

```
#From a journal article in wheat transcriptomics,
#retrieve the study accession number,
# search google with terms: "accession number E-MTAB-1729"
# this google search returns this url: https://www.ebi.ac.uk/arrayexpress/
experiments/E-MTAB-1729/
#
```

 European Bioinformatics Institute [GB] | <https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1729/> 

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ARRAYEXPRESS / BROWSE / E-MTAB-1729

### E-MTAB-1729 - RNA-seq of coding RNA from near-isogenic lines, harboring either the resistant or the susceptible allele for Fhb1 and Qfhs.ifa-5A, in response to *F. graminearum*

Status	Released on 10 October 2013, last updated on 9 March 2017
Organism	Triticum aestivum
Samples (60)	<a href="#">Click for detailed sample information and links to data</a>
Protocols (6)	<a href="#">Click for detailed protocol information</a>
Description	Near isogenic wheat lines, differing in the presence of the FHB-resistance QTL Fhb1 and Qfhs.ifa-5A, have been sequenced using Illumina HiSeq2000 under disease pressure (30 and 50 hai) as well as with mock-inoculation, to discern transcriptional differences induced by <i>Fusarium graminearum</i> .
Experiment types	RNA-seq of coding RNA, co-expression, in vivo, stimulus or stress
Contact	 Wolfgang Schweiger <wolfgang.schweiger@boku.ac.at>
Citations	<a href="#">Quantitative trait loci-dependent analysis of a gene co-expression network associated with Fusarium head blight resistance in bread wheat (Triticum aestivum L.)</a> , Kugler KG, Siegwart G, Nussbaumer T, Ametz C, Spannagl M, Steiner B, Lemmens M, Mayer KF, Buerstmayr H, Schweiger W., <a href="#">PMID:24152241</a> . <a href="#">Joint Transcriptomic and Metabolomic Analyses Reveal Changes in the Primary Metabolism and Imbalances in the Subgenome Orchestration in the Bread Wheat Molecular Response to <i>Fusarium graminearum</i></a> . Nussbaumer T, Warth B, Sharma S, Ametz C, Bueschl C, Parich A, Pfeifer M, Siegwart G, Steiner B, Lemmens M, Schuhmacher R, Buerstmayr H, Mayer KF, Kugler KG, Schweiger W., <a href="#">PMID:26438291</a>
MINSEQE	* - * - * Exp. design    Protocols    Variables    Processed    Seq. reads
Files	Investigation description  <a href="#">E-MTAB-1729.idf.txt</a> Sample and data relationship  <a href="#">E-MTAB-1729.sdrf.txt</a>  <a href="#">Click to browse all available files</a>
Links	<a href="#">Expression Atlas - E-MTAB-1729</a> <a href="#">ENA - ERP003465</a> <a href="#">Send E-MTAB-1729 data to GENOME SPACE</a>

#collect the link from the **Links section of url**: see here: "ENA-ERP003465" —  
>> Pressing on that one returns: [https://www.ebi.ac.uk/ena/data/view/  
PRJEB4202](https://www.ebi.ac.uk/ena/data/view/PRJEB4202)

European Bioinformatics Institute [GB] | <https://www.ebi.ac.uk/ena/data/view/PRJEB4202>

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<b>Name</b> FHB on wheat	<b>Submitting Centre</b> Institute for Biotechnol Sciences, A-3430 Tulln
<b>Secondary accession(s)</b> ERP003465	
<b>Broker Name</b> ArrayExpress	
<b>Description</b> Near isogenic wheat lines, differing in the presence of the FHB-resistance QTL Fhb1 and Qfhs.ifa-5A, have been sequenced using Illumina HiSeq2000 under disease pressure (30 and 50 hai) as well as with mock-inoculation, to discern transcriptional differences induced by Fusarium graminearum.	
<a href="#">Navigation</a> <a href="#">Read Files</a> <a href="#">Portal</a> <a href="#">Attributes</a>	
<b>↓ Sample:</b> <a href="#">ERS316935-ERS316994</a> <b>↓ Experiment:</b> <a href="#">ERX278615-ERX278674</a> <b>↓ Run:</b> <a href="#">ERR305274-ERR305333</a> <b>← Submission:</b> <a href="#">ERA234368</a> <b>→ ArrayExpress</b> <a href="#">E-MTAB-1724</a>	

European Bioinformatics Institute [GB] | <https://www.ebi.ac.uk/ena/data/view/PRJEB4202>

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<b>Study: PRJEB4202</b> FHB on wheat		<a href="#">Download: Project XML</a> <a href="#">Study XML</a>																																																																																						
<b>Name</b> FHB on wheat		<b>Submitting Centre</b> Institute for Biotechnology in Plant Production, IFA-Tulln, University of Natural Resources and Life Sciences, A-3430 Tulln, Austria																																																																																						
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<b>Showing results 1 - 10 of 60 results</b> <table border="1"> <thead> <tr> <th>Study accession</th> <th>Sample accession</th> <th>Secondary sample accession</th> <th>Experiment accession</th> <th>Run accession</th> <th>Tax ID</th> <th>Scientific name</th> <th>Instrument model</th> <th>Library layout</th> <th>FASTQ files (FTP)</th> <th>FASTQ files (Galaxy)</th> <th>Submitted files (FTP)</th> <th>Submitted files (Galaxy)</th> <th>NCBI SRA file (FTP)</th> <th>NCBI SRA file (Galaxy)</th> <th>CRAM Index files (FTP)</th> <th>CRAM Index files (Galaxy)</th> </tr> </thead> <tbody> <tr> <td>PRJEB4202</td> <td>SAMEA2151438</td> <td>ERS316984</td> <td>ERX278664</td> <td>ERR305274</td> <td>4565</td> <td>Triticum aestivum</td> <td>Illumina HiSeq 2000</td> <td>SINGLE</td> <td><a href="#">File 1</a></td> <td><a href="#">File 1</a></td> <td><a href="#">Fastq file 1</a></td> <td><a href="#">Fastq file 1</a></td> <td><a href="#">File 1</a></td> <td><a href="#">File 1</a></td> <td></td> <td></td> </tr> <tr> <td>PRJEB4202</td> <td>SAMEA2149084</td> <td>ERS316955</td> <td>ERX278635</td> <td>ERR305275</td> <td>4565</td> <td>Triticum aestivum</td> <td>Illumina HiSeq 2000</td> <td>SINGLE</td> <td><a href="#">File 1</a></td> <td><a href="#">File 1</a></td> <td><a href="#">Fastq file 1</a></td> <td><a href="#">Fastq file 1</a></td> <td><a href="#">File 1</a></td> <td><a href="#">File 1</a></td> <td><a href="#">File 1</a></td> <td></td> </tr> <tr> <td>PRJEB4202</td> <td>SAMEA2143535</td> <td>ERS316945</td> <td>ERX278625</td> <td>ERR305276</td> <td>4565</td> <td>Triticum aestivum</td> <td>Illumina HiSeq 2000</td> <td>SINGLE</td> <td><a href="#">File 1</a></td> <td><a href="#">File 1</a></td> <td><a href="#">Fastq file 1</a></td> <td><a href="#">Fastq file 1</a></td> <td><a href="#">File 1</a></td> <td><a href="#">File 1</a></td> <td><a href="#">File 1</a></td> <td></td> </tr> <tr> <td>PRJEB4202</td> <td>SAMEA2142276</td> <td>ERS316972</td> <td>ERX278652</td> <td>ERR305277</td> <td>4565</td> <td>Triticum aestivum</td> <td>Illumina HiSeq 2000</td> <td>SINGLE</td> <td><a href="#">File 1</a></td> <td><a href="#">File 1</a></td> <td><a href="#">Fastq file 1</a></td> <td><a href="#">Fastq file 1</a></td> <td><a href="#">File 1</a></td> <td><a href="#">File 1</a></td> <td><a href="#">File 1</a></td> <td></td> </tr> </tbody> </table>			Study accession	Sample accession	Secondary sample accession	Experiment accession	Run accession	Tax ID	Scientific name	Instrument model	Library layout	FASTQ files (FTP)	FASTQ files (Galaxy)	Submitted files (FTP)	Submitted files (Galaxy)	NCBI SRA file (FTP)	NCBI SRA file (Galaxy)	CRAM Index files (FTP)	CRAM Index files (Galaxy)	PRJEB4202	SAMEA2151438	ERS316984	ERX278664	ERR305274	4565	Triticum aestivum	Illumina HiSeq 2000	SINGLE	<a href="#">File 1</a>	<a href="#">File 1</a>	<a href="#">Fastq file 1</a>	<a href="#">Fastq file 1</a>	<a href="#">File 1</a>	<a href="#">File 1</a>			PRJEB4202	SAMEA2149084	ERS316955	ERX278635	ERR305275	4565	Triticum aestivum	Illumina HiSeq 2000	SINGLE	<a href="#">File 1</a>	<a href="#">File 1</a>	<a href="#">Fastq file 1</a>	<a href="#">Fastq file 1</a>	<a href="#">File 1</a>	<a href="#">File 1</a>	<a href="#">File 1</a>		PRJEB4202	SAMEA2143535	ERS316945	ERX278625	ERR305276	4565	Triticum aestivum	Illumina HiSeq 2000	SINGLE	<a href="#">File 1</a>	<a href="#">File 1</a>	<a href="#">Fastq file 1</a>	<a href="#">Fastq file 1</a>	<a href="#">File 1</a>	<a href="#">File 1</a>	<a href="#">File 1</a>		PRJEB4202	SAMEA2142276	ERS316972	ERX278652	ERR305277	4565	Triticum aestivum	Illumina HiSeq 2000	SINGLE	<a href="#">File 1</a>	<a href="#">File 1</a>	<a href="#">Fastq file 1</a>	<a href="#">Fastq file 1</a>	<a href="#">File 1</a>	<a href="#">File 1</a>	<a href="#">File 1</a>		
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{Ignore this section if starting with know the article name. Otherwise this is useful if starting from the EBI side. }Press on Study XML file url" <https://www.ebi.ac.uk/ena/data/view/ERP003465&display=xml> which contains <Description> tag, which has the abstract of the study. Take the text of that

element and Google search again, which should bring the Study. To confirm this is the correct study, search the article for the Institute name, and confirm that this is the same as the name of the institute in the EBA records. The authors are not recorded in EBA!!

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Study accession	Sample accession	Secondary sample accession	Experiment accession	Run accession	Tax ID	Scientific name	Instrument model	Library layout	FASTQ files (FTP)	FASTQ files (Galaxy)	Submitted files (FTP)	Submitted files (Galaxy)	Sample file
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**OR can access the TEXT link and the document itself via this url  
(which I found through developer tools:**

**Request URL:** [https://www.ebi.ac.uk/ena/data/warehouse/filereport?accession=PRJEB4202&result=read\\_run&fields=study\\_accession,sample\\_accession,secondary\\_sample\\_accession,experiment\\_accession,run\\_accession,tax\\_id,scientific\\_name,instrument\\_model,library\\_layout,fastq\\_ftp,fastq\\_galaxy,submitted\\_ftp,submitted\\_galaxy,sra\\_ftp,sra\\_galaxy,cram\\_index\\_ftp,cram\\_index\\_galaxy&download=txt](https://www.ebi.ac.uk/ena/data/warehouse/filereport?accession=PRJEB4202&result=read_run&fields=study_accession,sample_accession,secondary_sample_accession,experiment_accession,run_accession,tax_id,scientific_name,instrument_model,library_layout,fastq_ftp,fastq_galaxy,submitted_ftp,submitted_galaxy,sra_ftp,sra_galaxy,cram_index_ftp,cram_index_galaxy&download=txt)

- **Request Method:** GET
- **Status Code:** 200 OK
- **Remote Address:** 193.62.193.80:443
- **Referrer Policy:** no-referrer-when-downgrade

The screenshot shows the Network tab in the Chrome DevTools. The request details are as follows:

- Name:** PRJEB4202
- Request URL:** https://www.ebi.ac.uk/ena/data/warehouse/filereport?accession=PRJEB4202&result=read\_run&fields=study\_accession,sample\_accession,secondary\_sample\_accession,experiment\_accession,run\_accession,tax\_id,scientific\_name,instrument\_model,library\_layout,fastq\_ftp,fastq\_galaxy,submitted\_ftp,submitted\_galaxy,sra\_ftp,sra\_galaxy,cram\_index\_ftp,cram\_index\_galaxy&download=txt
- Request Method:** GET
- Status Code:** 200 OK
- Remote Address:** 193.62.193.80:443
- Referrer Policy:** no-referrer-when-downgrade

The Response Headers section shows:

- Access-Control-Allow-Headers: Origin, X-Requested-With, Content-Type, Accept
- Access-Control-Allow-Methods: GET

**This is how the PRJEB4202.txt text looks like: Which is all data and metadata for the user who wants to reproduce the article findings.**

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PRJEB4202.txt

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21	PRJEB4202	SAMEA214416936	ERS316936	ERX278616	ERR305293	4565	Triticum aestivum Illumina HiSeq	SINGLE		ftp.sra.ebi.ac.uk/vol1/err/ERR305/ERR305293						

on a different manuscript:

doi: <https://science.scienmag.org/content/345/6194/1250091/tab-pdf>

searching "accession → returned accession no.

**ACKNOWLEDGMENTS**

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Materials and Methods  
Supplementary Text  
Figs. S1 to S25  
Tables S1 to S31  
References (55–69)  
IWGSC Author List

23 December 2013; accepted 21 May 2014  
10.1126/science.1250091

If want to assess the Methodology reproducibility, this url gives:

<https://www.ebi.ac.uk/ena/data/view/ERX278664>

The EXPERIMENT description: <https://www.ebi.ac.uk/ena/data/view/ERX278664>

(NOTE: Assess how well this section is filled for each study. What scores could we take, what variables could we assess?).

The screenshot shows the EBI ENA experiment details page for ERX278664. The page includes the following sections:

- Submitting Centre:** Institute for Biotechnology in Plant Production, IFA-Tulln, University of Natural Resources and Life Sciences, A-3430 Tulln, Austria.
- Platform:** ILLUMINA
- Model:** Illumina HiSeq 2000
- Library Layout:** SINGLE
- Library Strategy:** WGS
- Library Source:** TRANSCRIPTOMIC
- Library Selection:** RANDOM
- Library Name:** Extract 53

**Broker Name:** ArrayExpress

**Library Construction Protocol:**

We utilized four early isogenic lines (NILs) previously generated from a cross of the resistant spring wheat line CM-82036 and Remus, a susceptible Austrian spring wheat cultivar. The NILs have Remus as the recurrent parent (5 backcrosses) and contain the resistance alleles from CM-82036 of both Fhb1 and Qfhs.lfa-5A (NIL1), or either Fhb1 (NIL2) or Qfhs.lfa-5A (NIL3) or none (NIL4). Additionally, CM-82036 was used in the subsequent experiments. In preparation for fungal inoculation, *F. graminearum* spores required for inoculation were produced on defined SNA medium under UV-light at 25 degrees C. After two weeks conidia were harvested and diluted to 50,000 conidia/mL in water. Aliquots were stored at -80 degrees C. Single seeds were sown and put at 4 C for one week. After vernalization, seeds were germinated at 20 degrees C for two weeks and each two plants were potted into 3 L pots. The plants were initially kept in a 18 degrees C/12 degrees C day/night cycle (12 hours light), which was gradually changed until anthesis to 21 degrees C/18 degrees C at 55 % relative humidity (16 hours light). At least 12 heads per experimental condition (three replications, *F. graminearum*/mock treatment; two time points) were subjected to further experiments. At anthesis, the plants were inoculated either with a *F. graminearum* spore suspensions or water: 10 ? of the respective inoculum was pipetted into one floret between palea and lemma, directly onto the generative part. Per head two outer floret of six spikelets in three central rows were treated in this way, while the central florets were not inoculated (in total 12 florets). The inoculated heads were moistened with distilled water and bagged into a plastic bag for 24 hours to provide favourable conditions for disease development. Tissues comprising only the initially inoculated spikelets were sampled 30 or 50 hours after inoculation (hai) and from these the generative parts (stigma, anthers, ovary) as well as the glumes and the central floret were discarded. Only palea, lemma and rachis were frozen immediately in liquid nitrogen and stored at -80 degrees C until use. Single seeds were sown and put at 4 degrees C for one week. After vernalization, seeds were germinated at 20 degrees C for two weeks and each two plants were potted into 3 L pots. The plants were initially kept in a 18 degrees C/12 degrees C day/night cycle (12 hours light), which was gradually changed until anthesis to 21 degrees C/18 degrees C at 55 % relative humidity (16 hours light). At least 12 heads per experimental condition (three replications, *F. graminearum*/mock treatment; two time points) were subjected to further experiments. 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To eliminate RNases, metal jars with inherent metal spheres for Retsch-mill (MM 301, Haan, Germany) were sterilized at 180 degrees C for 3 h and then stored at -80 degrees C. All tissue belonging to one sample was pooled in one precooled jar and clamped in Retsch-mill. Grinding was performed for 30 s at full speed to obtain a fine tissue powder and immediately put back at -80 degrees C. Total-RNA was extracted from 100 ? of frozen tissue powder using the RNeasy Plant Mini Kit (#74903, Qiagen, Venlo, Netherlands) according to manufacturers instructions. The extracted RNA was checked for quality and quantity on an automated electrophoresis-system (Experion, #701-7000, Bio-Rad, Hercules, CA, US). Sequencing was performed on an Illumina HiSeq2000 machine using 8x multiplexing, theoretically generating 22 M reads per sample by an external sequencing-provider ?ATC? (Konstanz, Germany). Each sample represents one experimental condition (pathogen/mock; time points; genotype) and comprises pools of 12 treated wheat heads. Each experimental condition has been replicated 3x. cDNA was sent to a service provider (GATC konstanz germany) who have performed the library construction following the Illumina TruSeq RNA sample preparation guide (version 2, [http://support.illumina.com/sequencing/sequencing\\_kits/truseq\\_rna\\_sample\\_prep\\_kit\\_v2/documentation.ilmn](http://support.illumina.com/sequencing/sequencing_kits/truseq_rna_sample_prep_kit_v2/documentation.ilmn))

**Description:**  
FHB on wheat

**Navigation:** Read Files Attributes

This table contains the files for experiment ERX278664

**Bulk Download Files** (If the downloader app doesn't open, please try using Firefox to launch it.)

Download: 1 - 1 of 1 results in TEXT

Select columns

Showing results 1 - 1 of 1 results

Study accession	Sample accession	Secondary sample accession	Experiment accession	Run accession	Tax ID	Scientific name	Instrument model	Library layout	FASTQ files (FTP)	FASTQ files (Galaxy)	Submitted files (FTP)	Submitted files (Galaxy)	NCBI SRA file (FTP)	NCBI SRA file (Galaxy)	CRAM Index files (FTP)	CRAM Index files (Galaxy)
PRJEB4202	SAMEA2151438	ERS316984	ERX278664	ERR305274	4565	<i>Triticum aestivum</i>	Illumina HiSeq 2000	SINGLE	<a href="#">File 1</a>	<a href="#">File 1</a>	<a href="#">Fastq file 1</a>	<a href="#">Fastq file 1</a>	<a href="#">File 1</a>	<a href="#">File 1</a>	<a href="#">File 1</a>	<a href="#">File 1</a>

## NOTE:

Re-read that article which assess the data availability of articles in one Journal, see how they scored it, what their methodology was, coders and then their statistics.

how from DOI to get the text format in order to query it for specific terms:

<https://marcobonzanini.com/2015/01/12/searching-pubmed-with-python/>  
(returns in XML or JSON format)

<https://www.ncbi.nlm.nih.gov/pmc/tools/ftp/>

Query **NCBI Entrez** and retrieve PubMed records in XML or TXT format. PubMed records can be downloaded and saved as XML or text files. Data integrity is enforced during data download, allowing to retrieve and save very large number of records effortlessly. PubMed records can be processed to extract publication- and author-specific information

R package: [https://www.data-pulse.com/projects/Rlibs/vignettes/easyPubMed\\_02\\_advanced\\_tutorial.html](https://www.data-pulse.com/projects/Rlibs/vignettes/easyPubMed_02_advanced_tutorial.html)

search PubMed with Python: to get XML and JSON with Biopython. <https://marcobonzanini.com/2015/01/12/searching-pubmed-with-python/>

<https://www.elsevier.com/about/open-science/research-data/text-and-data-mining>

<https://linux.die.net/man/1/pdftotext>

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Dear Evanthia, cc Cristobal,

I am happy to help but I am sorry but I don't think I will have good news for you.

When we did this I actually started at the NCBI SRA and searched for "wheat" or "Triticum aestivum". I then filtered for "RNA-seq" and then went manually through every sample (then there were ~400 samples, the last time I did this there were ~1,500, now there are even more!). I used google to see if the SRR number could be found in any publication (this approach is not very successful). I also then looked for the SRP or PRJEB number using google. Many times this did not work but sometimes it did. I then checked that those samples really were the correct ones in the paper (e.g. number of samples, tissues etc).

My next step was to google for the author who had deposited the data with some key words I could find associated with the SRA sample - e.g. wheat or the tissue or experimental conditions. Sometimes the person who deposited the paper was not in the author list so I also googled without the depositor's name. Sometimes using the Institution which deposited the data helped. This often found a paper which seemed possible, so I then read the paper to check if the deposited samples were the ones in that paper (same tissue, growth conditions etc). Often it was not that easy to tell and sometimes people deposit extra samples which are then not in the final paper. Using this approach I could identify a paper for ~95 % of samples but it takes a lot of manual curation.

I think in the end we only had a few samples which didn't have a paper associated to them.

By the way the data in the SRA for the second paper you mentioned (doi: 10.1126/science.1250091) is actually truncated so it should be downloaded from the URGI website instead (the links were in the excel sheet you sent).

It would be really useful to have an automated way to collect the RNA-seq data from the repositories (please keep me updated on how this goes!) I think this might require buy-in from journals to have a uniform way to report the NGS data deposition (e.g. a section called Data Availability where all the SRA codes could be written), and even more vital that everyone actually deposits their data.

Good luck with this and let me know if you need any more details.

Best wishes

Philippa

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