

Assignment-2

Q.1: How can I calculate the length of each gene from the ASM584v2 GTF file?

- Visit NCBI homepage: [National Center for Biotechnology Information](https://www.ncbi.nlm.nih.gov/)
- Choose 'Genome' from the dropdown menu.
- Type the scientific name of the organism you want to search for (e.g.: *Escherichia coli*). Click on 'search' button.
- Now, you will see a list of assemblies. Select the top one, i.e., ASM584v2 to download the GTF file.
- Run the below following -

```
(base) ibab@IBAB-MScBDB2-Comp007:~/NGS_Lab/ngs_files$ awk '$3 == "gene" {len = $5 - $4 + 1; print $1, len}' GCF_000005845.2_ASM584v2_genomic.gtf > gene_lengths.txt
```

```
(base) ibab@IBAB-MScBDB2-Comp007:~/NGS_Lab/ngs_files$ cat gene_lengths.txt
NC_000913.3 66
NC_000913.3 2463
NC_000913.3 933
NC_000913.3 1287
NC_000913.3 297
NC_000913.3 777
NC_000913.3 1431
NC_000913.3 954
NC_000913.3 588
NC_000913.3 567
NC_000913.3 714
NC_000913.3 486
NC_000913.3 405
NC_000913.3 1917
NC_000913.3 1131
NC_000913.3 1113
NC_000913.3 210
NC_000913.3 153
NC_000913.3 59
NC_000913.3 1167
NC_000913.3 906
NC_000913.3 504
NC_000913.3 276
NC_000913.3 264
NC_000913.3 219
NC_000913.3 942
NC_000913.3 2817
NC_000913.3 495
NC_000913.3 450
NC_000913.3 951
NC_000913.3 915
```

Q.2: Create a directory and download the reference genome of *Saccharomyces cerevisiae* along with annotation files in GTF and GFF formats.

- Create a directory using 'mkdir' command.
- Visit NCBI homepage: [National Center for Biotechnology Information](https://www.ncbi.nlm.nih.gov)
- Choose 'Genome' from the dropdown menu.
- Type the scientific name of the organism you want to search for (e.g.: *Saccharomyces cerevisiae*). Click on 'search' button.
- Now, you will see a list of assemblies. Select the top one (hint: green tick) as shown below.

NCBI Datasets Taxonomy **Genome** Gene Command-line tools Documentation

Genome

Download a genome data package including genome, transcript and protein sequence, annotation and a data report

Selected taxa
Saccharomyces cerevisiae (baker's yeast) Enter one or more taxonomic names

Filters

Download Select columns 1,666 Genomes Rows per page 20 1-20 of 1,666

Assembly	GenBank	RefSeq	Scientific name	Modifier	Annotation	Action
<input checked="" type="checkbox"/> R64	GCA_000146045.2	<u>GCF_000146045.2</u>	Saccharomyces cerevisiae S28...	S288C (strain)	NCBI RefSeq Submitter	
<input type="checkbox"/> ASM2117220v1	GCA_021172205.1		Saccharomyces cerevisiae (bre...	S288C-SK1-cross (s...		
<input type="checkbox"/> ASM2350882v1	GCA_023508825.1		Saccharomyces cerevisiae (bre...	CICC 1445 (strain)		
<input type="checkbox"/> ASM401491v1	GCA_004014915.1		Saccharomyces cerevisiae (bre...	Makgeolli (strain)		
<input type="checkbox"/> ASM30865v1	GCA_003086655.1		Saccharomyces cerevisiae (bre...	BY4742 (strain)		
<input type="checkbox"/> SX2 Assembly v2	GCA_903819175.2		Saccharomyces cerevisiae (bre...	SX2 (strain)	Submitter	
<input type="checkbox"/> ASM158042v1	GCA_001580425.1		Saccharomyces cerevisiae (bre...	BCAnc (strain)		

- Go to 'Action' and then click on 'Download'. Select 'RefSeq only' and choose those that you want to download.

Download Package

1 genome selected for download

Select file source [Select file types](#)

☐ All ☒ RefSeq only ☐ GenBank only

☒ Genome sequences (FASTA)
☒ Annotation features (GTF)
☒ Annotation features (GFF)
☐ Sequence and annotation (GBFF)
☐ Transcripts (FASTA)
☐ Genomic coding sequences (FASTA)
☐ Protein (FASTA)
☐ Sequence report (JSONL)
☒ Assembly data report (JSONL)

Your selected data will be downloaded as a ZIP archive
Estimated file size is 8 MB

Name your file
ncbi_dataset.zip

- Unzip the file using 'gunzip' command and navigate into the sub-folders in it to see and analyse the .fna / .gtf / .gff files.

- Another way to download is through ‘FTP’ links or even using CLI.

NCBI Datasets	Taxonomy	Genome	Gene	Command-line tools	Documentation
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Genome assembly ASM257140v2

Download datasets URL **FTP**

Submitted GenBank assembly	GCA_002571405.2
Taxon	Saccharomyces cerevisiae (brewer's yeast)
Strain	CEN.PK113-7D; CBS 8340
Assembly type	haploid
Submitter	Delft University of Technology
Date	Jan 2, 2020

Index of /genomes/all/GCA/002/571/405/GCA_002571405.2_ASM257140v2

Name	Last modified	Size
Parent Directory		-
GCA_002571405.2_ASM257140v2_assembly_structure/	2025-06-21 17:43	-
GCA_002571405.2_ASM257140v2_assembly_report.txt	2023-12-03 18:24	2.6K
GCA_002571405.2_ASM257140v2_assembly_stats.txt	2023-12-03 18:24	28K
GCA_002571405.2_ASM257140v2_cds_from_genomic.fna.gz	2020-02-05 01:12	2.7M
GCA_002571405.2_ASM257140v2_fcs_report.txt	2025-02-24 00:59	456
GCA_002571405.2_ASM257140v2_feature_count.txt	2023-12-03 18:24	902
GCA_002571405.2_ASM257140v2_feature_table.txt.gz	2020-02-05 01:12	250K
GCA_002571405.2_ASM257140v2_genomic.fna.gz	2021-03-04 17:34	3.6M
GCA_002571405.2_ASM257140v2_genomic.gbff.gz	2023-12-03 18:24	7.3M
GCA_002571405.2_ASM257140v2_genomic.gff.gz	2025-06-21 17:43	656K
GCA_002571405.2_ASM257140v2_genomic.gtf.gz	2025-06-21 17:43	648K
GCA_002571405.2_ASM257140v2_genomic.gaps.txt.gz	2020-02-05 01:12	133
GCA_002571405.2_ASM257140v2_protein.faa.gz	2020-02-05 01:12	1.7M
GCA_002571405.2_ASM257140v2_protein.gpff.gz	2023-12-03 18:24	3.7M
GCA_002571405.2_ASM257140v2_rna_from_genomic.fna.gz	2023-12-03 18:24	2.7M
GCA_002571405.2_ASM257140v2_translated_cds.faa.gz	2020-02-05 01:12	1.9M
README.txt	2024-08-27 13:56	55K
annotation_hashes.txt	2025-06-21 17:43	410
assembly_status.txt	2025-07-24 07:10	14
md5checksums.txt	2025-06-21 17:43	6.5K
uncompressed_checksums.txt	2025-06-21 17:43	3.6K

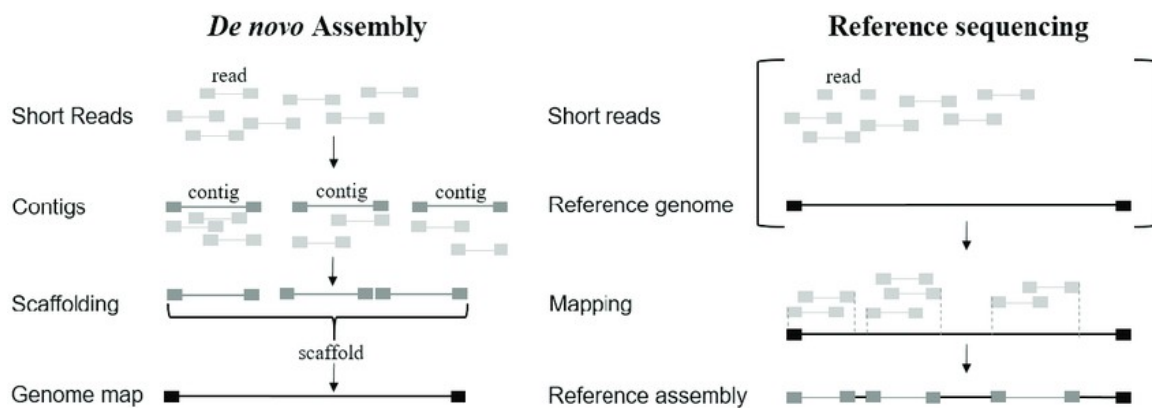
[HHS Vulnerability Disclosure](#)

Q.3: What is the difference between assembly and alignment?

	Assembly	Alignment
Definition Input Reference? Types	Computational construction of a longer sequence from smaller sequence reads. It can be de-novo (without a reference) or reference-guided.	Similarity-based arrangement of DNA, RNA or protein sequences. It matches sequencing reads to an existing reference genome to determine their origin. <u>Types:-</u> Global or local alignment
Purpose	To build the entire genome or transcript when the reference genome is missing or incomplete.	To find where each read maps on a known reference genome or transcriptome is.
Output	Contigs or scaffolds (assembled sequences) – FASTA format.	SAM or BAM files (coordinates of reads on the reference)
Tools Used	SPAdes, Velvet, MEGAHIT, Trinity (RNA)	BWA, Bowtie2, STAR, HISAT2, Minimap2

Use Cases	To find novel species, metagenomic studies, to discover structural variants, etc.	Variant calling, gene expression analysis, RNA-seq quantification, SNP detection, to annotate genomic features, etc.
Difficulty CPU usage Storage	Much more complex & resource-intensive, high CPU usage (especially for de-novo) and requires more storage (especially with intermediate contigs).	Relatively fast and lightweight, moderate to low CPU usage, easy to interpret results.
Disadvantages	Prone to fragmentation or misassembly.	Sensitive to reference genome errors.

Q.4: What is the difference between de-novo assembly and reference-based assembly?



	De-Novo Assembly	Reference-Based Assembly
Primary Goal	Reconstruct a genome or transcriptome without any reference.	Map reads to a known reference genome to infer variation or expression.
When to Use?	<ul style="list-style-type: none"> • New or poorly studied organisms. • Metagenomics • Novel virus or bacterial strains. 	<ul style="list-style-type: none"> • Model organisms (human, mouse, yeast) • Clinical genomics • Variant calling, RNA-seq quantification
Genome Bias	No bias; entire sequence assembled from scratch.	Biased towards the reference; novel sequences may be missed.
Data Requirement	Needs high coverage (30x – 100x +) & good quality data to generate reliable contigs.	Can work with lower coverage (~10x – 30x) since structure is already known.
Novel sequence detection	Can detect new genes, rearrangements, or repeat expansions.	Rare or novel variants may be missed or misaligned.

Repetitive Regions	Difficult to resolve repeats accurately; may result in gaps or fragmented assembly.	Easier to handle with reference, as repeats are known and aligned accordingly.
Output Examples	<ul style="list-style-type: none"> • FASTA files with contigs/scaffolds • Entire genome sequence • Graphs (e.g., De Bruijn) 	<ul style="list-style-type: none"> • BAM/SAM alignment files • VCF for SNP/indel calls • Coverage maps or expression matrices
Computational load	High RAM & CPU needed; more time-consuming (large genomes).	Faster & less memory-intensive due to guided alignment.
Error Sensitivity	Sensitive to sequencing errors; can affect assembly quality or contiguity.	Errors are easier to spot & correct against reference genome.
Tools (Genomic)	SPAdes, SOAPdenovo, ABySS, Canu (for long reads), Flye (for nanopore), etc.	BWA, Bowtie2, Minimap2, GATK, Samtools for post-processing, etc.
Tools (Transcriptomic)	Trinity, Oases (RNA-seq de-novo), RNA-Bloom (long-read RNA), etc.	HISAT2, STAR, Kallisto, Salmon (for quantification), etc.
Use in evolutionary studies	To discover divergent or unique genes in different species or populations.	To compare known variations & SNPs across individuals of the same species.
Scaffolding & Gap Filling	Often requires paired-end or mate-pair reads or long reads to scaffold properly.	Not needed as the reference already provides structure.

Q.5: What is the difference between FASTA and FASTQ file format?

	FASTA	FASTQ
Full name	FAST-All (because it can store any sequence type)	FASTQ (FAST + Quality)
Origin	Developed for the sequence databases like GenBank.	Developed by the Sanger Institute for storing raw sequencing reads.
Lines per entry	2 lines (or more if sequence wraps): Header line (starts with >) and sequence line.	Always 4 lines: header line (starts with @), sequence line, + separator, ASCII-encoded quality.
Quality encoding	Not supported	Usually Phred+33 (Illumina) or Phred+64 (older platforms) $Q = -10 * \log_{10}P$; where, P = Probability of error

Header format	Flexible	Must match the identifier in line 1 and line 3.
Common tools	BLAST, Bowtie (for index), genome browsers, Prokka	FastQC, Trimmomatic, BWA, STAR, kallisto, HISAT2, Salmon
Storage purpose	Reference sequence, consensus genomes, contigs, scaffolds	Raw read data from sequencers (prior to alignment/assembly)
Example	>NC_090774.1 Yarrowia lipolytica chromosome 1E, complete sequence GCGTGCTCAGTCGAATCCT CCACTA	 @seqA ATGCAAGTC + IIIIIII (I = high quality score)

Q.6: How can I download paired-end nucleotide sequencing data of *Saccharomyces cerevisiae* (e.g. – ERR11532742) from a whole genome sequencing (WGS) experiment using either the NCBI SRA or the ENA (European Nucleotide Archive)?

- Visit ENA homepage - <https://www.ebi.ac.uk/ena/browser/home>
- Enter the accession ID (ERR11532742) or organism name in the search bar and press 'Enter'.
- Select both the fastq.gz files (forward & reverse-end) and click on 'Get download script'. This contains wget links, so if you run the script then it will automatically both the fastq.gz files. And then gunzip or uncompress these.

Organism: [Saccharomyces cerevisiae \(brewer's yeast\)](#)

Instrument Platform: ILLUMINA

Instrument Model: NextSeq 500

Read Count: 7649718

Base Count: 1147457700

Center Name: University of Graz, Institute of Pharmaceutical Sciences

Library Layout: PAIRED

Library Strategy: AMPLICON

Library Source: OTHER

Library Selection: PCR

Show More

Read Files

Show Column Selection

Download report: JSON TSV

Get download script Download selected files

Download All

Study Accession	Sample Accession	Experiment Accession	Run Accession	Tax Id	Scientific Name	Generated FASTQ files: FTP
PRJEB60025	SAMEA113582077	ERX10937305	ERR11532742	4932	Saccharomyces cerevisiae	<input checked="" type="checkbox"/> ERR11532742_1.fastq.gz <input checked="" type="checkbox"/> ERR11532742_2.fastq.gz

```
(base) ibab@IBAB-MScBDB2-Comp007:~/Downloads$ cat ena-file-download-selected-files-20250823-0627.sh
wget -nc ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR115/042/ERR11532742/ERR11532742_2.fastq.gz
wget -nc ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR115/042/ERR11532742/ERR11532742_1.fastq.gz
```



```
(base) ibab@IBAB-MScBDB2-Comp007:~/Downloads$ chmod +x ena-file-download-selected-files-20250823-0627.sh
(base) ibab@IBAB-MScBDB2-Comp007:~/Downloads$ ./ena-file-download-selected-files-20250823-0627.sh
--2025-08-23 11:58:25-- ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR115/042/ERR11532742/ERR11532742_2.fastq.gz
Resolving proxy.ibab.ac.in (proxy.ibab.ac.in)... 192.168.1.254
Connecting to proxy.ibab.ac.in (proxy.ibab.ac.in)|192.168.1.254|:3128... connected.
Proxy request sent, awaiting response... 200 Gatewaying
Length: 229187791 (219M) [text/plain]
Saving to: 'ERR11532742_2.fastq.gz'

ERR11532742_2.fastq.gz      100%[=====>] 218.57M  2.44MB/s   in 99s

2025-08-23 12:00:16 (2.21 MB/s) - 'ERR11532742_2.fastq.gz' saved [229187791/229187791]

--2025-08-23 12:00:16-- ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR115/042/ERR11532742/ERR11532742_1.fastq.gz
Resolving proxy.ibab.ac.in (proxy.ibab.ac.in)... 192.168.1.254
Connecting to proxy.ibab.ac.in (proxy.ibab.ac.in)|192.168.1.254|:3128... connected.
Proxy request sent, awaiting response... 200 Gatewaying
Length: 232721564 (222M) [text/plain]
Saving to: 'ERR11532742_1.fastq.gz'

ERR11532742_1.fastq.gz    100%[=====>] 221.94M  3.03MB/s   in 76s

2025-08-23 12:01:34 (2.93 MB/s) - 'ERR11532742_1.fastq.gz' saved [232721564/232721564]
```

Q.7: Download the single-cell RNA-Seq data of E. Coli or Saccharomyces cerevisiae; the one having small size.

1. Go to the SRA website.
2. Type “Single cell RNA-seq E. Coli” in the search bar & press ‘Enter’.
3. Click on the first hit.
4. Go below the page and click on the SRA metadata link.
5. From the Data Access column, copy the NCBI link.
6. Open terminal and navigate to the required folder and download using the wget command.

Service Alert: Planned Maintenance beginning July 25th
 Most services will be unavailable for 24+ hours starting 9 PM EDT. [Learn more about the maintenance.](#)

SRA

Public (73)

Source RNA (73)

Library Layout paired (71) single (2)

Platform Illumina (73)

Strategy **RNASeq** (73)

Data in Cloud GS (73) S3 (73)

File Type fastq (73)

[Clear all](#)

[Show additional filters](#)

Summary 20 per page

View results as an expanded interactive table using the RunSelector. [Send results to Run selector](#)

Search results

Items: 1 to 20 of 73

Filters activated: RNASeq. [Clear all](#) to show 10532 items.

Quoted phrase not found.

- ☐ [GSM8128542: EsaTldR_RIP: Escherichia coli: RIP-Seq](#)
 1 ILLUMINA (NextSeq 550) run: 2.3M spots, 352.9M bases, 146.2Mb downloads
 Accession: SRX23848526
- ☐ [GSM8128541: EceTldR_RIP: Escherichia coli: RIP-Seq](#)
 1 ILLUMINA (NextSeq 550) run: 2.9M spots, 438.3M bases, 182.3Mb downloads
 Accession: SRX23848525
- ☐ [GSM8128540: EcaTldR_RIP: Escherichia coli: RIP-Seq](#)
 1 ILLUMINA (NextSeq 550) run: 2.2M spots, 333.7M bases, 139.3Mb downloads
 Accession: SRX23848524
- ☐ [GSM8128539: Efa2TldR_RIP: Escherichia coli: RIP-Seq](#)
 1 ILLUMINA (NextSeq 550) run: 2.1M spots, 315.9M bases, 131.9Mb downloads
 Accession: SRX23848523
- ☐ [GSM8128538: EmuTldR_RIP: Escherichia coli: RIP-Seq](#)
 1 ILLUMINA (NextSeq 550) run: 2.1M spots, 316.3M bases, 131.2Mb downloads
 Accession: SRX23848522

Send to: [Manage Filters](#)

Results by taxon

Top Organisms [Tree](#)

Homo sapiens (43)
 Escherichia coli (18)
 Mus musculus (12)

Top Bioprojects

Epigenomics projects for the... (392)
 NIH Epigenomics Roadmap Init... (57)

Search in related databases

Database	Access		all
	public	controlled	
BioSample	588		588
BioProject	54		54
dbGaP		1	1
GEO Datasets	26		26

Find related data

Database: [Select](#)

[Find items](#)

Search details

NIH

National Library of Medicine
National Center for Biotechnology Information

Sequence Read Archive

SearchRun BrowserAnalysesStudyProvisional SRADocumentationMirroring

Run Browser > SRR28237338

GSM8128542: EsaTldR_RIP; Escherichia coli; RIP-Seq (SRR28237338)

Metadata

Analysis

Reads

Data access

FASTA/FASTQ download

Run

Run	Spots	Bases	Size	GC Content	Data Status	Published
SRR28237338	2.3M	352.9M	146.2MB	52.9%	Public	2024-04-22

Quality graph (bigger)

This run has 2 reads per spot:

L=76, 100%

L=76, 100%

Legend

Experiment

Experiment	Library Name	Platform	Strategy	Source	Selection	Layout	Action
SRX23848526	GSM8128542	Illumina	RIP-Seq	TRANSCRIPTOMIC	other	PAIRED	BLAST

Biosample

Biosample	Sample Description	Organism	Links
SAMN40277727 (SRS20668610)		Escherichia coli str. K-12 substr. MG1655	TnpB homologs exapted from transposons are RNA-guided transcription factors

NIH

National Library of Medicine
National Center for Biotechnology Information

Sequence Read Archive

SearchRun BrowserAnalysesStudyProvisional SRADocumentationMirroring

Run Browser > SRR28237338

GSM8128542: EsaTldR_RIP; Escherichia coli; RIP-Seq (SRR28237338)

Metadata

Analysis

Reads

Data access

FASTA/FASTQ download

SRA archive data

SRA archive data is normalized by the SRA load process and used by the SRA Toolkit to read and produce formats like FASTQ, SAM, etc. The default toolkit configuration enables it to find and retrieve SRA runs by accession.
Public SRA files are now available from GCP and AWS cloud platforms as well as from NCBI. Access to most data in the cloud requires a user account with the cloud service provider. The user's account will incur costs for cloud compute or to copy data outside of the specified cloud service region.

Type	Version	Created	Size	Location	Name	Free Egress	Access Type
SRA Lite	1	2024-03-06	92.8MB	NCBI	https://sra-downloadb.be-md.ncbi.nlm.nih.gov/sos4/sra-pub-zq-5/SRR028/28237/SRR28237338/SRR28237338.lite.1	worldwide	anonymous
				AWS	s3://sra-pub-zq-7/SRR28237338/SRR28237338.lite.1	s3.us-east-1	aws identity
				GCP	gs://sra-pub-zq-100/SRR28237338/SRR28237338.lite.1	gs.us-east1	gcp identity
SRA Normalized	1	2024-03-06	146.2MB	AWS	https://sra-pub-run-odp.s3.amazonaws.com/sra/SRR28237338/SRR28237338	worldwide	anonymous

Original format

The original files submitted to SRA. These files may require specific software to open, read and interpret data.

Type	Version	Created	Size	Location	Name	Free Egress	Access Type
fastq	1	2024-03-06	106.6MB	AWS	s3://sra-pub-sra-9/SRR28237338/EsaTldR_RIP_R2.fastq.gz.1	-	Use Cloud Data Delivery
fastq	1	2024-03-06	91.3MB	AWS	s3://sra-pub-sra-9/SRR28237338/EsaTldR_RIP_R1.fastq.gz.1	-	Use Cloud Data Delivery

Egress and Access: what does it mean?

Why is SRA data in the cloud?

What is "Cloud Data Delivery"?

```
lhab@IBAB-MSCB002-Comp001:~/NCS Lab$ wget https://sra-downloadb.be-md.ncbi.nlm.nih.gov/sos4/sra-pub-zq-5/SRR028/28237/SRR28237338/SRR28237338.lite.1
--2025-07-24 21:17:48-- https://sra-downloadb.be-md.ncbi.nlm.nih.gov/sos4/sra-pub-zq-5/SRR028/28237/SRR28237338/SRR28237338.lite.1
Resolving sra-downloadb.be-md.ncbi.nlm.nih.gov (sra-downloadb.be-md.ncbi.nlm.nih.gov)... 130.14.250.18, 130.14.250.26, 130.14.250.24, ...
Connecting to sra-downloadb.be-md.ncbi.nlm.nih.gov (sra-downloadb.be-md.ncbi.nlm.nih.gov)|130.14.250.18|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 97328228 (93M) [application/x-troff-man]
Saving to: 'SRR28237338.lite.1'

SRR28237338.lite.1          72K[=====] 67.17M  6.24MB/s   eta 11s
```


Q.8: Download paired-end RNA-seq data of Escherichia coli from a public repository (NCBI SRA or ENA) with the following experimental design:

- 1. Conditions: 3 samples under healthy (control) condition, 3 samples under diseased treatment condition at different time points.**
- 2. Replicates: Each condition/time point has 3 biological replicates.**

GEO DataSets
GEO DataSets
Escherichia coli RNA-Seq
Create alert
Advanced

Entry type
DataSets (0)
Series (785)
Samples (1,824)
Platforms (0)
Organism
Customize ...
Study type
Expression profiling by array
Methylation profiling by array
Customize ...

Summary
20 per page
Sort by Default order
Send to:

Search results
Items: 1 to 20 of 2609
<< First
< Prev
Page 1 of 131
Next >
Last >>

☐ [Host transcriptomic responses of chicken embryos during Avian Pathogenic Escherichia coli infection reveal the significant role of the yolk sac in embryonic mortality](#)
1. (Submitter supplied) Colibacillosis caused by avian pathogenic **Escherichia coli** (APEC) is a major disease syndrome in poultry with the yolk sac infection recognized as a leading factor contributing to embryonic mortality. Yolk sac is the initial site of infection, however its contribution in embryonic mortality at molecular

☐ [RelA influence on antimicrobial action of t-cinnamaldehyde on Escherichia coli MG1655](#)
3. (Submitter supplied) Antimicrobial resistance poses a global threat. Natural-origin compounds represent a valuable source of antimicrobial agents used in both human and veterinary medicine. However, understanding their mechanisms of action at the molecular level is essential to support their safe and effective application. In this study, we evaluated the antimicrobial potential of trans-cinnamaldehyde (CNMA), a major constituent of cinnamon bark oil, which can account for up to 80% of the oil content in species such as Cinnamomum zeylanicum and cassia. [more...](#)
Organism: **Escherichia coli**
Type: Expression profiling by high throughput sequencing
Platform: GPL25368 12 Samples
Download data: XLSX
Series Accession: GSE301628 ID: 200301628

Samples (12)
Less...

GSM9086649	MG1655, control, 0min, biol rep1
GSM9086650	MG1655, control, 0min, biol rep2
GSM9086651	MG1655, control, 0min, biol rep3
GSM9086652	MG1655relA, control, 0min, rep1
GSM9086653	MG1655relA, control, 0min, rep2
GSM9086654	MG1655relA, control, 0min, rep3
GSM9086655	MG1655relA, CNMA, 30min, rep1
GSM9086656	MG1655relA, CNMA, 30min, rep2
GSM9086657	MG1655relA, CNMA, 30min, rep3
GSM9086658	MG1655relA, CNMA, 60min, rep1
GSM9086659	MG1655relA, CNMA, 60min, rep2
GSM9086660	MG1655relA, CNMA, 60min, rep3