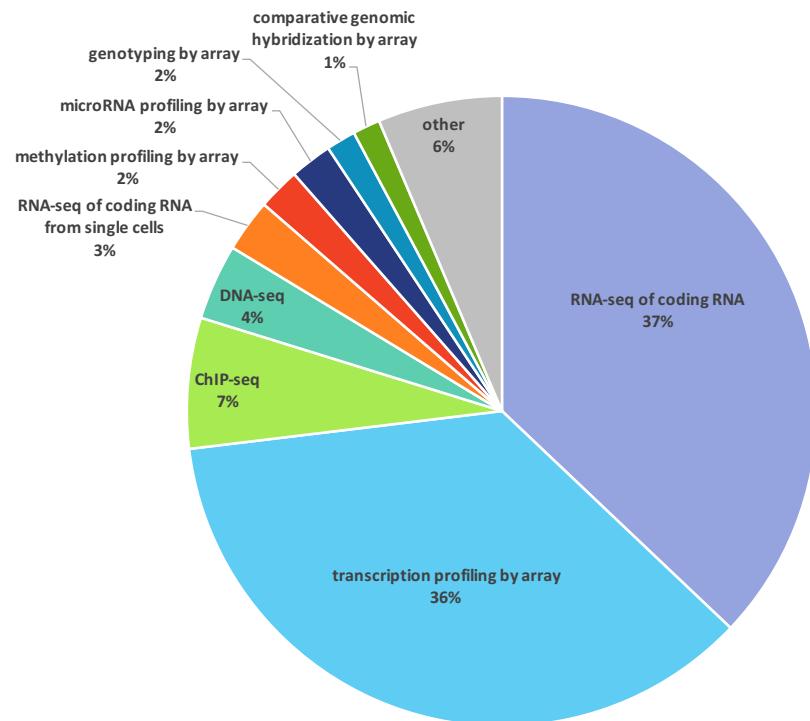
The screenshot shows the Annotare web application. At the top, there's a navigation bar with links for Home, Go to ArrayExpress, Help, About Annotare, Contact us, Register, and Login. The main area has a title "ArrayExpress: why and how to submit your data" and a sub-section "Submit your experiment". It features two prominent buttons: "Save as Spreadsheets" and "Submit to ArrayExpress". Below these buttons, the identifier "E-MTAB-9999" is displayed. A central diagram illustrates the submission process: two scientists (one female, one male) are shown with a document, which is then processed by a computer (indicated by a play button icon). The output is a circular icon with the letters "AE", representing ArrayExpress. To the right of this main panel is a "Please log in to Annotare" form with fields for Email address (lauhuema) and Password, and links for "Forgot your password?", "Log in", and "register". Further down, there's a "Tweets" section from @ArrayExpressEBI, showing a tweet from ArrayExpress (@ArrayExpressEBI) about ArrayExpress submitters and another from Yasset Perez-Riverol (@ypriverol) mentioning OmicsDI and various EBI teams.

www.ebi.ac.uk/fg/annotare/login/



What is Annotare?

Last year submissions by experiment type





What is Annotare?

Easy step-by-step web interface

UNACCESSIONED

[Help](#)[Curator's Edit](#)[Save as Spreadsheets](#)[Validate](#)[Submit to ArrayExpress](#)

Experiment Description Samples and Data Experiment Description Preview Sample and Data Preview

General Information

Contacts *

Publications

One-color microarray
- array design: A-AFFY-44
- label: biotin
change...

Title * Provide an informative experiment title (max. 255 characters), e.g. RNA-seq of human breast cancer cell line MCF-7 treated with tamoxifen against untreated controls

Description * Describe the biological relevance and intent of the experiment. Include an overview of the experimental workflow. Avoid copy-and-pasting your manuscript's abstract.

(at least 50 characters)
Experiment Type * transcription profiling by array

disease state design

Date of Experiment YYYY-MM-DD

Date of Public Release * YYYY-MM-DD

Hide my identity from reviewers

Related Accession Number Enter the accession number of related experiments in ArrayExpress or PRIDE e.g. E-MTAB-4688, PXD123456

Automatically generates
MAGE-TAB files

Upload Files

Drag-and-drop files here to start upload
or press the "Upload Files" button.

⚠ File names only contain letters [A-Z,a-z],
numbers [0-9], underscores [_], and dots [.]



What is Annotare?

Applies MIAME/MINSEQE guidelines

E-MTAB-5409

Experiment Description Samples and Data Experiment Description Preview Sample and Data Preview

General Information

Title *	Loss of miR-22 in white adipose tissue
Contacts *	
Publications	
Description *	Expression profiling of white adipose tissue isolated from WT and miR-22 KO animals

E-MTAB-5409

Experiment Description Samples and Data Experiment Description Preview Sample and Data Preview

Create samples, add attributes and experimental variables

Describe protocols

Upload and assign data files

One-color microarray
- array design: A-GEOID-10528
- label: biotin
change...

Add Sample Attributes and Variables * Add Samples Delete Samples Fill Down Value Import Values

	Name	Material Type	Organism	Sex	Genotype	Organism Part
<input type="checkbox"/>	Sample 1	organism part	Mus musculus	male	wild type genotype	white adipose tissue
<input type="checkbox"/>	Sample 2	organism part	Mus musculus	male	wild type genotype	white adipose tissue
<input type="checkbox"/>	Sample 3	organism part	Mus musculus	male	wild type genotype	white adipose tissue
<input type="checkbox"/>	Sample 4	organism part	Mus musculus	male	miR-22 KO	white adipose tissue
<input type="checkbox"/>	Sample 5	organism part	Mus musculus	male	miR-22 KO	white adipose tissue
<input type="checkbox"/>	Sample 6	organism part	Mus musculus	male	miR-22 KO	white adipose tissue



What is Annotare?

Built-in validation

✓ Validate

Validation failed with 14 errors, please fix:

ERROR: [Assign Files] A raw data file name can only contain alphanumeric characters, underscores and dots. Click on the file name in the upload panel to rename, then press 'Enter' to save the changes.

ERROR: [Assign Files] An assay name could not be generated automatically. You may not have assigned a data file to the sample(s). See [Assign files to samples \(Annotare Help\)](#) for more details.

ERROR: [Assign Files] At least one data file must be uploaded and assigned

ERROR: [Assign Files] The 'Raw Data File' column has not been filled in (completely). See [Assign files to samples \(Annotare Help\)](#) for more details.

ERROR: [Assign Files] The assignment between files and samples contains errors. You may have chosen the wrong type of data column (e.g. choose 'Raw Matrix', not 'Raw', if you have 1 file containing raw data for multiple samples). For two-color experiments, there may be a problem with the relationship between files and samples (expects 1 raw data file per 2 labeled extracts). See [Assign files to samples \(Annotare Help\)](#) and [Two-color experiments \(Annotare Help\)](#) for more details.

Instant accessioning

Open-source

Support

E-MTAB-5409



What is Annotare?

Ontology term suggestions from EFO

Organism	Disease	Individual
Homo sapiens	normal	H1
Homo sapiens	normal	H2
Homo sapiens	normal	H3
Homo sapiens	normal	H4
Homo sapiens	normal	H5
Homo sapiens	normal	H6
Homo sapiens	colorectal	C1
Homo sapiens	colorectal neoplasm (EFO_0004142)	
Homo sapiens	colorectal cancer (EFO_0005842)	
Homo sapiens	colorectal adenoma (EFO_0005406)	
Homo sapiens	Colorectal Adenosquamous Carcinoma (EFO_1000190)	
Homo sapiens	Colorectal Gastrointestinal Stromal Tumor (EFO_1000192)	
Homo sapiens	Colorectal Neuroendocrine Tumor G1 (EFO_1000195)	
Homo sapiens	Colorectal Hamartoma (EFO_1000193)	
Homo sapiens	colorectal adenocarcinoma (EFO_0000365)	
Homo sapiens	Colorectal Sessile Serrated Adenoma/Polyp (EFO_1000197)	
Homo sapiens	Colorectal Squamous Cell Carcinoma (EFO_1000198)	



What is Annotare?

Development is based on feedback

Submission Successful

Thanks for submitting!

You'll receive a stable accession number shortly for this submission. The accession can be cited in your manuscript, but is not valid until a curator has checked the raw data files, reviewed your submission and loaded it into the ArrayExpress database.

We will start checking the content of your raw data files as soon as possible. Sometimes this can take a few days, due to the sheer volume of data; please bear with us. If we detect problems with the files, we will provide information on how to fix the problems, and invite you to resubmit with valid files.

We value your feedback. Please rate your experience submitting with Annotare:



If you wish please leave a comment below:

Where did you first hear/learn about Annotare?

Journal Editor/Reviewer Search Engine ArrayExpress Help Word of Mouth Other



Average feedback score from submitters: 8 out of 9



What is Annotare?

E-MTAB-5409 - Transcription profiling by array of mouse white adipose tissue from miR-22 knockouts and littermates

Status	Submitted on 9 February 2012, last updated on 13 March 2017, released on 13 March 2017
Organism	Mus musculus
Samples (6)	Click for detailed sample information and links to data
Array (1)	A-AFFY-130 - Affymetrix GeneChip Mouse Gene 1.0 ST Array [MoGene-1_0-st-v1]
Protocols (5)	Click for detailed protocol information

E-MTAB-5409 - Transcription profiling by array of mouse white adipose tissue from miR-22 knockouts and littermates

[Display full sample-data table](#)

[Export table in Tab-delimited format](#)

6 rows

Source Name	Sample Attributes					Variables	Assay	Links to Data
	organism	sex	genotype	organism part	strain			
Sample 1	Mus musculus	male	wild type genotype	white adipose tissue	C57Bl6/129SV	wild type genotype	WT_WAT_1	↓
Sample 2	Mus musculus	male	wild type genotype	white adipose tissue	C57Bl6/129SV	wild type genotype	WT_WAT_2	↓
Sample 3	Mus musculus	male	wild type genotype	white adipose tissue	C57Bl6/129SV	wild type genotype	WT_WAT_3	↓
Sample 4	Mus musculus	male	miR-22 knockout	white adipose tissue	C57Bl6/129SV	miR-22 knockout	miR22KO_WAT_1	↓
Sample 5	Mus musculus	male	miR-22 knockout	white adipose tissue	C57Bl6/129SV	miR-22 knockout	miR22KO_WAT_2	↓
Sample 6	Mus musculus	male	miR-22 knockout	white adipose tissue	C57Bl6/129SV	miR-22 knockout	miR22KO_WAT_3	↓



What is Annotare?

Example of submission

Hands-on activity

RNA-seq of pancreatic islets cells from 6 patients with type II diabetes mellitus and 6 healthy individuals. We also know age and sex of each individual. Libraries were prepared with Illumina TruSeq Stranded mRNA Library prep kit and sequenced in a Illumina HiSeq 2500 System (paired-end 75 bp)



Getting started

Email to log in and
to contact you

Password: at least 4 characters
containing one digit

Please register with Annotare

Full name

Email address

Password

Confirm password

Already registered? Please [log in](#).

[Register](#)

Please log in to Annotare

Email address

Password

[Forgot your password?](#)

[Log in](#)

Don't have an account? Please [register](#).



EMBL-EBI



Getting started

My Submissions

+ Create Import

All Submissions

Completed

Incomplete

New Experiment Submission

Select Submission Template

⚠ Please ensure you have selected a template before proceeding!

A sequencing experiment produces raw sequence data files. These files can be generated by various sequencing platforms such as Illumina's NextSeq or MiSeq, ABI's 3730XL Analyzer/HiSeq or Ion Torrent. An example is E-MTAB-582.

Annotate expects the following experimental workflow (but is flexible with the number of files per sample, e.g. for paired-end samples):

paired-end

```
graph LR; S1[Sample 1] --> L1[Library 1]; S2[Sample 2] --> L2[Library 2]; S3[Sample 3] --> L3[Library 3]; L1 --> F1A[File A] --- F1B[File A2] --- F1C[File A3] --- F1D[File A4]; L2 --> F2A[File B] --- F2B[File B2] --- F2C[File B3] --- F2D[File B4]; L3 --> F3A[File C] --- F3B[File C2] --- F3C[File C3] --- F3D[File C4]
```

single-end technical replicates

Select the submission template for your experiment type

Please ensure you have selected the correct template as this cannot be changed later





Getting started

New Experiment Submission

Select Experiment Design(s) i

- binding site identification design
- case control design
- cell type comparison design
- clinical history design
- compound treatment design
- development or differentiation design
- disease state design
- dose response design
- genetic modification design
- genotype design
- growth condition design
- pathogenicity design
- injury design
- organism part comparison design
- sex design
- species design
- stimulus or stress design
- strain or line design
- time series design

Prev

Provide Experiment Details

How many samples does your experiment have? i 12

1 sample = 1 biological replicate

OK

Fill in experiment design and details to set up your submission



Describe your experiment

UNACCESSIONED

General Information
Contacts
Publications
Create samples, add attributes and experimental variables
Assign ENA library information
Describe protocols
Assign data files

High-throughput sequencing

Informative title highlighting its intention

Description *

Provide an informative title for your experiment, e.g. "Transcription profiling of mouse liver tissue with tamoxifen against Cdkn1a".

Background biology and aim of the experiment

Experiment Type *

disease state design

Add... Remove Selected

Date of Experiment

YYYY-MM-DD

Date of Public Release *

YYYY-MM-DD

Hide my identity from reviewers

Related Accession Number

Enter the accession number of related experiments

B-4688

Keep your experiment until you want Double-blind peer review Cross referencing datasets

Save a draft | Upload multiple files in one go | Submit to ArrayExpress

Upload

Name	Date	Status	File Size (Bytes)
------	------	--------	-------------------

FTP upload

Drag-and-drop files here to start upload or press the "Upload Files" button.

⚠ File names can only contain letters [A-Z,a-z], numbers [0-9], underscores [_], and dots [.]

Start uploading files from the beginning to save time



Provide contact details

General Information

Contacts

Publications

Create samples, add attributes and experimental variables

Assign ENA library information

Describe protocols

Assign data files

High-throughput sequencing

Add contacts

Remove contacts

+

Laura Huerta

First Name *	Laura	Middle Initials	Affiliation *
Last Name *	Huerta	Address *	
Email *	lauhuema@ebi.ac.uk	Roles *	submitter change...
Phone			
Fax			

At least one contact must have the role of “submitter”

Laura Huerta

First Name *	Middle Initials	Affiliation *
Last Name *	Address *	
Email *	Roles *	change...
Phone		
Fax		



What is Annotare?

Example of submission

Hands-on activity

RNA-seq of pancreatic islets cells from 6 patients with type II diabetes mellitus and 6 healthy individuals. We also know age and sex of each individual. Libraries were prepared with Illumina TruSeq Stranded mRNA Library prep kit and sequenced in a Illumina HiSeq 2500 System (paired-end 75 bp)

age

sex

tissue

cell type

disease



Sample attributes

Mandatory attributes

Sample Attributes and Experimental Variables

Material Type	<	Cell Line
Organism	>	Clinical History
Individual	↑	Compound (Experimental Variable)
Age	↓	Cultivar
Sex	=	Description
Organism Part		Developmental Stage
Cell Type		Diet
Disease (Experimental Variable)		Disease Staging
		Dose (Experimental Variable)
		Ecotype
		Environmental History
		Environmental stress
		Fraction
		Genetic Modification
		Genotype
		Growth Condition
		Immunoprecipitate (Experimental Variable)
		Infect
		Injury
		Irradiate (Experimental Variable)
		Karyotype
		Phenotype
		Provider
		RNA interference (Experimental Variable)
		Replicate
		Response to Treatment
		Sampling site
		Single Cell Well Quantity
		Specimen With Known S
		Stimulus

Sample Attribute Experimental Variable

Name: Age

EFO Term: age

Measurement Unit: ye
year (UO_0000036)

Select as many terms as possible to annotate your sample

For attribute/s related to measurements, e.g. age, time, dose, add also the units of measurement

Add your own attributes if it is not listed

[new attribute](#)

Cancel OK





How to annotate your samples

General Information Add Sample Attributes and Variables * Add Samples Delete Samples Fill Down Value Paste Into Column

	Name	Material Type	Organism	Individual	Age (year)	Sex	Organism Part	Cell Type	Disease
<input type="checkbox"/>	Sample 1	organism part	Homo sapiens						
<input type="checkbox"/>	Sample 2	organism part	Homo sapiens						
<input type="checkbox"/>	Sample 3	organism part	Homo sapiens						
<input type="checkbox"/>	Sample 4	organism part	Homo sapiens						
<input type="checkbox"/>	Sample 5	organism part	Homo sapiens						
<input type="checkbox"/>	Sample 6	organism part	Homo sapiens						
<input type="checkbox"/>	Sample 7	organism part	Homo sapiens						
<input type="checkbox"/>	Sample 8	organism part	Homo sapiens						
<input type="checkbox"/>	Sample 9	organism part	Homo sapiens						
<input type="checkbox"/>	Sample 10	organism part	Homo sapiens						
<input type="checkbox"/>	Sample 11	organism part	Homo sapiens						
<input type="checkbox"/>	Sample 12	organism part	Homo sapiens						

Copy value into all cells in a column



How to annotate your samples

General Information

Add Sample Attributes and Variables *

Add Samples Delete Samples Fill Down Value Paste Into Column

Contacts

Publications

Create samples, add attributes and experimental variables

Assign EN information

Describe

High-throughput

Metadata_slides.txt - OpenOffice Calc

Arial 10 B U E F G H I

D2:D13 N6

	A	B	C	D	E	F	G	H	I
1	Sample	Material Type	Organism	Individual	Age (year)	Sex	Organism Part	Cell Type	Disease
2	Sample 1	organism part	Homo sapiens	P1	21	male	pancreas	islet of Langerhans	type I diabetes mellitus
3	Sample 2	organism part	Homo sapiens	P2	32	female	pancreas	islet of Langerhans	type I diabetes mellitus
4	Sample 3	organism part	Homo sapiens	P3	37	female	pancreas	islet of Langerhans	type I diabetes mellitus
5	Sample 4	organism part	Homo sapiens	P4	24	male	pancreas	islet of Langerhans	type I diabetes mellitus
6	Sample 5	organism part	Homo sapiens	P5	45	male	pancreas	islet of Langerhans	type I diabetes mellitus
7	Sample 6	organism part	Homo sapiens	P6	56	female	pancreas	islet of Langerhans	type I diabetes mellitus
8	Sample 7	organism part	Homo sapiens	N1	43	male	pancreas	islet of Langerhans	type I diabetes mellitus
9	Sample 8	organism part	Homo sapiens	N2	52	male	pancreas	islet of Langerhans	normal
10	Sample 9	organism part	Homo sapiens	N3	39	female	pancreas	islet of Langerhans	normal
11	Sample 10	organism part	Homo sapiens	N4	27	male	pancreas	islet of Langerhans	normal
12	Sample 11	organism part	Homo sapiens	N5	48	female	pancreas	islet of Langerhans	normal
13	Sample 12	organism part	Homo sapiens	N6	33	female	pancreas	islet of Langerhans	normal
14									
15									
16									
17									
18									
19									
20									
21									

Sheet 1 / 3 Default STD Sum=0 100 %

Paste Into Column

Please enter values, one per line:

P1
P2
P3
P4
P5
P6
N1
N2
N3
N4
N5
N6

Cancel OK



How to annotate your samples

General Information	Add Sample Attributes and Variables * Add Samples Delete Samples Fill Down Value Paste Into Column																																																																																																																																												
Contacts	<table border="1"><thead><tr><th>Name</th><th>Material Type</th><th>Organism</th><th>Individual</th><th>Age (year)</th><th>Sex</th><th>Organism Part</th><th>Cell Type</th><th>Disease</th><th></th></tr></thead><tbody><tr><td>Sample 1</td><td>organism part</td><td>Homo sapiens</td><td>P1</td><td>21</td><td>male</td><td>pancreas</td><td>islet of Langerhans</td><td>type I diabetes mellitus</td><td></td></tr><tr><td>Sample 2</td><td>organism part</td><td colspan="2">Homo sapiens (NCBITaxon_9606)</td><td>male</td><td>pancreas</td><td>islet of Langerhans</td><td>type I diabetes mellitus</td><td></td><td></td></tr><tr><td>Sample 3</td><td>organism part</td><td>Homo sapiens</td><td>P3</td><td>37</td><td>female</td><td>pancreas</td><td>islet of Langerhans</td><td>type I diabetes mellitus (EFO_0001359)</td><td></td></tr><tr><td>Sample 4</td><td>organism part</td><td>Homo sapiens</td><td>P4</td><td>24</td><td>male</td><td>pancreas</td><td>islet of Langerhans</td><td>type I diabetes mellitus</td><td></td></tr><tr><td>Sample 5</td><td>organism part</td><td>Homo sapiens</td><td>P5</td><td>45</td><td>male</td><td>pancreas</td><td>islet of Langerhans</td><td>type I diabetes mellitus</td><td></td></tr><tr><td>Sample 6</td><td>organism part</td><td>Homo sapiens</td><td>P6</td><td>56</td><td>female</td><td colspan="2">pancreas (UBERON_0001264)</td><td></td><td></td></tr><tr><td>Sample 7</td><td>organism part</td><td>Homo sapiens</td><td>N1</td><td>43</td><td>male</td><td>pancreas</td><td>islet of Langerhans</td><td>normal</td><td></td></tr><tr><td>Sample 8</td><td>organism part</td><td>Homo sapiens</td><td>N2</td><td>52</td><td>male</td><td>pancreas</td><td>islet of Langerhans</td><td>normal</td><td></td></tr><tr><td>Sample 9</td><td>organism part</td><td>Homo sapiens</td><td>N3</td><td>39</td><td>female</td><td>pancreas</td><td>islet of Langerhans</td><td>normal</td><td></td></tr><tr><td>Sample 10</td><td>organism part</td><td>Homo sapiens</td><td>N4</td><td>27</td><td colspan="2">female (PATO_0000383)</td><td>islet of Langerhans</td><td>normal</td><td></td></tr><tr><td>Sample 11</td><td>organism part</td><td>Homo sapiens</td><td>N5</td><td>48</td><td>female</td><td>pancreas</td><td>islet of Langerhans</td><td>normal</td><td></td></tr><tr><td>Sample 12</td><td>organism part</td><td>Homo sapiens</td><td>N6</td><td>33</td><td>female</td><td>pancreas</td><td>islet of Langerhans</td><td>normal</td><td></td></tr></tbody></table>											Name	Material Type	Organism	Individual	Age (year)	Sex	Organism Part	Cell Type	Disease		Sample 1	organism part	Homo sapiens	P1	21	male	pancreas	islet of Langerhans	type I diabetes mellitus		Sample 2	organism part	Homo sapiens (NCBITaxon_9606)		male	pancreas	islet of Langerhans	type I diabetes mellitus			Sample 3	organism part	Homo sapiens	P3	37	female	pancreas	islet of Langerhans	type I diabetes mellitus (EFO_0001359)		Sample 4	organism part	Homo sapiens	P4	24	male	pancreas	islet of Langerhans	type I diabetes mellitus		Sample 5	organism part	Homo sapiens	P5	45	male	pancreas	islet of Langerhans	type I diabetes mellitus		Sample 6	organism part	Homo sapiens	P6	56	female	pancreas (UBERON_0001264)				Sample 7	organism part	Homo sapiens	N1	43	male	pancreas	islet of Langerhans	normal		Sample 8	organism part	Homo sapiens	N2	52	male	pancreas	islet of Langerhans	normal		Sample 9	organism part	Homo sapiens	N3	39	female	pancreas	islet of Langerhans	normal		Sample 10	organism part	Homo sapiens	N4	27	female (PATO_0000383)		islet of Langerhans	normal		Sample 11	organism part	Homo sapiens	N5	48	female	pancreas	islet of Langerhans	normal		Sample 12	organism part	Homo sapiens	N6	33	female	pancreas	islet of Langerhans	normal	
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Create samples, add attributes and experimental variables																																																																																																																																													
Assign ENA library information																																																																																																																																													
Describe protocols																																																																																																																																													
Assign data files																																																																																																																																													
High-throughput sequencing																																																																																																																																													

www.ebi.ac.uk/ols/index



How to annotate your samples

Sample annotation with ontology terms

Pancreatic islets cells isolated from 23-year old male with type I diabetes

OLS Ontology Lookup Service

Home | Ontologies | Documentation | About | Contact Us

OLS > Search

islet of Langerhans

Exact match Obsolete terms

Filters

Term type

Filter by type

class	1296298
individual	21582
property	1475
ontology	115

Ontologies

Filter by ontology

Search results for *islet of Langerhans*

Showing 1 to 10 of 1319470 results

Islet of Langerhans NCIT_C12608
http://purl.obolibrary.org/obo/NCIT_C12608
The pancreatic tissue that contains the islets of Langerhans. It is responsible for the production and secretions of the pancreatic hormones.
Ontology: NCI Thesaurus OBO Edition NCIT

Islet of Langerhans UBERON:0000006
http://purl.obolibrary.org/obo/UBERON_0000006
the clusters of hormone-producing cells that are scattered throughout the pancreas
Ontology: Uber-anatomy ontology UBERON
Also in: EFO OBA BCGO CL ENVO OAE DOID HP CLO MP

www.ebi.ac.uk/ols/index



Sequencing library information

General Information										
Fill Down Value										
	Name	Library Layout *	Library Source *	Library Strategy *	Library Selection *	Library Strand	Nominal Length	Nominal SDev	Orientation	
	Sample 1	SINGLE	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	not applicable	5		5'-3'-3'-5'	
	Sample 2	SINGLE	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	first strand	5		5'-3'-3'-5'	
	Sample 3	PAIRED	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	second strand	5		5'-3'-3'-5'	
	Sample 4	PAIRED	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	first strand	75		5'-3'-3'-5'	
	Sample 5	PAIRED	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	first strand	75		5'-3'-3'-5'	
	Sample 6	PAIRED	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	first strand	75		5'-3'-3'-5'	
	Sample 7	PAIRED	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	first strand	75		5'-3'-3'-5'	
	Sample 8	PAIRED	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	first strand	75		5'-3'-3'-5'	
	Sample 9	PAIRED	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	first strand	75		5'-3'-3'-5'	
	Sample 10	PAIRED	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	first strand	75		5'-3'-3'-5'	
	Sample 11	PAIRED	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	first strand	75		5'-3'-3'-5'	
	Sample 12	PAIRED	TRANSCRIPTOMIC	RNA-Seq (Random)	PolyA (PolyA selecti	first strand	75		5'-3'-3'-5'	

www.ebi.ac.uk/fg/annotare/help/seq_lib_spec.html

Single-end and paired-end sequencing

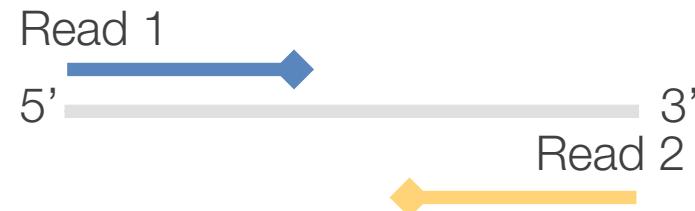
Single-end sequencing



my_sequence.fastq

```
@HWI-BRUNOP16X_0001:1:1:1466:1018#0/1  
AAGGAAGTGCCTGTCTGGCTAACACAGCNAGNCACGTGAC  
+  
aVfbe`^__^_TTTSSdfffffdfffabbZbbfebafbbbbbb
```

Paired-end sequencing



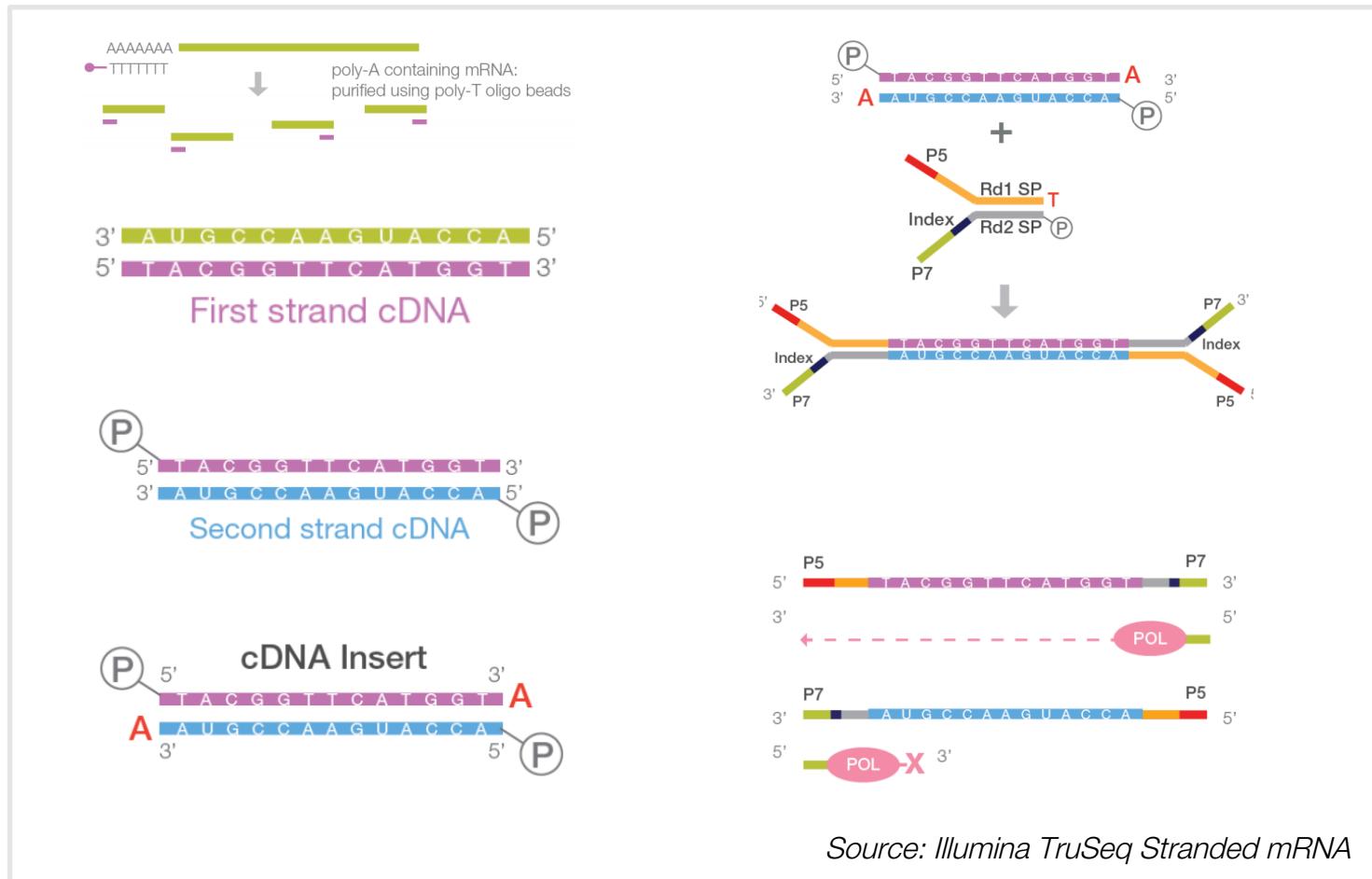
my_sequence_1.fastq

```
@HWI-BRUNOP16X_0001:1:1:1278:989#0/1  
NAAATTCGAATTCTGTGAAGTAAGCATCTTCTTGCA  
+  
BJJGGKIIINN^^^^^QQNTUQOOTTTRTOTY^^Y^\\^
```

my_sequence_2.fastq

```
@HWI-BRUNOP16X_0001:1:1:1278:989#0/2  
AACCCACACAGGAGAGCAGCCTACAGATGCAAATACTGTG  
+  
]K___fffffggghgeggggggdggggggfgggggeggggghh
```

Strand specific mRNA library





Add information about protocols

General Information

Add Protocol *

Name

sample collection protocol
Please enter the description for the sample collection protocol

nucleic acid extraction protocol
Please enter the description for the nucleic acid extraction protocol

nucleic acid library construction protocol
Please enter the description for the nucleic acid library construction protocol

nucleic acid sequencing protocol
Please enter the description for the nucleic acid sequencing protocol

Additional Protocols

growth protocol
Please enter the description for the growth protocol

treatment protocol
Please enter the description for the treatment protocol

normalization data transformation protocol
Please enter the description for the normalization data transformation protocol

conversion protocol
Please enter the description for the conversion protocol

Performer Hardware

Cancel Create

One-color microarray
- array design: A-AFFY-44
- label: biotin
[change...](#)



Upload files and assign samples

Annotare 2.0

UNACCESSIONED

Experiment Description Samples and Data

Create samples, add attributes and experimental variables

Describe protocols

Assign data files

One-color microarray
- array design: A-AFFY-44
- label: biotin
change...

Name Sample 1:biotin Sample 2:biotin Sample 3:biotin Sample 4:biotin Sample 5:biotin Sample 6:biotin Sample 7:biotin Sample 8:biotin Sample 9:biotin Sample 10:biotin Sample 11:biotin Sample 12:biotin

Favorites iCloud Drive Applications Documents lahuema Desktop Downloads Devices laura-ml Remote Disc Shared All... Tags Media Music Photos Movies

raw_data

Name Date Modified

66SML_PrimColt_C_06110962_Exon1.0_18.04.11.CEL Today, 16:35
66SML_PrimColt_T_06110962_Exon1.0_14.04.11.CEL Today, 16:35
70LS_PrimColt_C_06117914_Exon1.0_14.04.11.CEL Today, 16:35
70LS_PrimColt_T_06117914_Exon1.0_14.04.11.CEL Today, 16:35
72FG_PrimColt_C_06119711_Exon1.0_14.04.11.CEL Today, 16:35
95RA_PrimColt_C_0818806_Exon1.0_13.04.11.CEL Today, 16:35
95RA_PrimColt_T_0818806_Exon1.0_13.04.11.CEL Today, 16:35
106CS_PrimColt_C_08122156_Exon1.0_13.04.11.CEL Today, 16:35
106CS_PrimColt_T_08122156_Exon1.0_13.04.11.CEL Today, 16:35
121GIC_PrimColt_C_09114599_Exon1.0_18.04.11.CEL Today, 16:35
121GIC_PrimColt_T_09114599_Exon1.0_18.04.11.CEL Today, 16:35
124LR_PrimColt_T_09116420_Exon1.0_14.04.11.CEL Today, 16:35
143PG_PrimColt_C_1014386_Exon1.0_18.04.11.CEL Today, 16:35
143PG_PrimColt_T_1014386_Exon1.0_18.04.11.CEL Today, 16:35
148GB_PrimColt_C_1010898_Exon1.0_13.04.11.CEL Today, 16:35
148GB_PrimColt_T_1010898_Exon1.0_13.04.11.CEL Today, 16:35

Format: All Files

Options Cancel Open

Laura Huerta Sign Out

Get Us Save as Spreadsheets Validate Submit to ArrayExpress

Upload Files... FTP Upload... Delete Files

Name Date Status File Size (Bytes)

Upload files – Make sure the files have status “uploaded” before you try assigning them to samples



Send data files by FTP

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Send data files to ArrayExpress by FTP

ArrayExpress provides a FTP repository for submitters to upload a large volume of data files associated with their experiment submissions. FTP upload is also useful if you would like to send files to us prior to a submission (e.g. for us to check if they are in a suitable format).

Before you start transferring files, please note the following points:

1. **File preparation:** Please check our guidelines on submitting files for a [microarray experiment](#), [sequencing experiment](#) or [array design](#). E.g. microarray data files should not be compressed, but fastq files from sequencing experiments must be individually compressed by gzip or bzip2 (as a requirement from the Sequence Read Archive).
2. **Data privacy:** All ArrayExpress submitters use the same account to upload files (see below). As most of the files are un-/pre-published, we make all uploaded files "private", which means you will not be able to see any files or directories already on the FTP site, including those that you uploaded or created. You will only be able to see your files if you are uploading to your personal Annotare submission directory. The FTP server is a temporary storage space, where we will keep your files for two months, counting from the date of file upload, after which we will delete them without warning. This is to comply with the [fair usage policy](#) of the disc space which we share with the European Nucleotide Archive.
3. **No whitespaces or special characters in file names:** Make sure the file names are constructed only from alphanumerals [A-Z,a-z,0-9], underscores [_] and dots [.], with no whitespaces, brackets, other punctuations or symbols.

www.ebi.ac.uk/arrayexpress/help/ftp_upload.html

Outline of the session

- ✓ What is Annotare?
 - ✓ Getting started
 - ✓ Describe your experiment
 - ✓ Sample attributes
 - ✓ Microarray experiment
 - ✓ Sequencing experiment
 - ✓ Upload files and assign to samples
- ✓ Data submission with Annotare
 - ✓ Hands-on exercise



Let's try Annotare

Submit microarray data

Hands-on activity

Submitting microarray data for this experiment



In pairs

<http://europepmc.org/abstract/MED/27449199>

EMBL-EBI workshop: Tools for functional genomics data

Annotare: “your” web-form submission tool

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Senior Scientific Curator

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24 May 2018

