

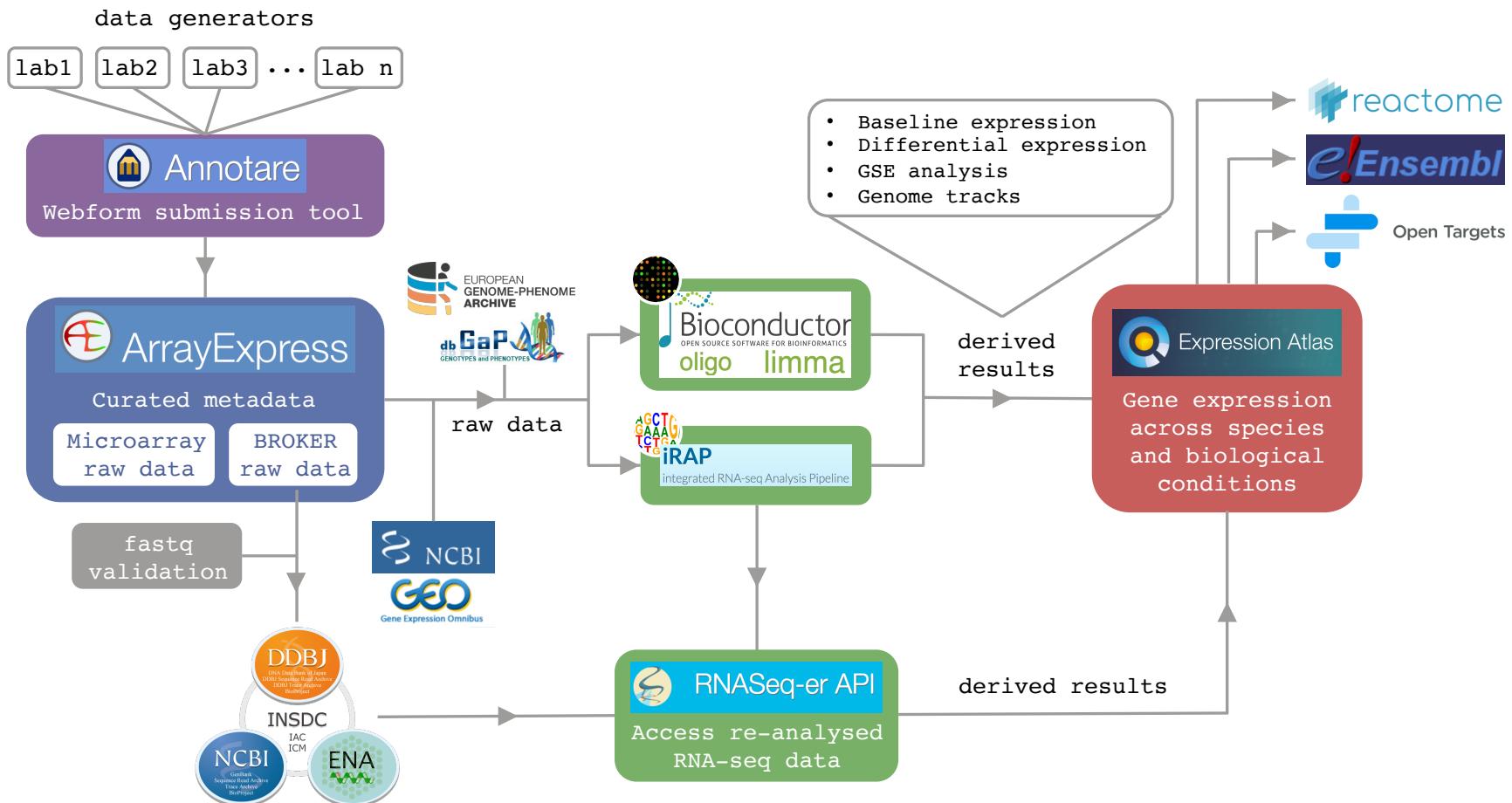
# EMBL-EBI Resources and tools for genomics and proteomics

Discover functional genomics data  
with ArrayExpress

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6 December 2017



# Functional genomics resources at EMBL-EBI





# ArrayExpress: functional genomics data archive

Home    Browse    Submit    Help    About ArrayExpress    Contact Us    Login

## ArrayExpress – functional genomics data

ArrayExpress Archive of Functional Genomics Data stores data from high-throughput functional genomics experiments, and provides these data for reuse to the research community.

[Browse ArrayExpress](#)

### Latest News

13 October 2017 - **ArrayExpress is stopping import of GEO data**

Unfortunately, we are stopping the regular imports of Gene Expression Omnibus (GEO) data into ArrayExpress. We will keep using data from GEO to build our added value database [Expression Atlas](#), and the reprocessed and additionally annotated data for selected datasets will be available from there.

### Links

Information about how to search ArrayExpress, understand search results, how to submit data and FAQ can be found in our [Help section](#).

Find out more about the [Functional Genomics group](#).

### Tools and Access

[Annotare](#): web-based submission tool for ArrayExpress.

[ArrayExpress Bioconductor package](#): an R package to access ArrayExpress and build data structures.

[Programmatic access](#): query and download data using web services or JSON.

### Data Content

Updated today at 03:00

- 70487 experiments
- 2231358 assays
- 46.08 TB of archived data

### Related Projects

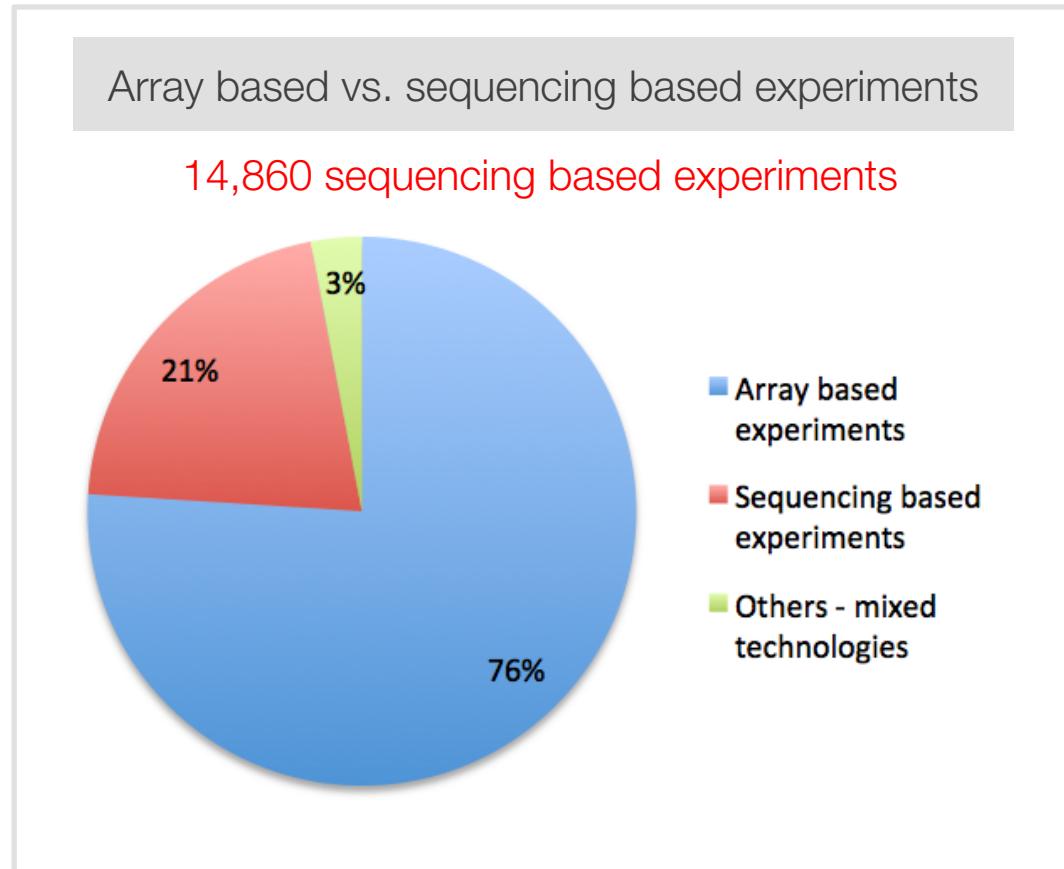
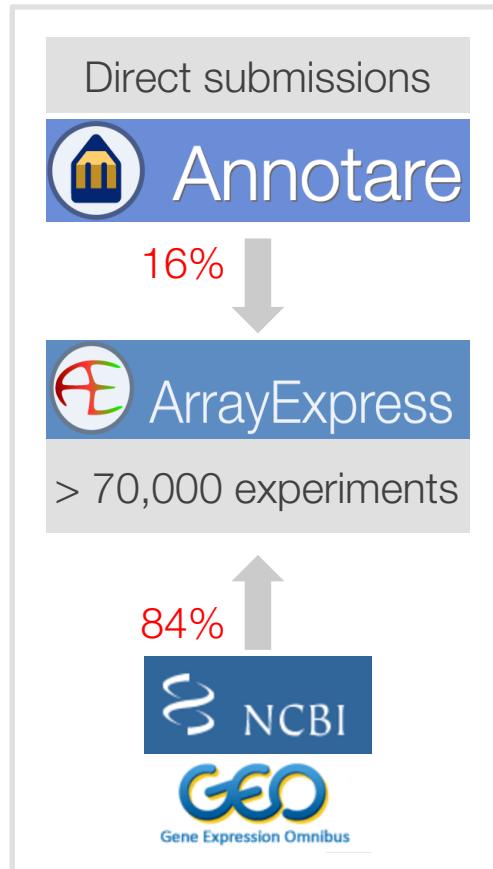
Discover up and down regulated genes in numerous experimental conditions in the [Expression Atlas](#).

Explore the [Experimental Factor Ontology](#) used to support queries and annotation of ArrayExpress data.

[www.ebi.ac.uk/arrayexpress](http://www.ebi.ac.uk/arrayexpress)



# ArrayExpress: functional genomics data archive

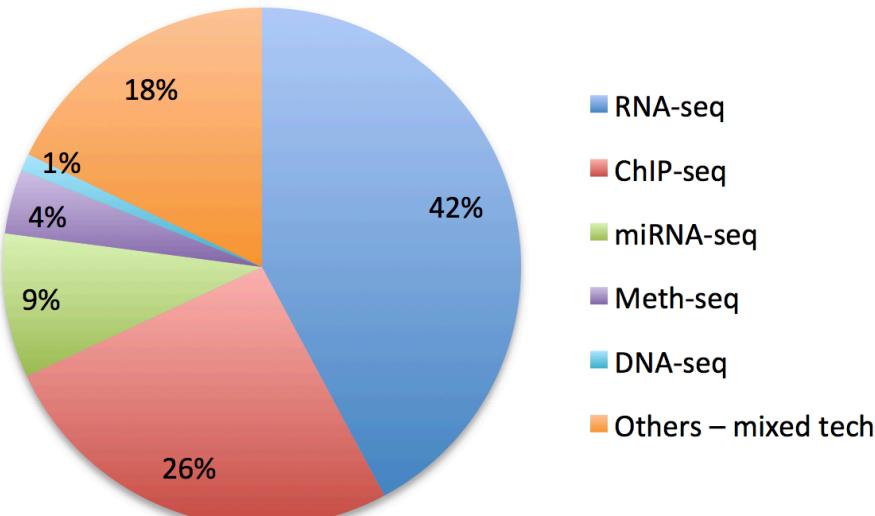




# ArrayExpress: functional genomics data archive

Sequencing based experiments

6,266 RNA-seq of coding RNA experiments





# ArrayExpress: functional genomics data archive

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

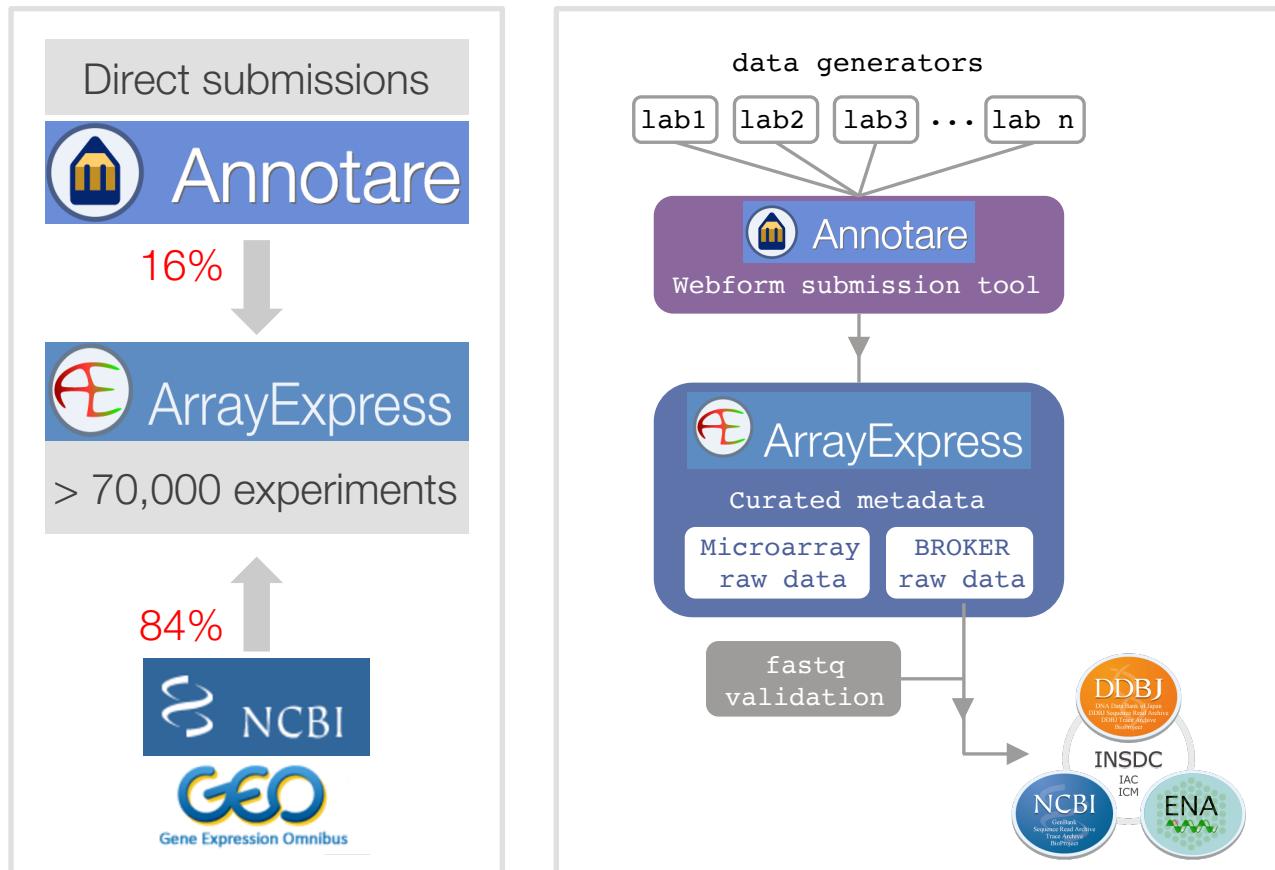
## Experiment types in ArrayExpress

Experiment Type	Definition (EFO term accession)	Example
4C	EFO_0007690	E-MTAB-2180
antigen profiling	EFO_0000747	E-MTAB-3606
ATAC-seq	EFO_0007045	E-MTAB-3972
Bisulfite-seq	EFO_0003753	E-MTAB-1042
Capture-C	EFO_0007691	E-MTAB-4845
ChIP-chip by array	EFO_0002760	E-MTAB-2804
ChIP-chip by SNP array	EFO_0002764	E-GEOID-22306
ChIP-chip by tiling array	EFO_0002762	E-MTAB-1402
ChIP-seq	EFO_0002692	E-MTAB-3631
CLIP-seq	EFO_0003143	E-MTAB-1371
comparative genomic hybridization by array	EFO_0000749	E-MTAB-2293
DNA-seq	EFO_0002693	E-MTAB-3109
FAIRE-seq	EFO_0004428	E-MTAB-3199

[www.ebi.ac.uk/arrayexpress/help/experiment\\_types.html](http://www.ebi.ac.uk/arrayexpress/help/experiment_types.html)



# ArrayExpress: archive for direct submissions





# Raw data – stable archiving at INSDC

- ✓ INSDC (3 partners) runs the sequence read archive (SRA)
- ✓ ArrayExpress brokers raw NGS data to ENA & GEO to NCBI SRA

INSDC – International Nucleotide Sequence Database Collaboration

The image shows a world map centered on Europe and North America. Overlaid on the map are three logos: NCBI (National Center for Biotechnology Information) on the left, ENA (European Nucleotide Archive) in the center, and DDBJ (DNA Data Bank of Japan) on the right. The NCBI logo consists of a blue square with a white stylized DNA helix and the acronym 'NCBI' below it. The ENA logo features the acronym 'ENA' in large letters with a green wavy line graphic to its right, and the full name 'European Nucleotide Archive' below. The DDBJ logo has a stylized orange and yellow 'S' shape followed by the acronym 'DDBJ' and the full name 'DNA Data Bank of Japan'. A grey banner at the bottom of the map contains the text 'Daily data exchange - mirroring'.

Daily data exchange - mirroring



# Data mining with ArrayExpress

## ArrayExpress

Home Browse Submit Help About ArrayExpress

Search Examples: E-MEXP-31, cancer, p53, Geuvadis [advanced search](#)

Contact Us Login

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[www.ebi.ac.uk/arrayexpress](http://www.ebi.ac.uk/arrayexpress)



# Data mining with ArrayExpress

ArrayExpress

Search Examples: E-MEXP-31, cancer, p53, Geuvadis [advanced search](#)

Home Browse Submit Help About ArrayExpress Contact Us Login

Filter search results

Page 1 2 3 4 5 6 .. 2820 Showing 1 - 25 of 70485 experiments

Sortable headings

Accession	Title	Type	Organism	Assays	Released	Processed	Raw	Views	Atlas
E-MTAB-5910	Toxicity of the main electronic cigarette components, propylene glycol, glycerin and nicotine in Sprague Dawley rats in a 90-day OECD inhalation study complemented with molecular endpoints (RNE)	transcription profiling by array	Rattus norvegicus	48	03/11/2017	<a href="#">Download</a>	<a href="#">Download</a>	-	-
E-MTAB-5545	Toxicity of the main electronic cigarette components, propylene glycol, glycerin and nicotine in Sprague Dawley rats in a 90-day OECD inhalation study complemented with molecular endpoints (Lung)	transcription profiling by array	Rattus norvegicus	48	03/11/2017	<a href="#">Download</a>	<a href="#">Download</a>	-	-
E-MTAB-5544	Toxicity of the main electronic cigarette components, propylene glycol, glycerin and nicotine in Sprague Dawley rats in a 90-day OECD inhalation study complemented with molecular endpoints (Liver)	transcription profiling by array	Rattus norvegicus	32	03/11/2017	<a href="#">Download</a>	<a href="#">Download</a>	-	-
E-MTAB-6129	Determination by ChIP-chip of the binding sites of the developmental transcription regulator BldC in the genome of Streptomyces venezuelae ATCC 33323	ChIP-chip by array	Streptomyces venezuelae	4	01/11/2017	<a href="#">Download</a>	<a href="#">Download</a>	15	-

Accession number

Experiment type

Number of hybridisations, sequencing libraries



# Data mining with ArrayExpress

Browse ArrayExpress

## Hands-on activity

Find the biggest experiments (in terms of number of assays). Now display the top 100 most viewed experiments on one page



[www.ebi.ac.uk/arrayexpress/experiments/browse.html](http://www.ebi.ac.uk/arrayexpress/experiments/browse.html)



# ArrayExpress: Experimental variable

Experimental variable



It is the main factor that you are investigating

Transcription profiling of blood from smokers, non-smokers and former smokers to identify gene expression signature for cigarette smoke exposure response

organism > Homo sapiens

age > 22, 57, 43, 39 year, etc.

sex > male OR female

organism part > blood

disease > normal

ethnic group > Caucasian OR African American

clinical history > smoker, former smoker OR non-smoker



# ArrayExpress: Experimental variable

Experimental variable



It is the main factor that you are investigating

Transcription profiling of blood from smokers (with or without COPD), non-smokers and former smokers to identify gene expression signature for cigarette smoke exposure response

organism > Homo sapiens

age > 22, 57, 43, 39 year, etc.

sex > male OR female

organism part > blood

ethnic group > Caucasian OR African American

disease > normal OR COPD

clinical history > smoker, former smoker OR non-smoker



# ArrayExpress: Experimental variable

MIAME & MAGE-TAB

## Hands-on activity

Go to experiment E-GEO-49515, find the experimental variable and the groups of samples compared. Download the SDRF file and figure out which file belongs to each category



[www.ebi.ac.uk/arrayexpress](http://www.ebi.ac.uk/arrayexpress)



# ArrayExpress: Experimental variable

	A	B	C
1	Source Name	Array Data File	FactorValue [disease]
2	GSM1200316 1	GSM1200316_PAN-PBMC-S03.CEL	pancreatic cancer
3	GSM1200315 1	GSM1200315_PAN-PBMC-S02.CEL	pancreatic cancer
4	GSM1200314 1	GSM1200314_PAN-PBMC-S01.CEL	pancreatic cancer
5	GSM1200313 1	GSM1200313_NOR-PBMC-S10.CEL	normal
6	GSM1200312 1	GSM1200312_NOR-PBMC-S09.CEL	normal
7	GSM1200311 1	GSM1200311_NOR-PBMC-S08.CEL	normal
8	GSM1200310 1	GSM1200310_NOR-PBMC-S07.CEL	normal
9	GSM1200309 1	GSM1200309_NOR-PBMC-S06.CEL	normal
10	GSM1200308 1	GSM1200308_NOR-PBMC-S05.CEL	normal
11	GSM1200307 1	GSM1200307_NOR-PBMC-S04.CEL	normal
12	GSM1200306 1	GSM1200306_NOR-PBMC-S03.CEL	normal
13	GSM1200305 1	GSM1200305_NOR-PBMC-S02.CEL	normal
14	GSM1200304 1	GSM1200304_NOR-PBMC-S01.CEL	normal
15	GSM1200303 1	GSM1200303_HCC-PBMC-S10.CEL	hepatocellular carcinoma
16	GSM1200302 1	GSM1200302_HCC-PBMC-S09.CEL	hepatocellular carcinoma
17	GSM1200301 1	GSM1200301_HCC-PBMC-S08.CEL	hepatocellular carcinoma
18	GSM1200300 1	GSM1200300_HCC-PBMC-S07.CEL	hepatocellular carcinoma
19	GSM1200299 1	GSM1200299_HCC-PBMC-S06.CEL	hepatocellular carcinoma
20	GSM1200298 1	GSM1200298_HCC-PBMC-S05.CEL	hepatocellular carcinoma
21	GSM1200297 1	GSM1200297_HCC-PBMC-S04.CEL	hepatocellular carcinoma
22	GSM1200296 1	GSM1200296_HCC-PBMC-S03.CEL	hepatocellular carcinoma
23	GSM1200295 1	GSM1200295_HCC-PBMC-S02.CEL	hepatocellular carcinoma
24	GSM1200294 1	GSM1200294_HCC-PBMC-S01.CEL	hepatocellular carcinoma
25	GSM1200293 1	GSM1200293_GAS-PBMC-S03.CEL	gastric cancer
26	GSM1200292 1	GSM1200292_GAS-PBMC-S02.CEL	gastric cancer
27	GSM1200291 1	GSM1200291_GAS-PBMC-S01.CEL	gastric cancer



# Data mining with ArrayExpress

Data mining: Discover datasets to analyse yourself

*Find RNA-seq experiments related to human autoimmune disease*

main search box

filter search box

The screenshot shows the ArrayExpress homepage. At the top right is a search bar with a placeholder 'Search' and a magnifying glass icon. Below it is an 'advanced search' link. A red box highlights the search bar area. At the bottom left, there is a yellow button labeled 'Filter search results' with a funnel icon. A red box highlights this button. The navigation bar at the top includes links for Home, Browse (which is highlighted), Submit, Help, About ArrayExpress, Contact Us, and Login.

[www.ebi.ac.uk/arrayexpress/browse.html](http://www.ebi.ac.uk/arrayexpress/browse.html)



# Data mining with ArrayExpress

Data mining: Discover datasets to analyse yourself

*Find RNA-seq experiments related human autoimmune disease*

Filter search results

By organism:

Homo sapiens

By experiment type:

RNA assay

Sequencing assay

By array:

All arrays

ArrayExpress data only

Reset filters

Filter

"autoimmune dis

autoimmune disease

- Autoimmune Hepatitis
- Behcet's syndrome
- CNS demyelinating **autoimmune disease**
- Eosinophilia-Myalgia Syndrome
- Guillain-Barre syndrome
- Myasthenia gravis
- Sjogren syndrome
- Susac Syndrome
- Vitiligo
- Wegener's granulomatosis
- anti-neutrophil antibody associated vasculitis
- antiphospholipid antibodies
- arthritis
- autoimm

Efficient search via  
ontology-driven query  
expansion



# Ontology-driven query expansion

**Ontology Lookup Service**

Home | **Ontologies** | Documentation | About

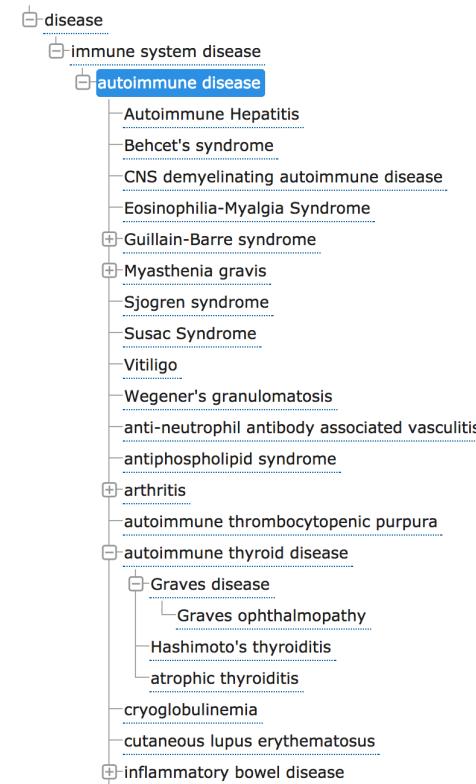
OLS > Experimental Factor Ontology > EFO:0005140

## autoimmune disease

[http://www.ebi.ac.uk/efo/EFO\\_0005140](http://www.ebi.ac.uk/efo/EFO_0005140)

Much richer queries by  
using the hierarchy within  
the ontology

Return subclasses when a  
higher level superclass is  
used in the query



[www.ebi.ac.uk/ols/ontologies/efo](http://www.ebi.ac.uk/ols/ontologies/efo)



# Data mining with ArrayExpress

Data mining: Discover datasets to analyse yourself

*Find RNA-seq experiments related human autoimmune disease*

Search results for "autoimmune disease"

Filtered by organism **Homo sapiens**, experiment type "sequencing assay", experiment type "rna assay"

Page 1 2

Showing 1 - 25 of 36 experiments

Page size 25 50 100 250 500

Accession	Title	Type	Organism	Assays	Released	Processed	Raw	Views	Atlas
E-GEOD-60424	Next generation sequencing of human immune cell subsets across diseases	RNA-seq of coding RNA	Homo sapiens	134	06/01/2015	-		3054	
E-MTAB-1568	RNA-seq of coding RNA in human plasma cells isolated from individuals with colorectal cancer, ulcerative colitis and normal individuals	RNA-seq of coding RNA	Homo sapiens	9	29/03/2013	-		1078	-
E-GEOD-46579	A blood based 12-miRNA signature of Alzheimer patients	RNA-seq of non coding RNA	Homo sapiens	70	17/06/2013	-		824	-
E-GEOD-57945	Core Ileal Transcriptome in Pediatric Crohn Disease	RNA-seq of coding RNA	Homo sapiens	359	24/07/2014			623	-
E-MTAB-4304	RNA-Seq analysis of human intact and damaged osteoarthritic cartilage following total knee replacement	RNA-seq of coding RNA	Homo sapiens	22	06/04/2016	-		487	-
E-GEOD-83139	Single cell RNA-seq of human pancreatic endocrine cells from Juvenile, adult control and type 2 diabetic donors	RNA-seq of coding RNA	Homo sapiens	635	05/07/2016	-		328	-



# Data mining with ArrayExpress

Samples  
and files

Experiment  
description

Experiment  
type

MINSEQE  
compliance score

Links to  
data

## E-GEOD-60424 - Next generation sequencing of human immune cell subsets across diseases

Status *Released on 6 January 2015, last updated on 25 February 2016*

Organism **Homo sapiens**

Samples (134) [Click for detailed sample information and links to data](#)  
*↳ found inside: multiple sclerosis, Type 1 Diabetes*

Protocols (2) [Click for detailed protocol information](#)

Description This study compared whole transcriptome signatures of 6 immune cell subsets and whole blood from patients with an array of immune-associated diseases. Fresh blood samples were collected from healthy subjects and subjects diagnosed **type 1 diabetes**, amyotrophic lateral sclerosis, and sepsis, as well as **multiple sclerosis** patients before and 24 hours after the first treatment with IFN-beta. At the time of blood draw, an aliquot of whole blood was collected into a Tempus tube (Invitrogen), while the remainder of the primary fresh blood sample was processed to highly pure populations of neutrophils, monocytes, B cells, CD4 T cells, CD8 T cells, and natural killer cells. RNA was extracted from each of these cell subsets, as well as the whole blood samples, and processed into RNA sequencing (RNAseq) libraries (Illumina TruSeq). Sequencing libraries were analyzed on an Illumina HiScan, with a target read depth of ~20M reads. Reads were demultiplexed, mapped to human gene models (ENSEMBL), and tabulated using HTSeq. Read count data were normalized by the TMM procedure (edgeR package). We performed whole genome RNAseq profiling of immune cell subsets and whole blood from subjects with an array of immune-associated diseases.

Experiment type **RNA-seq of coding RNA**

Contacts Scott Presnell <SPresnell@benaroyaresearch.org>, Carla J Greenbaum, Cate Speake, Damien Chaussabel, Elizabeth Whalen, Jane H Buckner, Kimm K O'Brien, Michael J Mason, Peter S Linsley, Quynh-Anh Nguyen, Scott R Presnell, Uma Malhotra, Vivian H Gersuk

Citation [Copy number loss of the interferon gene cluster in melanomas is linked to reduced T cell infiltrate and poor patient prognosis.](#) Linsley PS, Speake C, Whalen E, Chaussabel D. , [Europe PMC 25314013](#)

MINSEQE \* \* \* - \*

Exp. design Protocols Variables Processed Seq. reads

Files Investigation description [↓ E-GEOD-60424.idf.txt](#)  
Sample and data relationship [↓ E-GEOD-60424.sdrf.txt](#)  
Additional data (1) [↓ E-GEOD-60424.additional.1.zip](#)

Links [Click to browse all available files](#)

Expression Atlas - E-GEOD-60424

ENA - SRP045500, GEO - GSE60424

Send E-GEOD-60424 data to



# Data mining with ArrayExpress

E-GEOD-60424 - Next generation sequencing of human immune cell subsets across diseases

[Display full sample-data table](#)

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

Page 1 2 3 4 5 6 .. 11

Showing 1 - 25 of 268 rows

Page size 25 50 100 250 500

Source Name	name	Sample Attributes							cell type	disease	ENA	FASTQ
		age	cell type	disease	individual	organism	ethnic group	sex				
GSM1479433 1	32 (year)	whole blood	normal	44	Homo sapiens	hispanic	female		whole blood	norm	<a href="#">EN</a>	<a href="#">FT</a>
GSM1479433 1	32 (year)	whole blood	normal	44	Homo sapiens	hispanic	female		whole blood	norm	<a href="#">EN</a>	<a href="#">FT</a>
GSM1479434 1	52 (year)	whole blood	multiple sclerosis	31	Homo sapiens	white	female	smoker	whole blood	multi	<a href="#">EN</a>	<a href="#">FT</a>
GSM1479434 1	52 (year)	whole blood	multiple sclerosis	31	Homo sapiens	white	female	smoker	whole blood	multi	<a href="#">EN</a>	<a href="#">FT</a>
GSM1479435 1	52 (year)	whole blood	multiple sclerosis	33	Homo sapiens	white	female	smoker	whole blood	multi	<a href="#">EN</a>	<a href="#">FT</a>
GSM1479435 1	52 (year)	whole blood	multiple sclerosis	33	Homo sapiens	white	female	smoker	whole blood	multi	<a href="#">EN</a>	<a href="#">FT</a>
GSM1479436 1	24 (year)	whole blood	Type 1 Diabetes	34	Homo sapiens	white	female		whole blood	Type	<a href="#">EN</a>	<a href="#">FT</a>
GSM1479436 1	24 (year)	whole blood	Type 1 Diabetes	34	Homo sapiens	white	female		whole blood	Type	<a href="#">EN</a>	<a href="#">FT</a>
GSM1479437 1	27 (year)	whole blood	Type 1 Diabetes	37	Homo sapiens	white	female		whole blood	Type	<a href="#">EN</a>	<a href="#">FT</a>
GSM1479437 1	27 (year)	whole blood	Type 1 Diabetes	37	Homo sapiens	white	female		whole blood	Type	<a href="#">EN</a>	<a href="#">FT</a>
GSM1479438 1	32 (year)	neutrophils	normal	44	Homo sapiens	hispanic	female		neutrophils	norm	<a href="#">EN</a>	<a href="#">FT</a>
GSM1479438 1	32 (year)	neutrophils	normal	44	Homo sapiens	hispanic	female		neutrophils	norm	<a href="#">EN</a>	<a href="#">FT</a>
		(year)	monocytes	normal		hispanic	female		monocytes	norm	<a href="#">EN</a>	<a href="#">FT</a>
		(year)	monocytes	normal		hispanic	female					
		(year)	B-Cells	normal		hispanic	female					
		(year)	B-Cells	normal		hispanic	female					

Unique sample name for each biological replicate

Sample attributes describing the source material

Experimental variables

Links to download data



# Data mining with ArrayExpress

Data mining: Discover datasets to analyse yourself

*Find RNA expression arrays from human patients with diabetes*

## Search results for diabetes

Filtered by organism **Homo sapiens**, experiment type **"array assay"**, experiment type **"rna assay"**

Page **1** 2 3 4 5 6 .. 11

Showing **1 - 25** of **253** experiments

Page size **25** 50 100 250 500

Accession	Title	Type	Organism	Assays	Released	Processed	Raw	Views	Atlas
E-MTAB-2976	Global gene expression of bone marrow multipotent mesenchymal stromal cells isolated from <b>type 1 diabetes</b> patients and healthy donors	transcription profiling by array	<b>Homo sapiens</b>	8	01/12/2014		-	272	-
E-MTAB-2902	Transcriptional profiling by array of microRNAs of human peripheral blood mononuclear cells - PBMC - from control individuals for <b>Type 2 diabetes mellitus</b> patients	microRNA profiling by array	<b>Homo sapiens</b>	9	01/04/2015		255	-	
E-MTAB-2899	Transcriptional profiling by array of microRNAs from human peripheral blood mononuclear cells - PBMC - of <b>Type 2 diabetes mellitus</b> patients	microRNA profiling by array							
E-MTAB-2896	Transcriptional Profiles in Peripheral Blood Mononuclear Cells - PBMC - from individual controls for <b>Type 2 Diabetes Mellitus</b>	transcription profiling by array							

Exact match to search term

Matched EFO synonyms to search term

Matched EFO child term of search term



# ArrayExpress – Advanced search

diabetes

Examples: E-MEXP-31, cancer, p53, Geuvadis

advanced search

Search in all experimental fields,  
e.g. experiment description,  
protocols, publication title...

evv:diabetes

advanced search

fieldname:value

Limit your search only to  
experiments in which “diabetes” is  
the value of the experimental variable

## Search results for evv:diabetes

Filtered by organism **Homo sapiens**, experiment type **"rna assay"**, experiment type **"sequencing assay"**

3 experiments

Accession	Title	Type	Organism	Assays	Released	Processed	Raw	Views	Atlas
E-MTAB-5061	Single-cell RNA-seq analysis of human pancreas from healthy individuals and type 2 diabetes patients	RNA-seq of coding RNA from single cells	Homo sapiens	3514	22/09/2016			3091	
E-MTAB-5060	Whole-islet RNA-sequencing analysis of human pancreas from healthy individuals and type 2 diabetes patients	RNA-seq of coding RNA	Homo sapiens	7	22/09/2016			903	
E-GEO-60424	Next generation sequencing of human immune cell subsets across diseases	RNA-seq of coding RNA	Homo sapiens	134	06/01/2015	-		3163	

Export table in Tab-delimited format

Export matching metadata in XML format

Subscribe to RSS feed matching this search



# ArrayExpress – Advanced search

Field name	Search scope	Example use case
<b>accession</b>	Experiment primary or secondary accession	accession:E-MTAB-1234
<b>array</b>	Array design accession or name	array:A-AFFY-33
<b>ev (or ef)</b>	Experimental variable (or factor), the name of the main variable under study in an experiment. E.g. if the variable is "sex" in a human study, the researchers would be comparing between male and female samples, and "sex" is not merely an attribute the samples happen to have. Has <a href="#">EFO expansion</a> .	ev:genotype
<b>evv (or efv)</b>	The value of an experimental variable (or factor). E.g. The values for "genotype" factor can be "wild type", "p53-/-". Has <a href="#">EFO expansion</a> .	evv:"wild type"
<b>expdesign</b>	Experiment design type, related to the questions being addressed by the study, e.g. "time series design", "stimulus or stress design", "genetic modification design". Has <a href="#">EFO expansion</a> .	expdesign:"time series"
<b>exptype</b>	Experiment type, related to the assay technology used. See the full <a href="#">list of experiment types in ArrayExpress</a> . Has <a href="#">EFO expansion</a> .	exptype:"RNA-seq of coding RNA"
<b>gxa</b>	Presence/absence of an ArrayExpress experiment in the <a href="#">Expression Atlas</a> . Use values "true" and "false" respectively.	gxa:true
<b>pmid</b>	PubMed identifier for a publication.	pmid:16553887
<b>sa</b>	Sample attribute values. Has <a href="#">EFO expansion</a> .	sa:fibroblast
<b>sac</b>	Sample attribute category. Find experiments that have a specific sample attribute defined, e.g. "age", "strain". Has <a href="#">EFO expansion</a> .	sac:age
<b>organism</b>	Species of the samples. Can use common name (e.g. "mouse") or binomial nomenclature/Latin names (e.g. "Mus musculus"). Has <a href="#">EFO expansion</a> .	organism:"homo sapiens"



# ArrayExpress – Advanced search

Data mining: Discover datasets to analyse yourself

*Find experiments comparing healthy (normal) and rheumatoid arthritis patients*

evv: "rheu

**rheumatic**

**rheumatic disease**

**rheumatic fever**

**rheumatic heart disease**

**Rheumatic Nodule**

**rheumatoid**

**rheumatoid arthritis**

Felty's syndrome

chronic childhood arthritis

pauciarticular juvenile **rheumatoid arthritis**

systemic juvenile idiopathic arthritis

**rheumatoid factor measurement**

**rheumatoid factor seropositivity measurement**

**rheumatology**

Search results for evv: "rheumatoid arthritis"

Showing 1 - 25 of 50 experiments



# ArrayExpress – Advanced search

Data mining: Discover datasets to analyse yourself

*Find experiments comparing healthy (normal) and rheumatoid arthritis patients*

evv:"rheumatoid arthritis" AND evv:normal

19 experiments

evv:"rheumatoid arthritis" AND (evv:normal OR evv:healthy)

Showing 1 - 25 of 28 experiments



# ArrayExpress – Advanced search

Data mining: Discover datasets to analyse yourself

*Find RNA expression arrays from human cancer samples  
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Examples: E-MEXP-31, cancer, p53, Geuvadis

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In pairs

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# Let's try ArrayExpress

 **ArrayExpress**

"Barrett's esophagus" AND ev:"disease staging" 

Examples: E-MEXP-31, cancer, p53, Geuvadis 

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Filtered by organism **Homo sapiens**, experiment type **"rna assay"**, experiment type **"sequencing assay"**

1 experiment

Accession	Title	Type	Organism	Assays	Released	Processed	Raw	Views	Atlas
E-MTAB-4054	Whole transcriptome profiling of Esophageal adenocarcinoma and Barrett's	RNA-seq of coding RNA	Homo sapiens	63	23/07/2017	-		177	-

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## E-MTAB-4054 - Whole transcriptome profiling of Esophageal adenocarcinoma and Barrett's

Status	<i>Submitted on 11 November 2015, released on 23 July 2017, last updated yesterday</i>
Organism	Homo sapiens
Samples (51)	<a href="#">Click for detailed sample information and links to data</a>
Protocols (4)	<a href="#">Click for detailed protocol information</a>
Description	RNA-seq was performed on esophageal adenocarcinoma (EAC), Barrett's without dysplasia, Barrett's with low-grade dysplasia (LGD) and normal squamous esophagus tissue to find early alterations in the transcriptome level turning Barrett's dysplastic.
Experiment types	RNA-seq of coding RNA, disease state design
Contact	<a href="mailto:j.maag@garvan.org.au">✉ Jesper LV Maag &lt;j.maag@garvan.org.au&gt;</a>
Citation	<a href="#">Novel Aberrations Uncovered in Barrett's Esophagus and Esophageal Adenocarcinoma Using Whole Transcriptome Sequencing</a> . Maag J, Fisher OM, Levert-Mignon AJ, Kaczorowski DC, Thomas ML, Hussey D, Watson D, Wettstein A, Bobryshev YV, Edwards M, Dinger ME, Lord RV, Europe PMC 28751461
MINSEQE	— — — —
	Exp. design   Protocols   Variables   Processed   Seq. reads
Files	Investigation description <a href="#"> E-MTAB-4054.idf.txt</a> Sample and data relationship <a href="#"> E-MTAB-4054.sdrf.txt</a> <a href="#">Click to browse all available files</a>
Links	<a href="#">ENA - ERP013206</a> <a href="#">Send E-MTAB-4054 data to  GENOMESPACE</a>



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E-MTAB-4054 - Whole transcriptome profiling of Esophageal adenocarcinoma and Barrett's

Display summary				Export table in Tab-delimited format		
Source Name	Protocol REF	Performer	Assay Name	Comment[technical replicate group]	Technology Type	Comment[ENA_EX]
N09	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N09_R		sequencing assay	ERX1220581
N10	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N10_R		sequencing assay	ERX1220582
N10	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N10_R		sequencing assay	ERX1220582
B05	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B05_Human_CCGTCC_R	group1	sequencing assay	ERX1220524
B05	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B05_Human_CCGTCC_R	group1	sequencing assay	ERX1220524
B05	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B05_R	group1	sequencing assay	ERX1220525
B05	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B05_R	group1	sequencing assay	ERX1220525
LNC14	P-MTAB-47385	Dominik C. Kaczorowski	LNC_14_Human_GTGAAA_R	group10	sequencing assay	ERX1220566
LNC14	P-MTAB-47385	Dominik C. Kaczorowski	LNC_14_Human_GTGAAA_R	group10	sequencing assay	ERX1220566
				group10	sequencing assay	ERX1220567
				group10	sequencing assay	ERX1220567
				group11	sequencing assay	ERX1220575
				group11	sequencing assay	ERX1220575
				group11	sequencing assay	ERX1220576
				group11	sequencing assay	ERX1220576
				group12	sequencing assay	ERX1220579
N08	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N08_Human_CCGTCC_R	group12	sequencing assay	ERX1220579
N08	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N08_R	group12	sequencing assay	ERX1220580
N08	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N08_R	group12	sequencing assay	ERX1220580
B06	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B06_Human_ATGTCA_R	group2	sequencing assay	ERX1220526
B06	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B06_Human_ATGTCA_R	group2	sequencing assay	ERX1220526
B06	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B06_R	group2	sequencing assay	ERX1220527
B06	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B06_R	group2	sequencing assay	ERX1220527
B07	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B07_Human_GATCAG_R	group3	sequencing assay	ERX1220528
B07	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B07_Human_GATCAG_R	group3	sequencing assay	ERX1220528

12 samples (2 normal, 5 Barrett's esophagus without dysplasia and 5 esophageal adenocarcinoma)



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E-MTAB-4054 - Whole transcriptome profiling of Esophageal adenocarcinoma and Barrett's

Display summary		Showing 76 - 100 of 126 rows			Export table in Tab-delimited format	
Source Name	Protocol REF	Performer	Assay Name	Comment[technical replicate group]	Technology Type	Comment[ENA_EX]
N09	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N09_R		sequencing assay	ERX1220581
N10	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N10_R		sequencing assay	ERX1220582
N10	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N10_R		sequencing assay	ERX1220582
B05	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B05_Human_CCGTCC_R	group1	sequencing assay	ERX1220524
B05	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B05_Human_CCGTCC_R	group1	sequencing assay	ERX1220524
B05	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B05_R	group1	sequencing assay	ERX1220525
B05	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B05_R	group1	sequencing assay	ERX1220525
LNC14	P-MTAB-47385	Do			sequencing assay	ERX1220566
LNC14	P-MTAB-47385	Do			sequencing assay	ERX1220566
LNC14	P-MTAB-47385	Do			sequencing assay	ERX1220567
LNC14	P-MTAB-47385	Dominik C. Kaczorowski	LNC_14_R	group10	sequencing assay	ERX1220567
N04	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N04_Human_AGTTCC_R	group11	sequencing assay	ERX1220575
N04	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N04_Human_AGTTCC_R	group11	sequencing assay	ERX1220575
N04	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N04_R	group11	sequencing assay	ERX1220576
N04	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N04_R	group11	sequencing assay	ERX1220576
N08	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N08_Human_CCGTCC_R	group12	sequencing assay	ERX1220579
N08	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N08_Human_CCGTCC_R	group12	sequencing assay	ERX1220579
N08	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N08_R	group12	sequencing assay	ERX1220580
N08	P-MTAB-47385	Dominik C. Kaczorowski	LNC_N08_R	group12	sequencing assay	ERX1220580
B06	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B06_Human_ATGTCA_R	group2	sequencing assay	ERX1220526
B06	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B06_Human_ATGTCA_R	group2	sequencing assay	ERX1220526
B06	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B06_R	group2	sequencing assay	ERX1220527
B06	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B06_R	group2	sequencing assay	ERX1220527
B07	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B07_Human_GATCAG_R	group3	sequencing assay	ERX1220528
B07	P-MTAB-47385	Dominik C. Kaczorowski	LNC_B07_Human_GATCAG_R	group3	sequencing assay	ERX1220528



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Disease cohort	Number of samples	Number of technical replicates
normal	17	2
Barrett's esophagus non-dysplastic	14	5
Barrett's esophagus low-grade dysplasia	8	0
esophageal adenocarcinoma	12	5
<b>Total number of samples</b>	<b>51</b>	12
Number of files (paired-end libraries)	102	24
<b>Total number of files</b>	<b>126</b>	

# EMBL-EBI Resources and tools for genomics and proteomics

Discover functional genomics data  
with ArrayExpress

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6 December 2017

