


**Using  
ArrayStar  
with a  
public dataset**

Jean-Yves Sgro



**ArrayStar**

Part of Lasergene Genomics Suite for analysis:

- Global gene expression
- Variation across groups

Optional Qseq module to analyze RNA-Seq, ChIP-Seq, CNV, and miRNA data.

# Public repositories

2 cross referenced world databases for microarray and Next Gen data:

USA: Gene Omnibus (GEO)  
([www.ncbi.nlm.nih.gov/geo](http://www.ncbi.nlm.nih.gov/geo))

Europe (UK): ArrayExpress (EMBL/EBI)  
([www.ebi.ac.uk/arrayexpress](http://www.ebi.ac.uk/arrayexpress))

## Search example: rhinovirus

The screenshot shows the ArrayExpress search results for 'rhinovirus'. The search bar at the top contains the text 'rhinovirus'. Below the search bar, the page displays 'ArrayExpress search results for rhinovirus'. There are filters for 'By organism' (set to 'All organisms') and 'By experiment type' (set to 'All assays by molecule'). A table of results is shown below, with columns for Accession, Title, Type, Organism, Assays, Released, Processed, Raw, and Atlas. The table lists several experiments related to rhinovirus, such as 'Identification of candidate rhinovirus C (RV-C) receptors by gene expression analysis' and 'Whole blood mRNA expression profiling of host molecular networks in neonatal sepsis'.

Accession	Title	Type	Organism	Assays	Released	Processed	Raw	Atlas
E-GEOD-41395	Identification of candidate rhinovirus C (RV-C) receptors by gene expression analysis	transcription profiling by array	Homo sapiens	18	01/11/2014	▲	▲	-
E-GEOD-23504	Whole blood mRNA expression profiling of host molecular networks in neonatal sepsis	transcription profiling by array	Homo sapiens	170	12/08/2014	▲	▲	-
E-GEOD-40113	Concordance between ex vivo PBMC and in vivo human infections confirmed by high-throughput analysis of single-subject transcriptomes	transcription profiling by array	Homo sapiens	8	07/08/2014	▲	▲	-
E-GEOD-53274	Human rhinovirus infection causes different DNA methylation changes in nasal epithelial cells from healthy and asthmatic subjects	methylation profiling	Homo sapiens	18	28/07/2014	▲	▲	-
E-GEOD-29385	Influenza virus serotype association to global whole blood transcriptional changes	transcription profiling by array	Homo sapiens	465	01/04/2014	▲	▲	-
E-GEOD-29384	Global transcriptional changes induced by rhinovirus infection in-vitro	transcription profiling by array	Homo sapiens	120	01/04/2014	▲	▲	-
E-GEOD-49371	Major and Minor Group Human Rhinovirus Response in Human Macrophages	RNA-seq of coding RNA	Homo sapiens	3	14/03/2014	▲	▲	-
E-GEOD-34558	Lipopolysaccharide modulates rhinovirus-induced chemokine secretion in monocytes and macrophages	transcription profiling by array	Homo sapiens	2	31/01/2014	▲	▲	-
E-GEOD-38960	Genome-wide analysis of whole blood transcriptional response to Respiratory Syncytial Virus, Influenza and Rhinovirus lower respiratory tract infection (LRTI) in children	transcription profiling by array	Homo sapiens	241	12/11/2013	▲	▲	-
E-GEOD-51292	Expression data from airway epithelial cells stimulated with Reovirus C from patients with asthma, rhinitis, and healthy controls	transcription profiling by array	Homo sapiens	68	18/10/2013	▲	▲	-
E-GEOD-49396	Whole blood transcriptional signature distinguishes viral infection from bacterial infection in healthy young children	transcription profiling by array	Homo sapiens	65	15/10/2012	▲	▲	-
E-GEOD-27972	Human airway epithelial responses to rhinovirus infection and cigarette smoke extract alone and in combination	transcription profiling by array	Homo sapiens	16	13/03/2011	▲	▲	-
E-GEOD-2228	E-Predict Training Data Set and Examples	unknown experiment type	Viruses	56	10/06/2010	▲	▲	-
E-GEOD-11396	Transcription profiling by array of cultured bronchial epithelial cells from patients with asthma and healthy individuals after infection with human rhinovirus	transcription profiling by array	Homo sapiens	22	13/11/2008	▲	▲	▲
E-GEOD-11348	Transcription profiling by array of human nasal epithelium from patients infected with HRV-16 rhinovirus	transcription profiling by array	Homo sapiens	93	12/06/2008	▲	▲	▲
E-GEOD-470	Transcription profiling of human bronchial epithelial cells from normal and asthmatic subjects exposed to either ozone or rhinovirus	transcription profiling by array	Homo sapiens	12	12/12/2007	▲	▲	-

At the bottom of the page, there are links for 'Export table in Tab-delimited format', 'Export matching metadata in XML format', and 'Subscribe to RSS feed matching this search'.

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

EMBL-EBI Services Research Training About us

# ArrayExpress

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

Home **Experiments** Arrays Submit Help About ArrayExpress Feedback Login

ArrayExpress > Experiments > E-GEOD-27973

## E-GEOD-27973 - Human airway epithelial responses to rhinovirus infection and cigarette smoke extract alone and in combination

Status	Released on 15 March 2011												
Organism	Homo sapiens												
Samples (16)	<a href="#">Click for detailed sample information and links to data</a>												
Array (1)	A-AFFY-44 - Affymetrix GeneChip Human Genome U133 Plus 2.0 [HG-U133_Plus_2]												
Protocols (8)	<a href="#">Click for detailed protocol information</a>												
Description	This study was performed to test the hypothesis that cigarette smoke extract would alter the responses of primary cultures of human bronchial epithelial cells to infection with purified human rhinovirus 16. The data show marked alterations in rhinovirus-induced expression profiles of a number of genes in the presence of cigarette smoke extract (CSE). Cultured epithelial cells from each of 4 donors were exposed to medium alone, rhinovirus 16 (RV16) alone, CSE alone, or RV16 in the presence of CSE. After a 24 h incubation gene expression was assessed.												
Experiment type	transcription profiling by array												
Contacts	David Proud <dproud@ucalgary.ca>, Richard Leigh												
MIAME	<table border="1"> <thead> <tr> <th>Platforms</th> <th>Protocols</th> <th>Factors</th> <th>Processed</th> <th>Raw</th> </tr> </thead> <tbody> <tr> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> </tbody> </table>	Platforms	Protocols	Factors	Processed	Raw							
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Links	<a href="#">GEO - GSE27973</a> <a href="#">Send E-GEOD-27973 data to GENOMESPACE</a>												

## Today: GEO series GSE27973

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE27973>

Or short URL version: (see page 14)

[1.usa.gov/WiUkmP](http://1.usa.gov/WiUkmP)

NCBI GEO Gene Expression Omnibus

NCBI > GEO > Accession Display

Scope: Self Format: HTML Amount: Quick GEO accession: GSE27973

**Series GSE27973** Query DataSets for GSE27973

Status Public on Mar 15, 2011

Title Human airway epithelial responses to rhinovirus infection and cigarette smoke extract alone and in combination

Organism [Homo sapiens](#)

Experiment type Expression profiling by array

Summary This study was performed to test the hypothesis that cigarette smoke extract would alter the responses of primary cultures of human bronchial epithelial cells to infection with purified human rhinovirus 16. The data show marked alterations in rhinovirus-induced expression profiles of a number of genes in the presence of cigarette smoke extract (CSE).

Overall design Cultured epithelial cells from each of 4 donors were exposed to medium alone, rhinovirus 16 (RV16) alone, CSE alone, or RV16 in the presence of CSE. After a 24 h incubation gene expression was assessed.

Contributor(s) [Proud D, Leigh R](#)

Citation(s) Proud D, Hudy MH, Wiehler S, Zaheer RS et al. Cigarette smoke modulates expression of human rhinovirus-induced airway epithelial host defense genes. *PLoS One* 2012;7(7):e40762. PMID: 22808255

Submission date Mar 15, 2011

Last update date Nov 10, 2014

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Country Canada

## 4 groups

### Series GSE27973

Query DataSets for GSE27973

Status	Public on Mar 15, 2011
Title	Human airway epithelial responses to rhinovirus infection and cigarette smoke extract alone and in combination
Organism	<a href="#">Homo sapiens</a>
Experiment type	Expression profiling by array
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Overall design	Cultured epithelial cells from each of 4 donors were exposed to <b>medium alone</b> , <b>rhinovirus 16 (RV16) alone</b> , <b>CSE alone</b> , or <b>RV16 in the presence of CSE</b> . After a 24 h incubation gene expression was assessed.

**Our analysis today with 2 groups: find the difference between medium alone and RV16 alone**

Platforms (1) [GPL570](#) [HG-U133\_Plus\_2] Affymetrix Human Genome U133 Plus 2.0 Array

Samples (16) [Less...](#)

- [GSM692115](#) Donor 1 - medium
- [GSM692116](#) Donor 1 - RV16
- [GSM692117](#) Donor 1 - CSE
- [GSM692118](#) Donor 1 - RV16+CSE
- [GSM692119](#) Donor 2 - medium
- [GSM692120](#) Donor 2 - RV16
- [GSM692121](#) Donor 2 - CSE
- [GSM692122](#) Donor 2 - RV16+CSE
- [GSM692123](#) Donor 3 - medium
- [GSM692124](#) Donor 3 - RV16
- [GSM692125](#) Donor 3 - CSE
- [GSM692126](#) Donor 3 - RV16+CSE
- [GSM692127](#) Donor 4 - medium
- [GSM692128](#) Donor 4 - RV16
- [GSM692129](#) Donor 4 - CSE
- [GSM692130](#) Donor 4 - RV16+CSE

Relations  
BioProject [PRJNA137767](#)

Analyze with GEO2R

Download family	Format
<a href="#">SOFT formatted family file(s)</a>	SOFT <a href="#">?</a>
<a href="#">MINIML formatted family file(s)</a>	MINIML <a href="#">?</a>
<a href="#">Series Matrix File(s)</a>	TXT <a href="#">?</a>

Supplementary file	Size	Download	File type/resource
<a href="#">GSE27973_RAW.tar</a>	76.5 Mb	<a href="#">(http)(custom)</a>	TAR (of CEL, CHP)

Raw data provided as supplementary file  
Processed data included within Sample table  
Processed data provided as supplementary file

# Sample files

Supplementary file	Size	Download	File type/resource
<a href="#">GSE27973_RAW.tar</a>	76.5 Mb	<a href="#">(http)(custom)</a>	TAR (of CEL, CHP)

Raw data provided as supplementary file  
Processed data included within Sample table  
Processed data provided as supplementary file

Custom GSE27973\_RAW.tar archive:

Supplementary file	File size
<input type="checkbox"/> <a href="#">GSM692115.CEL.gz</a>	4.6 Mb
<input type="checkbox"/> <a href="#">GSM692115.CHP.gz</a>	300.1 Kb
<input type="checkbox"/> <a href="#">GSM692116.CEL.gz</a>	4.5 Mb
<input type="checkbox"/> <a href="#">GSM692116.CHP.gz</a>	301.1 Kb
<input type="checkbox"/> <a href="#">GSM692117.CEL.gz</a>	4.5 Mb
<input type="checkbox"/> <a href="#">GSM692117.CHP.gz</a>	302.2 Kb
<input type="checkbox"/> <a href="#">GSM692118.CEL.gz</a>	4.3 Mb
<input type="checkbox"/> <a href="#">GSM692118.CHP.gz</a>	301.9 Kb
<input type="checkbox"/> <a href="#">GSM692119.CEL.gz</a>	4.6 Mb
<input type="checkbox"/> <a href="#">GSM692119.CHP.gz</a>	299.8 Kb
<input type="checkbox"/> <a href="#">GSM692120.CEL.gz</a>	4.6 Mb
<input type="checkbox"/> <a href="#">GSM692120.CHP.gz</a>	300.3 Kb
<input type="checkbox"/> <a href="#">GSM692121.CEL.gz</a>	4.5 Mb
<input type="checkbox"/> <a href="#">GSM692121.CHP.gz</a>	300.8 Kb
<input type="checkbox"/> <a href="#">GSM692122.CEL.gz</a>	4.5 Mb
<input type="checkbox"/> <a href="#">GSM692122.CHP.gz</a>	303.4 Kb
<input type="checkbox"/> <a href="#">GSM692123.CEL.gz</a>	4.5 Mb
<input type="checkbox"/> <a href="#">GSM692123.CHP.gz</a>	300.4 Kb
<input type="checkbox"/> <a href="#">GSM692124.CEL.gz</a>	4.6 Mb
<input type="checkbox"/> <a href="#">GSM692124.CHP.gz</a>	300.5 Kb

**Select All**   **0 file(s), 0 b**

2 types:  
 - CEL  
 - CHP

We want the CEL (raw data) files

## Essential: rename files

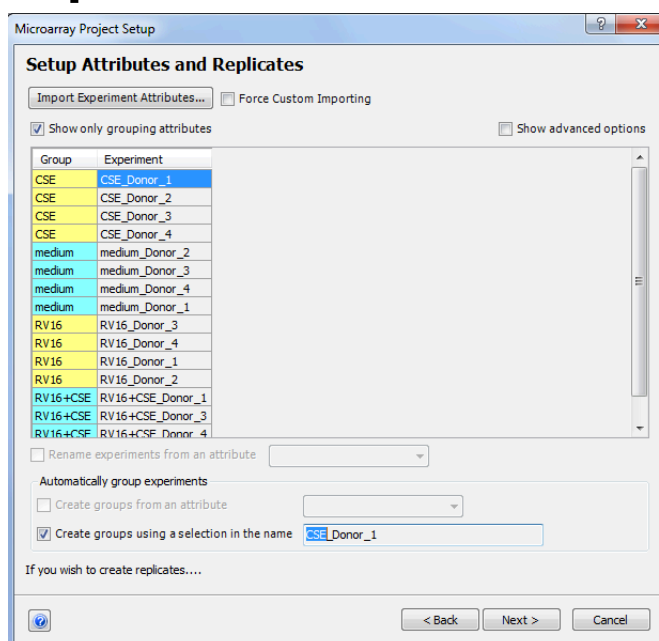
```

RENAME GSM692115.CEL medium_Donor_1.CEL
RENAME GSM692116.CEL RV16_Donor_1.CEL
RENAME GSM692117.CEL CSE_Donor_1.CEL
RENAME GSM692118.CEL RV16+CSE_Donor_1.CEL
RENAME GSM692119.CEL medium_Donor_2.CEL
RENAME GSM692120.CEL RV16_Donor_2.CEL
RENAME GSM692121.CEL CSE_Donor_2.CEL
RENAME GSM692122.CEL RV16+CSE_Donor_2.CEL
RENAME GSM692123.CEL medium_Donor_3.CEL
RENAME GSM692124.CEL RV16_Donor_3.CEL
RENAME GSM692125.CEL CSE_Donor_3.CEL
RENAME GSM692126.CEL RV16+CSE_Donor_3.CEL
RENAME GSM692127.CEL medium_Donor_4.CEL
RENAME GSM692128.CEL RV16_Donor_4.CEL
RENAME GSM692129.CEL CSE_Donor_4.CEL
RENAME GSM692130.CEL RV16+CSE_Donor_4.CEL

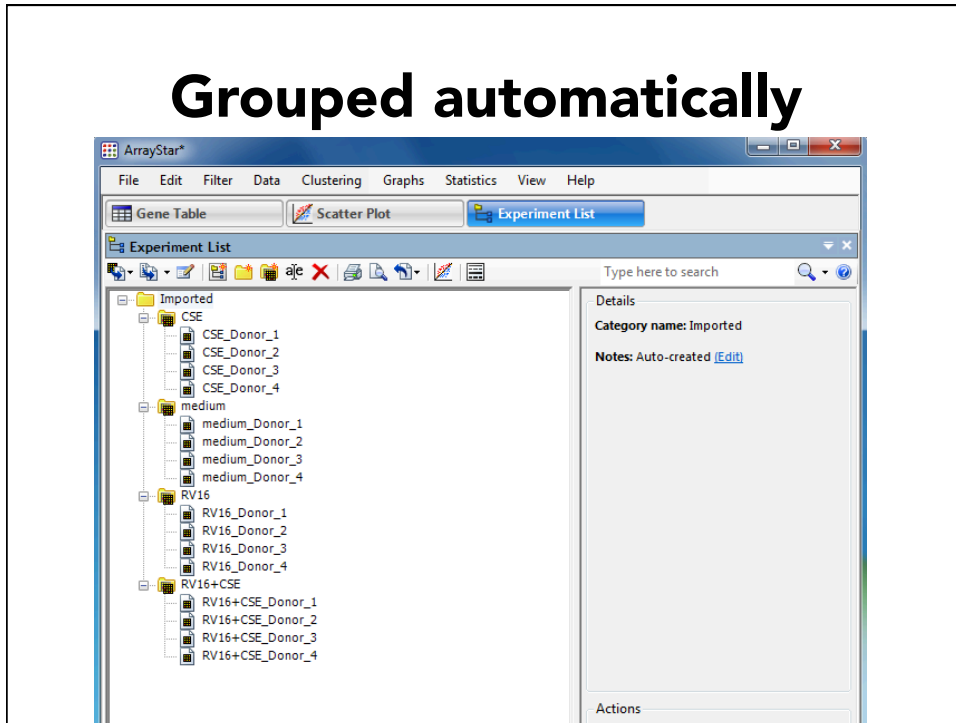
```

Files are ALREADY RENAMED and on the Windows Desktop

## Replicate names: automatic

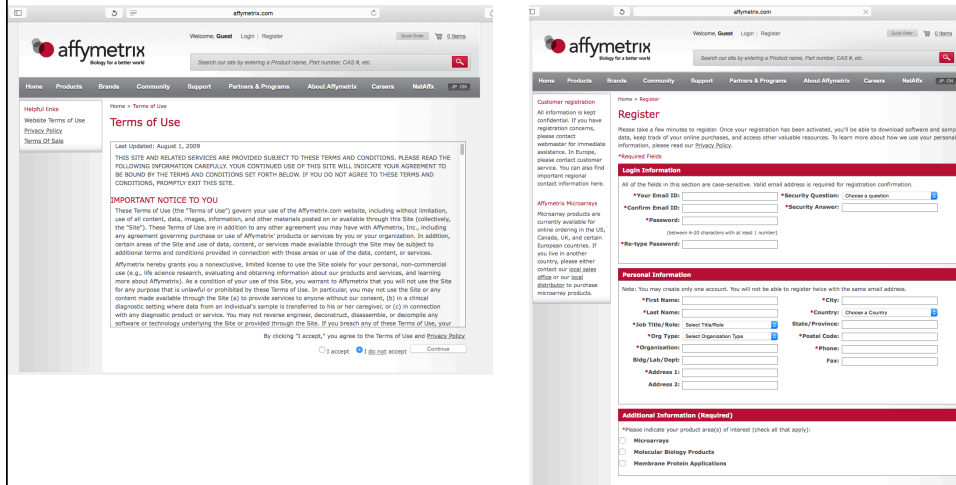


# Grouped automatically



# Register with Affymetrix

Affymetrix.com

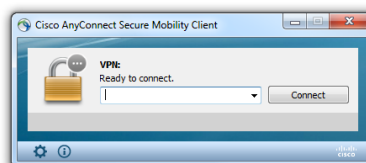


## From home / outside Biochem department

### Step 1:

VPN connection

*See also page 8*



**dept-ra-cssc.vpn.wisc.edu**

### Step 2:

Lasergene software: ArrayStar

