

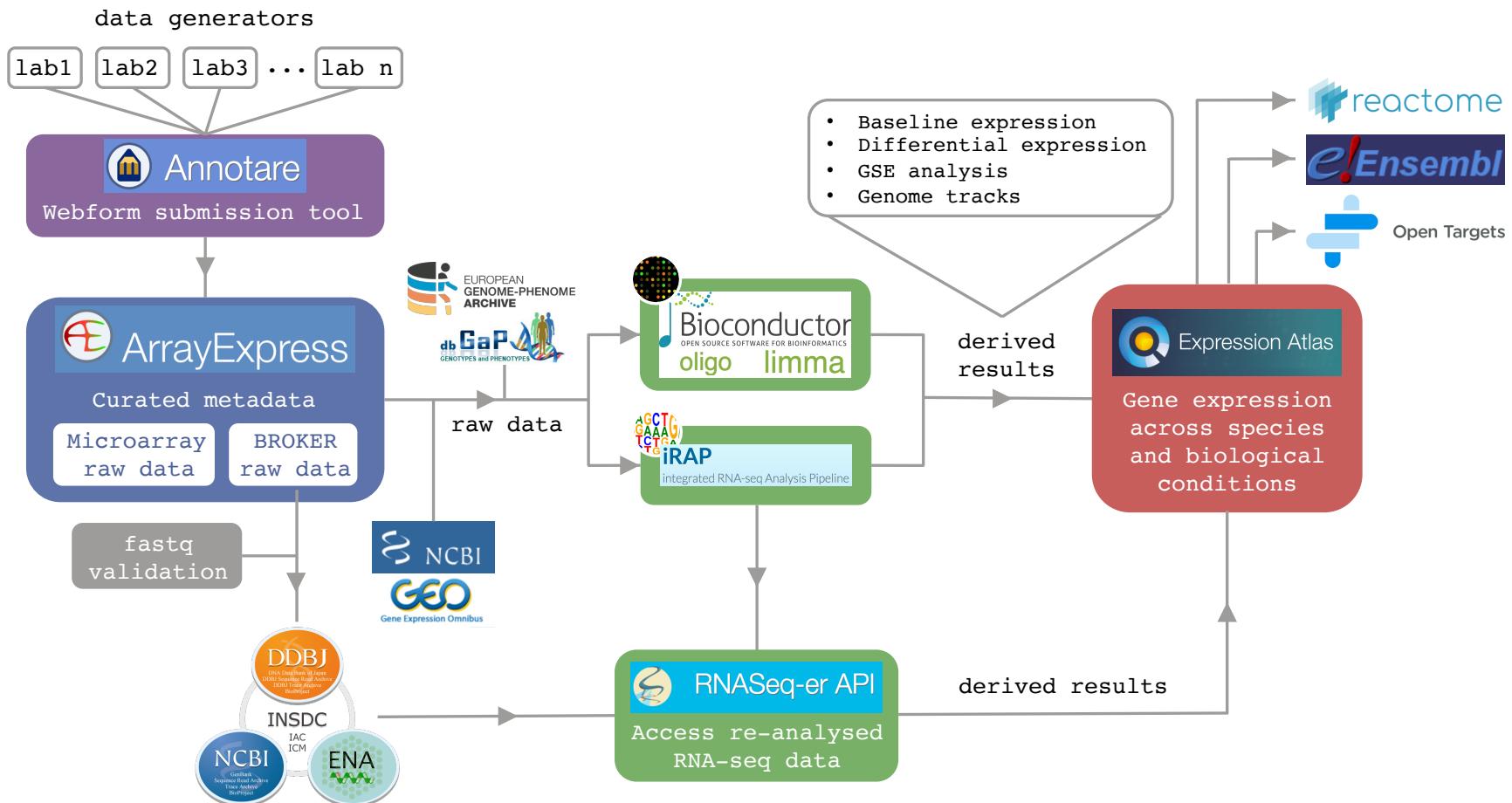
EMBL-EBI Bioinformatics resources for exploring functional genomics data

Annotare: “your” web-form submission tool

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9 November 2017



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?

ArrayExpress: why and how to submit your data

Submit your experiment

[Save as Spreadsheets](#) [Submit to ArrayExpress](#)

E-MTAB-9999

The diagram illustrates the submission process. On the left, two researchers (a woman and a man) are shown with a stack of papers. A large arrow points from them to a central video camera icon, which then points to a row of three small portrait photos of people. A final large arrow points down to the ArrayExpress logo.

ArrayExpress

EMBL-EBI

Please log in to Annotare

Email address

Password

[Forgot your password?](#) [Log in](#)

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

Tweets by @ArrayExpressEBI

 **ArrayExpress** @ArrayExpressEBI It's Friday. There are those who often work at wknds to look after #AnnotareEBI submitters depositing data in ArrayExpress. Meet the team! 

12 May

 **ArrayExpress** Retweeted  **Yasset Perez-Riverol** @ypriverol @OmicsDI nature.com/nbt/journal/v3... major coll. of 6 #EBI teams @pride_ebi @MetaboLights @ExpressionAtlas @ArrayExpressEBI @emblebies @ega_ebi

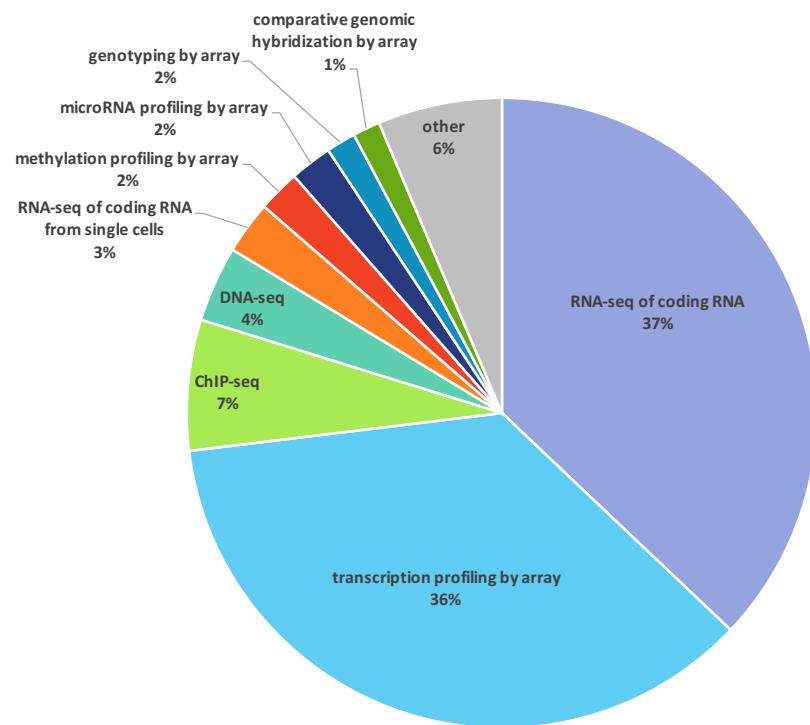
12 May

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

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
Sample 1	organism part	Mus musculus	male	wild type genotype	white adipose tissue
Sample 2	organism part	Mus musculus	male	wild type genotype	white adipose tissue
Sample 3	organism part	Mus musculus	male	wild type genotype	white adipose tissue
Sample 4	organism part	Mus musculus	male	miR-22 KO	white adipose tissue
Sample 5	organism part	Mus musculus	male	miR-22 KO	white adipose tissue
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

Transcription profile of pancreatic islets cells from 6 patients with type I diabetes mellitus and 6 healthy individuals. We also know age and sex of each individual. The array used was Affymetrix GeneChip Human Genome U133 Plus 2.0.



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

My Submissions

+ Create

Import

All Submissions

Completed

Incomplete



Getting started

Submission type:

- One-color microarray
- Two-color microarray
- High-throughput sequencing

Select a submission type

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

New Experiment Submission

How many hybridizations did you perform?

12

What array did you use?

A-AFFY-44

Affymetrix GeneChip Human Genome U133 Plus 2.0 [HG-U133_Plus_2] : A-AFFY-44

biotin

Enter the ArrayExpress Accession number

One hybridization is where one labeled sample is hybridized on an array chip

An example is E-MTAB-641, Europe PMC 21980142. A one colour experiment uses one dye or label. For example experiments using an Affymetrix array use the label biotin. For one colour data one row in the SDRF (Sample and Data Relationship Format) file is equal to one assay.

Not sure if your array is already accessioned in ArrayExpress, or not sure what an array is? [Here's a quick guide.](#)

OK



Finding an array in ArrayExpress

ARRAYEXPRESS / ARRAYS

Search arrays by accessions, names, descriptions, or providers

Affymetrix GeneChip Human Genome U133 Plus 2.0

ArrayExpress data only

2 arrays

Accession	Name	Organism	Files
A-AFFY-44	Affymetrix GeneChip Human Genome U133 Plus 2.0 [HG-U133_Plus_2]	Homo sapiens	
A-MTAB-599	Almac Xcel Array [ADXECv1a520743]	Homo Sapiens	

www.ebi.ac.uk/arrayexpress/arrays/browse.html?directsub=on



Finding an array in ArrayExpress

A-AFFY-44 - Affymetrix GeneChip Human Genome U133 Plus 2.0 [HG-U133_Plus_2]

Organism	Homo sapiens
Version	1.0
Provider	Affymetrix, Inc. (support@affymetrix.com)
Links	All 4412 experiments done using A-AFFY-44
Files	Array Design Browse all available files



A	B	C
1 Array Design Name	Affymetrix GeneChip Human Genome U133 Plus 2.0 [HG-U133_Plus_2]	
2 Comment[AdditionalFile:CDF]	HG-U133_Plus_2.CDF	
3 Comment[AdditionalFile:CDF]	HG-U133_Plus_2.cdf	
4 Version		1
5 Provider	Affymetrix, Inc. (support@affymetrix.com)	
6 Comment[ArrayExpressAccession]	A-AFFY-44	
7 Comment[SubmittedName]	Affymetrix GeneChip Human Genome U133 Plus 2.0 [HG-U133_Plus_2]	
8 Comment[Organism]	Homo sapiens	
9 Technology Type	in_situ oligo features	
10 Technology Type Term Accession Number	#in_situ_oligo_features	
11 Technology Type Term Source REF	The MGED Ontology	
12 Surface Type	glass	
13 Surface Type Term Accession Number	#glass	
14 Surface Type Term Source REF	mo	
15 Term Source Name	The MGED Ontology	mo
16 Term Source File	http://mgd.sourceforge.net/ontologies/MGEDontology.php	http://mgd.sourceforge.net/ontologies/MGEDontology.php
17 Term Source Version		
18 Comment[AdditionalFile:txt]	A-AFFY-44_comments.txt	
19		
20 [main]		
21 Composite Element Name	Composite Element Database Entry[affymetrix_netaffx]	Composite Element Database Entry[emb]
22 AFFX-BioB-5_at	AFFX-BioB-5_at	AFFX-BioB-5
23 AFFX-BioB-M_at	AFFX-BioB-M_at	AFFX-BioB-M
24 AFFX-BioB-3_at	AFFX-BioB-3_at	AFFX-BioB-3
25 AFFX-BioC-5_at	AFFX-BioC-5_at	AFFX-BioC-5
26 AFFX-BioC-3_at	AFFX-BioC-3_at	AFFX-BioC-3
27 AFFX-BioDn-5_at	AFFX-BioDn-5_at	AFFX-BioDn-5
28 AFFX-BioDn-3_at	AFFX-BioDn-3_at	AFFX-BioDn-3
29 AFFX-CreX-5_at	AFFX-CreX-5_at	AFFX-CreX-5



Getting started

New Experiment Submission

Submission type:

- One-color microarray
- Two-color microarray
- High-throughput sequencing

How many hybridizations did you perform?

What array did you use?
Affymetrix GeneChip Human Genome U133 Plus 2.0 [HG-U133_Plus_2] : A-AFFY-44

What label did you use?

One hybridization is where one labeled sample is hybridized on an array chip

An example is E-MTAB-641, Europe PMC 21980142. A one colour experiment uses one dye or label. For example experiments using an Affymetrix array use the label biotin. For one colour data one row in the SDRF (Sample and Data Relationship Format) file is equal to one assay.

Not sure if your array is already accessioned in ArrayExpress, or not sure what an array is? [Here's a quick guide.](#)

 OK



Describe your experiment

UNACCESSIONED

Experiment Description Samples and Data

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 (copy-and-pasting your manuscript's abstract)

(at least 50 characters)

Experiment Type *

transcription profiling by array

Experimental Designs

Informative title highlighting its intention

Background biology and aim of the experiment

Keep your experiment private until you want

Cross referencing datasets

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 experiment

Contact Us



Submit to ArrayExpress



Upload multiple files in one go

Upload Files...

FTP Upload...

Delete Files

Name File Size (Bytes)

FTP upload

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 [.]

Start uploading files from the beginning to save time



Describe your experiment

UNACCESSIONED

Experiment Description Samples and Data

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 with tamoxifen against untreated controls

Description * Describe the biological relevance and intent of the experiment. Include an or copy-and-pasting your manuscript's abstract.
(at least 50 characters)

Experiment Type * transcription profiling by array

Experimental Designs 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 in ArrayExpress or PRIDE

Double-blind peer review

Experimental Designs

[sheets](#) [Validate](#) [Submit to ArrayExpress](#)

biological variation design

- cell component comparison design
- cell cycle design
- cell type comparison design
- cellular modification design
- clinical history design
- compound treatment design
- cross sectional design
- development or differentiation design
- disease state design
- dose response design
- family based design
- genetic modification design

biomolecular annotation design

methodological variation design

[Upload...](#) [Delete Files](#)

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

Upload Files

Drop-and-drag 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 [.]

[Cancel](#) [Add](#)



Describe your experiment

Experiment Description

Samples and Data

General Information



Add contacts

Remove contacts

Contacts *

Publications

One-color microarray

- array design: A-AFFY-44
- label: biotin
change...

One-color microarray settings

What array design did you use?

A-AFFY-44

What label did you use?

biotin

▼ Laura Huerta

First Name
*

Laura

Middle Initials

Last Name
*

Huerta

Email
*

lauhuema@ebi.ac.uk

Phone

Fax

Affiliation

Address

Roles *
submitter
change...

At least one contact
must have the
role "submitter"

Change array
and label

Cancel Save



Sample attributes

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...](#)

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

	Name	Material
<input type="checkbox"/>	Sample 1	
<input type="checkbox"/>	Sample 2	
<input type="checkbox"/>	Sample 3	
<input type="checkbox"/>	Sample 4	
<input type="checkbox"/>	Sample 5	
<input type="checkbox"/>	Sample 6	Number of samples 1 Naming pattern Sample # Starting number 1 Will create samples named: Sample 13
<input type="checkbox"/>	Sample 7	
<input type="checkbox"/>	Sample 8	
<input type="checkbox"/>	Sample 9	
<input type="checkbox"/>	Sample 10	
<input type="checkbox"/>	Sample 11	
<input type="checkbox"/>	Sample 12	

Cancel Create



What is Annotare?

Example of submission

Hands-on activity

Transcription profile of pancreatic islets cells from 6 patients with type I diabetes mellitus and 6 healthy individuals. We also know age and sex of each individual. The array used was Affymetrix GeneChip Human Genome U133 Plus 2.0.



Sample attributes

Mandatory attributes

Sample Attributes and Experimental Variables	
Material Type	<
Organism	>
Age	↑
Sex	↓
Organism Part	=
Cell Type	
Disease (Experimental Variable)	

Sample Attribute Experimental Variable

Name: Disease
EFO Term: disease
Measurement Unit:

Indicate which attribute/s is also the main variable

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

Select as many terms to annotate your sample as possible

Cell Line
Clinical History
Compound (Experimental Variable)
Cultivar
Description
Developmental Stage
Diet
Disease Staging
Dose (Experimental Variable)
Ecotype
Environmental History
Environmental stress
Fraction
Genetic Modification
Genotype
Growth Condition
Immunoprecipitate (Experimental Variable)
Individual
Infect
Injury
Irradiate (Experimental Variable)
Karyotype
Phenotype
Provider
RNA interference (Experimental Variable)
Replicate
Response to Treatment
Sampling site
Single Cell Well Quantity
[new attribute](#)

Add your own attributes if it is not listed



How to annotate your samples

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...

Add Sample Attributes and Variables *									Add Samples	Delete Samples	Fill Down Value	Import Values	1-12 of 12
	Name	Material Type	Organism	Age (year)	Sex	Organism Part	Cell Type	Disease					
	Sample 1	cell	Homo sapiens	21	male	pancreas	islet of Langerhans	type I diabetes mellitus					
	Sample 2	cell	Homo sapiens	32	female	pancreas	islet of Langerhans	type I diabetes mellitus					
	Sample 3	cell	Homo sapiens (NCBITaxon_9606)			pancreas	islet of Langerhans	type I diabetes mellitus					
	Sample 4	cell	Homo sapiens	24	male	pancreas	islet of Langerhans	type I diabetes mellitus					
	Sample 5	cell	Homo sapiens	45	male	pancreas	islet of Langerhans	type I diabetes mellitus					
	Sample 6	cell	Homo sapiens	56	female	pancreas	type I diabetes mellitus (EFO_0001359)						
	Sample 7	cell	Homo sapiens	43	male	pancreas	islet of Langerhans	normal					
	Sample 8	cell	Homo sapiens	52	male	pancreas (UBERON_0001264)							
	Sample 9	cell	Homo sapiens	39	female	pancreas	islet of Langerhans	normal					
	Sample 10	cell	Homo sapiens	27	male	pancreas	islet of Langerhans	normal					
	Sample 11	cell	Homo sapiens	48	female	pancreas	islet of Langerhans	normal					
	Sample 12	cell	Homo sapiens	33		female (PATO_0000383)	angerhans	normal					

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



Sample attributes

Annotate your sample

Hands-on activity

What attributes will you use to annotate samples from 14 primary prostate cancers and their paired normal counterparts



www.ebi.ac.uk/ols/index



Add information about protocols

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...](#)

Add Protocol *
 Name
Del

New Protocol

Minimum Protocols Required

sample collection protocol

Please enter the description of sample collection protocol

nucleic acid extraction protocol

Please enter the description of nucleic acid extraction protocol

nucleic acid labeling protocol

Please enter the description of nucleic acid labeling protocol

nucleic acid hybridization to array protocol

Please enter the description of nucleic acid hybridization to array protocol

array scanning and feature extraction protocol

Please enter the description of array scanning and feature extraction protocol

Optional Protocols

growth protocol

Please enter the description of growth protocol

treatment protocol

Please enter the description of treatment protocol

normalization data transformation protocol

[Cancel](#)

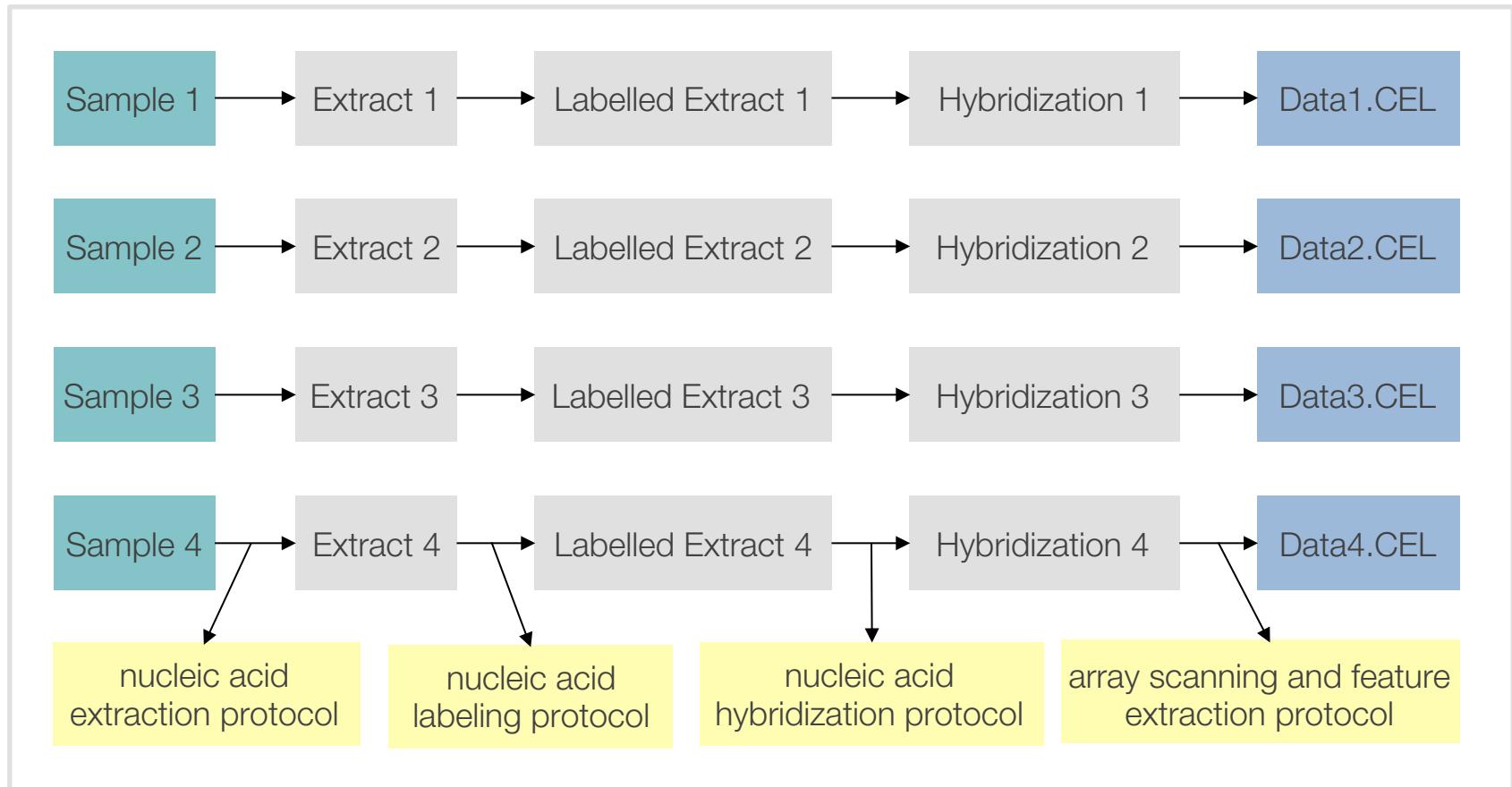
[Create](#)

1-1 of 0

Descrip



Metadata is stored in MAGE-TAB format





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

[Home](#)[Browse](#)[Submit](#)[Help](#)[About ArrayExpress](#)

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 Bioinformatics resources for exploring functional genomics data

Annotare: “your” web-form submission tool

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