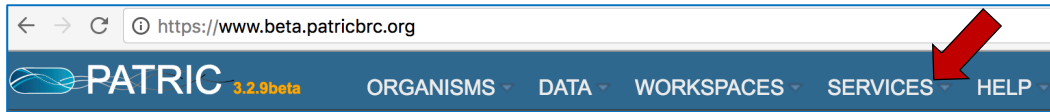
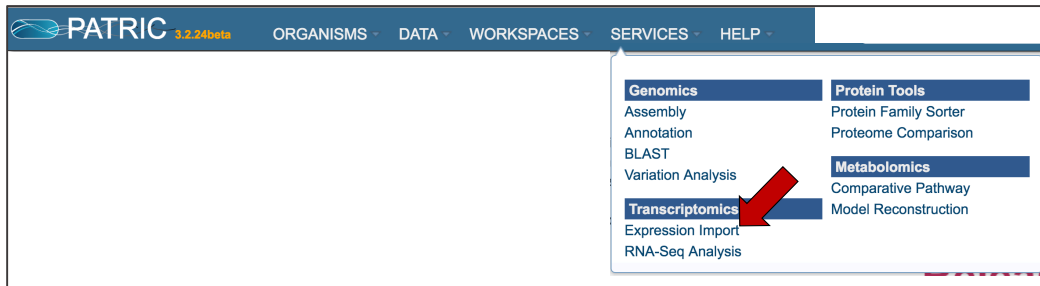


	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
1	UID	NAME	5min	10min	15min	30min	45min	60min	90min	120min	180min	270min	360min	540min	810min	1080min	1620min	2160min	3240min	360min	Norm	24h
2	000001	thvA	0.193	0.225	0.522	0.174	0.273	0.05	0.04	0.181	-2.29	-1.50	-4.44	-0.509	-4.44	-0.222	-0.129	0.131	0.091	0.094	0.316	-0.47
3	000002	thvB	0.015	-0.037	-0.055	0.005	0.044	0.018	-2.29	-1.50	-4.44	-0.509	-4.44	-0.509	-4.44	-0.222	-0.129	0.131	0.091	0.094	0.316	-0.47
4	000003	thvC	0.193	0.155	0.229	0.159	0.159	0.728	-0.454	-1.156	-0.921	-1.219	-0.662	-0.346	-0.454	-0.107	0.135	0.093	0.1	0.354	0.448	-0.043
5	000004	thvD	0.42	0.071	0.127	0.108	0	-1.793	-1.587	-1.582	-1.268	-0.888	-0.392	-0.48	-0.882	0.221	0.15	0.219	0.21	0.454	-0.294	
6	000005	ysaA	-0.008	0.299	0.172	0.085	0.626	0.832	0.173	0.327	-0.073	-0.015	0.062	0.11	0.007	0.493	0.137	0.306	0.136	0.129	0.591	0.384
7	000006	hnt	2.032	1.656	1.854	1.726	1.635	0.813	0.678	-0.446	-2.312	-0.291	-0.39	0.418	0.533	0.477	0.448	-0.181	-0.39	0.487	0.051	
8	000009	msu	0.571	0.421	0.155	0.199	-0.369	-0.333	-0.192	-0.033	0.128	0.082	0.056	-0.015	0.236	-0.058	0.04	-0.208	-0.181	-0.126	0.051	
9	0001010	ysaB	-1.796	-0.308	-1.206	-0.684	-0.185	0.21	0.405	0.28	0.093	0.132	0.041	-0.166	-0.023	0.302	0.302	0.34	0.297	0.342	0.161	0.442
10	000102	hgtA	0.598	-0.273	-0.088	-0.135	-0.107	0.665	0.301	0.682	-0.176	0.081	-0.125	0.351	0.177	0.202	0.298	0.74	0.573	0.733	0.479	
11	000103	hgtB	-0.605	-0.406	-0.382	-0.361	-0.391	-0.425	-0.425	-0.425	-0.425	-0.425	-0.425	-0.425	-0.425	-0.425	-0.425	-0.425	-0.425	-0.425	-0.425	-0.425
12	000104	hgtC	1.757	1.358	1.946	1.73	2.936	-1.805	-1.737	-1.899	-0.122	0.662	0.73	0.73	0.73	0.73	0.73	0.73	0.73	0.73	0.73	0.73
13	000105	dnal	1.248	1.322	1.239	1.068	2.342	-0.069	-0.99	-0.925	-0.175	0.34	0.297	0.219	0.081	0.567	1.3	1.214	0.204	0.095	0.968	0.7
14	000106	yfB1.1	0.158	-0.95	-0.104	0	1.662	-0.572	-0.252	-0.641	-0.134	-0.113	-0.083	-0.138	-0.221	-0.902	-0.132	-0.462	-0.596	0.102	0.102	
15	000107	yfB2.1	-0.479	-0.255	-0.304	0.051	0.919	-0.113	0.007	-0.049	-0.318	-0.119	-0.115	-0.33	-0.241	-0.646	-0.2	-0.413	-0.585	-0.428	-0.321	-0.428
16	000108	hnt	0.813	-0.111	-0.059	0.099	0.112	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589
17	000109	pnaA	-0.154	-0.343	-0.612	-0.432	1.406	-0.442	0.445	0.828	-0.346	0.136	0.135	0.309	0.171	0.591	0.88	0.864	0.764	0.749	1.049	0.749
18	000200	nhaR	0.33	-0.558	-0.761	-0.563	0.327	0.325	0.144	0.604	-0.249	-0.417	-0.359	-0.469	-0.459	0.446	0.291	0.244	0.535	0.098	0.373	0.749
19	000201	msu	-0.02	0.006	-0.104	-0.102	-0.786	-0.933	0.253	1.181	-0.118	0.221	-0.267	-0.401	-0.267	-1.391	-1.003	-1.03	-0.655	-0.97	-0.276	-0.276
20	000202	hnt	0.813	-0.111	-0.059	0.099	0.112	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589	-0.589
21	000203	msu	1.555	1.077	1.195	0.878	0.55	0.212	0.277	0.203	0.222	0.213	0.275	0.287	0.377	0.478	0.221	0.568	0.445	0.416	-0.229	-0.428
22	000205	ribE	0.612	0.337	0.552	0.447	0.718	0	-0.124	-0.23	0.236	0.261	0.37	0.449	0.262	-0.35	-0.234	-0.715	-0.459	-0.37	-0.196	-0.196
23	000206	lrf5	0.485	0.398	0.182	0.022	1.34	-0.242	-0.424	-0.507	-0.219	0.33	0.469	0.595	0.451	-0.412	-1.225	-2.122	-1.837	-3.84	-0.42	-0.42
24	000207	pnaB	-0.013	-0.009	-0.394	-0.448	-0.551	-0.552	-0.251	-0.596	-0.278	-0.114	0.104	0.082	0.056	0.051	-0.256	-0.089	-0.713	-0.113	-0.156	-0.156
25	000208	hnt	0.808	0.072	0.109	0.062	0.635	0.592	0	0.065	0.055	0.002	0.029	0.002	0.32	0.385	0.352	0.305	0.057	0.057	0.057	0.057
26	000301	dupB	2.1	2.056	1.221	1.748	-0.224	-0.138	-0.436	-0.631	-0.089	-0.235	-0.225	-0.772	-0.197	0.033	0.073	-0.579	-0.227	0.118	-0.491	-0.491
27	000302	carA	2.309	2.381	2.833	2.773	-0.235	-0.074	-0.904	-1.189	0.8	0.645	0.278	0.229	-0.006	-0.968	-1.868	-2.028	-2.092	-2.531	-2.003	-2.003
28	000303	carB	1.218	1.536	1.49	1.74	-0.795	-0.504	-0.666	-1.143	0.129	0.324	0.312	0.006	-0.091	-1.436	-1.3	-1.604	-1.942	-1.996	-0.591	-0.591
29	000304	hnt	0.813	0.083	0.163	0.075	0.603	-0.118	-0.272	-0.312	0.129	0.324	0.312	0.006	-0.091	-1.436	-1.3	-1.604	-1.942	-1.996	-0.591	-0.591
30	000305	carE	1.39	0.704	0.508	0.525	0.008	-0.053	-0.07	0.108	0.034	0.076	0.031	0.311	0.317	-0.063	0.23	0.003	0.248	0.295	-0.179	-0.179
31	000306	carD	0.951	0.881	0.096	0.087	0.473	-0.48	-0.399	-0.499	0.157	0.033	0.136	0.175	0.21	-0.047	0.325	0.549	0.568	0.719	-0.172	-0.172
32	000307	carC	0.751	-0.528	-0.889	-0.721	0.083	-0.562	-0.369	-0.513	0.062	0.092	-0.122	-0.217	0.001	0.559	0.266	0.563	0.596	0.719	0.26	0.26
33	000308	carB	-0.311	-0.4	-0.894	-0.875	-0.383	-0.506	-0.377	-0.24	0.166	0.008	0.255	0.077	0.371	0.117	0.116	0.218	0.321	0.31	0.263	0.263
34	000309	hnt	0.813	0.083	0.163	0.075	0.603	-0.118	-0.272	-0.312	0.129	0.324	0.312	0.006	-0.091	-1.436	-1.3	-1.604	-1.942	-1.996	-0.591	-0.591
35	000407	lecA	-1.222	-1.308	-1.549	-1.2	0.071	0.19	0.177	0.05	-0.126	-0.078	0.022	0.007	-0.148	0.532	0.174	0.499	0.473	0.516	0.131	0.131
36	000408	lecB	-0.436	-0.044	-0.561	-0.582	-0.497	0.618	0.142	0.384	-0.198	0.034	0.133	0.416	0.109	-0.358	0.448	-0.101	-0.064	-0.133	-0.469	-0.469

3. To upload this data into a private workspace, open the Services tab in PATRIC.



4. Click Experiment Import.



5. This opens a page where experimental data can be uploaded.

Differential Expression Import
Transform differential expression data for viewing on PATRIC

Experiment Data <i>i</i>	Experiment Information <i>i</i>
EXPERIMENT DATA FILE <input type="text"/>	EXPERIMENT TITLE <input type="text" value="Title"/>
EXPERIMENT TYPE <input type="text" value="Transcriptomics"/>	EXPERIMENT DESCRIPTION <input type="text" value="Description"/>
TARGET GENOME <input type="text" value="Optional"/>	ORGANISM NAME <input type="text" value="e.g. Bacillus Cereus"/>
	PUBMED ID <input type="text" value="Optional"/>
	OUTPUT FOLDER <input type="text" value="Experiments"/>
Optional Metadata <i>i</i> METADATA FILE <input type="text"/>	

II. Data Format

1. The data should be loaded into a particular format into PATRIC, an example of which can be seen below (A). The first column has the gene locus tag (RefSeq, GenBank, or PATRIC), and the second and later columns will have the log ratios for each gene in each condition. The column headers in the first row can have the name of that condition. You can see in B below that the second column has the gene name. That must be deleted before it can be uploaded.

1. Gene Matrix:

A

Gene ID	Comparison1	Comparison2
b0002	0.767	-1.316
b0003	0.815	-1.841
b0004	0.856	-1.643

	A	B	C	D	E	F	G	H
1	UID	NAME	5min .02M S	15min .02M	300min .02M	600min .02M	C410+0Ecb0	10' trp star
2	B0001	thrL	0.784	0.522	0.528	0.357	-0.273	0.088
3	B0002	thrA	0.215	-0.037	0.005	0.044	0.818	-2.409
4	B0003	thrB	0.193	0.155	0.229	0.159	0.728	-0.545
5	B0004	thrC	0.42	-0.071	0.127	0.108	0	-1.793
6	B0006	yaaA	-0.008	0.299	0.172	0.085	0.626	0.832
7	B0008	talB	2.032	1.656	1.854	1.726	-0.535	0.813
8	B0009	mog	0.571	0.421	0.155	0.199	-0.369	-0.333
9	B0010	yaaH	-1.796	-1.308	-1.206	-0.684	-0.185	0.21
10	B0012	htgA	0.598	-0.273	-0.088	-0.135	-0.107	0.665
11	B0013	yaaI	-0.803	-0.406	-0.782	-0.791	0.361	-0.391
12	B0014	dnaK	1.757	1.358	1.946	1.73	2.936	-1.895
13	B0015	dnaJ	1.248	1.322	1.239	1.068	2.342	-0.069
14	B0016	yi81_1	0.158	-0.95	-0.104	0	1.662	-0.572
15	B0017	yi82_1	-0.479	-0.255	-0.304	0.051	0.919	-0.113
16	B0018	gef	0.823	-0.111	-0.059	0.009	0.112	-0.589
17	B0019	nhaA	-0.154	-0.343	-0.612	-0.432	1.406	0.442
18	B0020	nhaR	-0.33	-0.558	-0.761	-0.563	0.327	0.325
19	B0021	insB_1	-0.02	0.006	-0.104	-0.102	-0.786	0.939


B

III. Uploading the Experimental Data

1. To upload the data sheet, which can either be txt or excel, click on the folder in the “Experiment Data” box that follows the text box under the words “Experiment Data File”.

Differential Expression Import
Transform differential expression data for viewing on F


Experiment Data ⓘ

EXPERIMENT DATA FILE
 

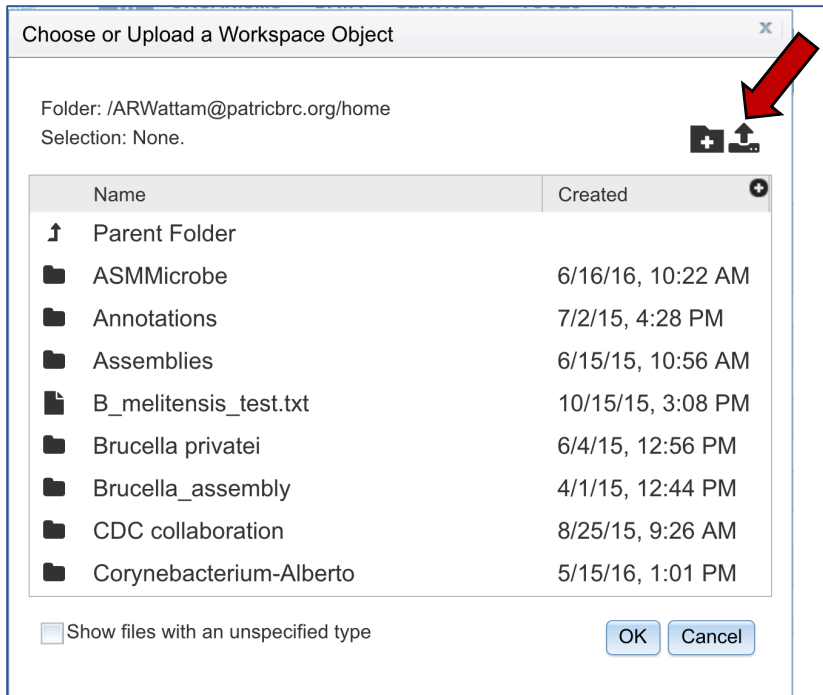
EXPERIMENT TYPE
Transcriptomics

TARGET GENOME
Optional

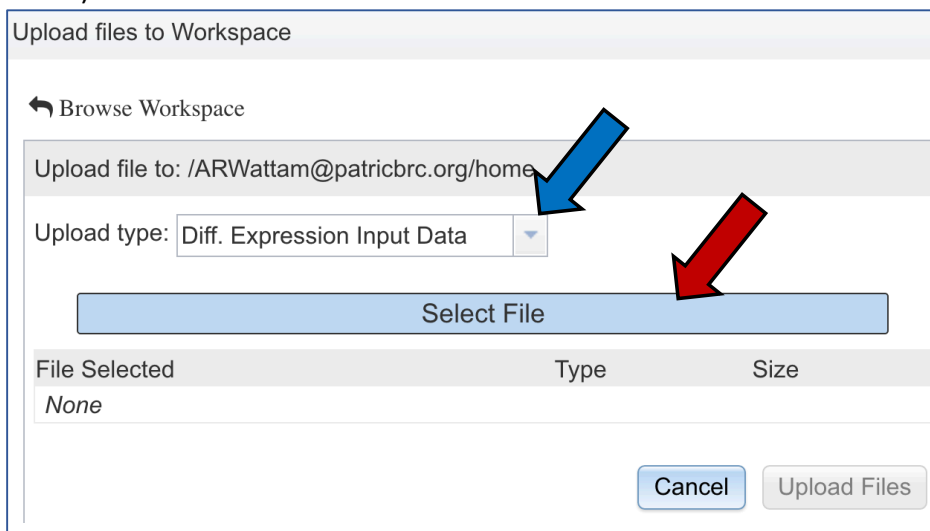
Optional Metadata ⓘ

METADATA FILE
 

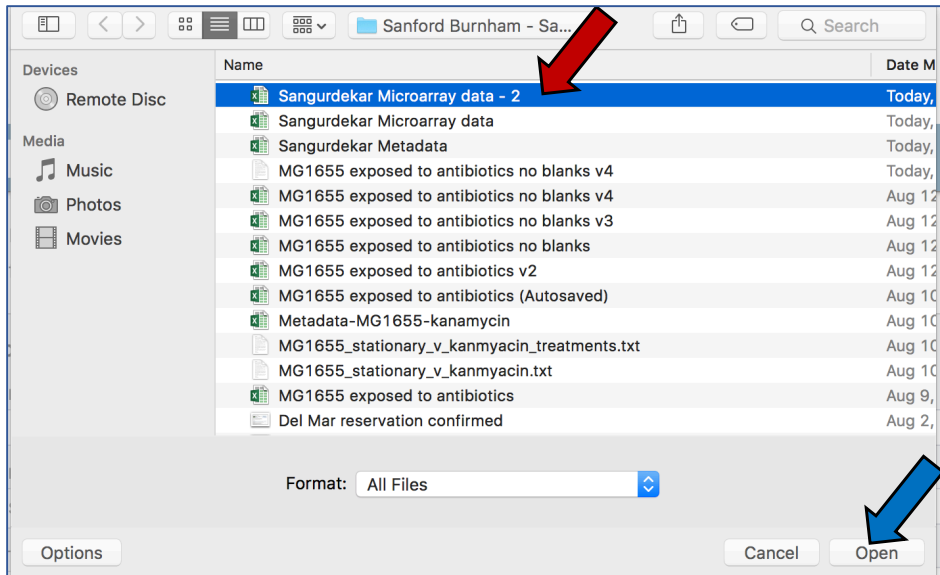
2. This will open a window that shows you data you have in uploaded or collected in PATRIC. If you had previously uploaded this data, you could find it here. To upload new data, click on the upload icon.



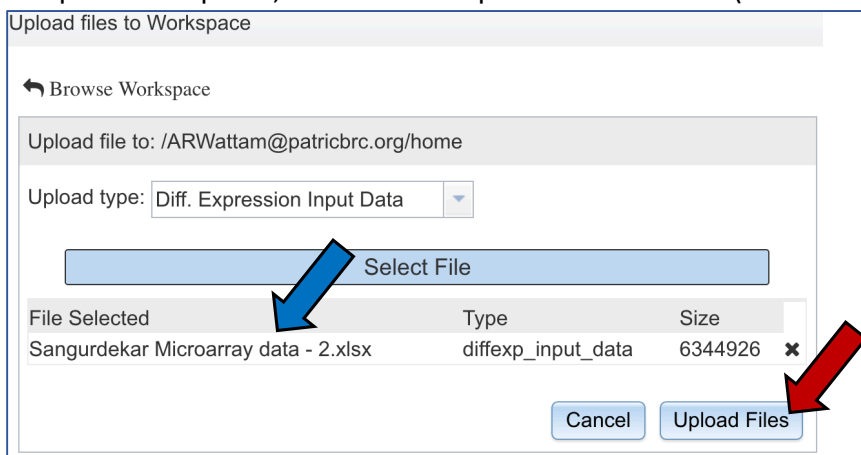
3. The pop-up widow will flip, and you will be able to select a file. Make sure you have the right type of data selected (Blue arrow). Then click on the blue “Select File” bar (Red arrow).



4. Select the file you want to upload (Red arrow) and then open it (Blue arrow).



5. The name of the file you selected will now appear on the page (Blue arrow). To complete the upload, click on the “Upload Files” button (Red arrow).



IV. Selecting a Target Genome

1. The next task is to select the target genome. It has to be the same as the genome in the experimental data you uploaded. In this instance, the reference genome was *Escherichia coli* MG1655. If you start typing MG1655 in the text box under “Target Genome” (Red arrow), PATRIC will display the best hits. There are quite a few there...how do you know that the one shown as selected (Blue arrow) is the right one.

Experiment Data

EXPERIMENT DATA FILE

Sangurdekar Microarray data - 2.xlsx

EXPERIMENT TYPE

Transcriptomics

TARGET GENOME

Optional

Experiment Data

EXPERIMENT DATA FILE

Sangurdekar Microarray data - 2.xlsx

EXPERIMENT TYPE

Transcriptomics

TARGET GENOME

MG1655
Escherichia coli strain K-12 substrain MG1655 [511145.209]
Escherichia coli str. K-12 substr. MG1655 JW5437-1 [511145.209]
Escherichia coli str. K-12 substr. MG1655 K-12 [511145.208]
Escherichia coli str. K-12 substr. MG1655star [879462.4]
Escherichia coli str. K-12 substr. MG1655 K-12 [511145.180]
Escherichia coli str. K-12 substr. MG1655 K-12 [511145.181]
Escherichia coli str. K-12 substr. MG1655 K-12 [511145.182]
Escherichia coli str. K-12 substr. MG1655 K-12 [511145.183]
Escherichia coli str. K-12 substr. MG1655 K-12 [511145.184]
Escherichia coli str. K-12 substr. MG1655 K12 [511145.12]

- The number that follows the name is the genome ID. If you click the Organism tab at the top of any PATRIC page, and then click on *Escherichia*, you will go to the landing page for that genus. Clicking on genome list will show all the genomes in *Escherichia*. MG1655 is a reference genome. You can find the genome ID by clicking on "Reference" in the filter (Red arrow). This will only show the reference genomes in the table

Taxon View

Bacteria » Proteobacteria » Gammaproteobacteria » Enterobacteriales » Enterobacteriaceae » **Escherichia** (4837 Genomes)

Overview

Phylogeny

Taxonomy

Genomes

Sequences

Features

Specialty Genes

Protein Families

Pathways

Transcriptomics

DOWNLOAD

KEYWORDS

REFERENCE

REFERENCE_GENOME x

HIDE

APPLY

Collection Year	Disease	Genome Status	Isolation Country	Public	Reference Genome
1922 (1)	Urinary tract infection (2)	Complete (6)	Japan (1)	true (6)	Reference (6)
1997 (1)	Hemolytic uremic syndrome (HUS) (1)				Representative (7)
	Hemorrhagic colitis (1)				

Genome Name	Genome ID	Genome Status	Sequence	PATRIC CDS	Isolation Country	Host Name	Disease	Collection Year	Completion Date
Escherichia coli IA139	585057.6	Complete	1	5094			Urinary tract infection		12/17/08
Escherichia coli O104:H4 str. 201	1133852.3	Complete	4	5479			Hemolytic uremic syndrome		9/26/12
Escherichia coli O83:H1 str. NRG	685038.3	Complete	2	4686					11/29/10
Escherichia coli UMN026	585056.7	Complete	3	5198			Urinary tract infection		12/17/08
Escherichia coli O157:H7 str. Sak	386585.9	Complete	3	5602	Japan		Hemorrhagic colitis	1997	3/28/00
Escherichia coli str. K-12 substr. MG1655	511145.12	Complete	1	4549				1922	9/4/97

- Click on the MG1655 genome (Red Arrow). This will load the vertical green bar with all the downstream processes that you can do with this genome. Click on the Genome icon (Blue arrow).

Overview Phylogeny Taxonomy **Genomes** Sequences Features Specialty Genes Protein Families Pathways Transcriptomics

DOWNLOAD KEYWORDS REFERENCE GENOME x HIDE APPLY


Collection Year	Disease	Genome Status	Isolation Country	Public	Reference Genome
1922 (1)	Urinary tract infection (2)	Complete (6)	Japan (1)	true (6)	Reference (6)
1997 (1)	Hemolytic uremic syndrome (HUS) (1)				Representative (7)
	Hemorrhagic colitis (1)				

↓ DWNLD GENOME GROUP

Genome Name	Genome ID	Genome Status	Sequenc	PATRIC CDS	Isolation Country	Host Name	Disease	Collectio Year	Comple Date
<input type="checkbox"/> Escherichia coli IA39	585057.6	Complete	1	5094			Urinary tract infection		12/17/08
<input type="checkbox"/> Escherichia coli O104:H4 str. 201	1133852.3	Complete	4	5479			Hemolytic uremic syndro		9/26/12
<input type="checkbox"/> Escherichia coli O83:H1 str. NRG	685038.3	Complete	2	4686					11/29/10
<input type="checkbox"/> Escherichia coli UMN026	585056.7	Complete	3	5198			Urinary tract infection		12/17/08
<input type="checkbox"/> Escherichia coli O157:H7 str. Sak	386585.9	Complete	3	5602	Japan		Hemorrhagic colitis	1997	3/28/00
<input checked="" type="checkbox"/> Escherichia coli str. K-12 substr. H	511145.12	Complete	1	4549				1922	9/4/97

1 - 6 of 6 results < 1 >

4. This will take you to the landing page for that genome, where you can see the specific genome ID (red box).

 **Escherichia coli str. K-12 substr. MG1655**

Length: 4639675bp, Chromosomes: 1, Plasmids: 0, Contigs: 0

Organism Info

Genome ID	511145.12
Genome Name	Escherichia coli str. K-12 substr. MG1655
NCBI Taxon ID	511145
Genome Status	Complete
Strain	K12
MLST	MLST.Escherichia_coli_1.10
Reference	Reference
Genome	

V. Experiment Information and Job Submission

- Next you will need to fill in all the metadata in the "Experiment Information" box (Red arrow). The PubMed ID is optional. When the information is filled out, click the submit button at the bottom of the page (Blue arrow).

Differential Expression Import
Transform differential expression data for viewing on PATRIC

Experiment Data

EXPERIMENT DATA FILE
Sangurdekar Microarray data - 2.xlsx

EXPERIMENT TYPE
Transcriptomics

TARGET GENOME
Escherichia coli str. K-12 substr. MG

Experiment Information

EXPERIMENT TITLE
Sangurdekar MG1655 data

EXPERIMENT DESCRIPTION
MG1655 stationary v stress conditions

ORGANISM NAME
Escherichia coli str. K-12 substr. MG1655

PUBMED ID
6626502

OUTPUT FOLDER
Experiments

Optional Metadata

METADATA FILE

Reset Submit

- A message appears underneath indicating that the data has been submitted (Red arrow).

Sangurdekar Microarray data - 2.xlsx

EXPERIMENT TYPE
Transcriptomics

TARGET GENOME
Escherichia coli str. K-12 substr. MG

Optional Metadata

METADATA FILE

Title

EXPERIMENT DESCRIPTION
MG1655 stationary v stress conditions

ORGANISM NAME
Escherichia coli str. K-12 substr. MG1655

PUBMED ID
6626502

OUTPUT FOLDER
Experiments

Conversion should be finished shortly. Check workspace for results.

Reset Submit

- Clicking on the Jobs button at the bottom of the page will show you the status of the job you submitted.

Uploads 0/0

Jobs 138/0/24

Status	Submit	App	Output Name	Start	Completed
completed	8/18/16, 9:23 AM	DifferentialExpression	Sangurdekar MG1655 data	8/18/16, 9:23 AM	8/18/16, 9:24 AM
completed	8/17/16, 6:19 PM	DifferentialExpression	MG 1655 exposed to kanamycin	8/17/16, 6:19 PM	8/17/16, 6:19 PM
completed	8/16/16, 11:05 AM	Proteome Comparison	B microti v GenBank microti	8/16/16, 11:05 AM	8/16/16, 11:06 AM
completed	8/15/16, 3:57 PM	DifferentialExpression	MG1655 exposed to antibiotics 5	8/15/16, 3:57 PM	8/15/16, 3:57 PM
completed	8/15/16, 3:08 PM	DifferentialExpression	MG1655 exposed to kanamycin 3	8/15/16, 3:08 PM	8/15/16, 3:09 PM
completed	8/12/16, 7:48 AM	DifferentialExpression	MG1655 exposed to kanamycin v2	8/12/16, 7:48 AM	8/12/16, 7:49 AM
completed	8/12/16, 7:40 AM	DifferentialExpression	MG1655 exposed to	8/12/16, 7:40 AM	8/12/16, 7:41 AM