

Find papers where a gene is differentially expressed

1) Click here to go to the expression page



The screenshot shows the PortEco website interface. At the top, the browser address bar displays "http://www.porteco.org/". The website header features the "PORT Eco" logo and a navigation menu with the following items: Home, About PortEco, Gene Expression, Genetics/Phenotypes, EcoWiki, EcoCyc, Community, Databases & Downloads, and Help/Tutorials. A blue arrow points from the text "1) Click here to go to the expression page" to the "Gene Expression" link in the navigation menu. Below the navigation menu, there are three main sections:

- WHAT CAN I DO?**
 - Find data for a particular gene**: Includes a search input field and a "Search" button.
 - Find and analyze datasets**: Includes a list of options: "Browse and select experimental conditions or specific publications", "Optionally specify a list of genes", "Cluster selected datasets", and "Find genes with significant phenotypes or expression in selected datasets". Below this list are two buttons: "Phenotype Data" and "Expression Data".
 - Browse and search other datasets**: Includes the text "Browse and search other high-throughput datasets available in a genome browser" and a "Go" button.
- PortEco is a next-generation data resource for the bacterial model organism, Escherichia coli**: Includes a "[Read more...]" link.
- PortEco Resources**: Includes a list of resources:
 - Pathway/Genome Databases for 130 E. coli genomes are available at BioCyc.org including curated databases for *E. coli* B Rel 606 and *E. coli* W3110
 - EcolHouse provides a publicly queryable MySQL database warehouse for E. coli data
 - Community features including colleague search, event calendar, job postings
 - E. coli systems models at BioModels
 - PortEco data downloads and database access
 - PortEco also supports manual curation of Gene Ontology terms from published papers at EcoCyc
- PortEco News and Events**: Includes two news items, each with a title and a "[Read more...]" link:
 - Bioinformatics ?office hours? at the Phage Meeting**: PortEco blog > PortEco: by jimhu (1 month ago.): We will be having "bioinformatics office hou...[Read more...]
 - Ribosome profiling phage lambda induction**: PortEco blog > PortEco: by jimhu (1 month ago.): The lysis-lysogeny switch of bacteriophage lambda ...[Read more...]

2) Enter the gene name in the Profiles search box and click 'Go'

PortEco : Expression

http://expression.porteco.org/

PORT *Eco*

portal for *E. coli* research

Home About PortEco Gene Expression Genetics/Phenotypes EcolWiki EcoCyc Community Databases & Downloads Help/Tutorials

Search Create Gene List (Beta) Cluster My Genes Gene Profiles Samples & Conditions Download Data Publications

PortEco: Expression holds post-publication microarray gene expression data from *E. coli* experiments. Our goal is to provide free access to all published *E. coli* expression data. If you would like to use PortEco: Expression to share your expression data, please [contact us](#).

Many of the search items below require a search term. Some of the queries expect a gene locus term such as 'lacZ' (without the quotes). Wildcard characters, '*' and '%' may also be used. For example 'lac*' (without quotes).

SEARCH

- Genes
 - Conditions Go
 - Profiles Go
 - Cluster My Genes ClusterMyGenes
- Experiments
 - Publications Go
 - Samples Go
 - Analyze Analyze

DOWNLOAD

- Array Data Go

Upload genelist, select samples, cluster.

select experiments and enter the analysis pipeline

News:

February 20, 2013: We are in the process of migrating published *E. coli* microarray data into PortEco: Expression. Currently we have 2056 published microarrays from 117 publications. For more information about our import plans, please refer to our [progress page](#).

Recent publication:

Vinella D, Potrykus K, Murphy H, Cashel M (2012): Effects on growth by changes of the balance between GreA, GreB, and DksA suggest mutual competition and functional redundancy in *Escherichia coli*. *J Bacteriol* 194(2):261-73

To cite SMD, please refer to:
Hubble J, Demeter J, Jin H, Mao M, Nitzberg M, Reddy TB, Wymore F, Zachariah ZK, Sherlock G, Ball CA. Implementation of GenePattern within the Stanford Microarray Database. *Nucleic Acids Res* 2009 Jan 1; **37(Database Issue)**:D898-901
Full text | PubMed

3) *fepB* is differentially expressed in 75 experiment sets. Scroll down to browse the experiment sets and find one of interest.

The screenshot shows a web browser window with the URL <http://expression.porteco.org/cgi-bin/expression/geneExpression.pl?name=fepB>. The page title is "PortEco : Expression". The header features the "PORT Eco" logo and a navigation menu with items like Home, About PortEco, Gene Expression, Genetics/Phenotypes, EcoI/WMI, EcoCyc, Community, Databases & Downloads, and Help/Tutorials. A search bar and a "Sign In" link are also present.

The main content area is titled "Gene Profiles" and displays a list of experiments where the gene *fepB/EG10294* is profiled. The first entry is titled "Antagonistic regulation of motility and transcriptome expression by RpoN and RpoS in Escherichia coli." by Dong T, et al. (2011) *Mol Microbiol* 79(2):375-86. It includes a brief abstract, a link to "View *fepB/EG10294* gene profile across 9 experiments" with a small heatmap icon, and a "Download gene expression data in PCL format" link.

The second entry is titled "Rapid acid treatment of Escherichia coli: transcriptomic response and recovery." by Kannan G, et al. (2008) *BMC Microbiol* 8():37. It includes a background paragraph, a link to "View *fepB/EG10294* gene profile across 20 experiments" with a heatmap icon, and a "Download gene expression data in PCL format" link.

4) Let's look at how *fepB* is expressed during biofilm maturation by clicking on the profile icon for Ito et al. (2009).

PortEco - Expression


http://expression.porteco.org/cgi-bin/expression/geneExpression.pl?name=fepB

Google

Increased antibiotic resistance of Escherichia coli in mature biofilms.

Ito A, et al. (2009) Appl Environ Microbiol 75(12):4093-100

Gene expression changes during biofilm formation processes were investigated. The gene expression was compared at attachment, colony formation and maturation during biofilm formation. At the same time, the gene expressions were also compared with exponential phase and stationary phase in planktonic cells. The gene expression pattern at attachment and colony formation processes showed similar pattern with those in ... [Expand](#)


[View fepB/EG10294 gene profile across 9 experiments](#) 

[Download gene expression data in PCL format](#)

The expression profile of Escherichia coli K-12 in response to minimal, optimal and excess copper concentrations.

Kershaw CJ, et al. (2005) Microbiology 151(Pt 4):1187-98

The gene expression profile of E. coli K-12 MG1655 Seq (CGSC7740) grown in minimal medium supplemented with elevated copper concentrations (as copper-glycine) has been analysed using whole genome oligonucleotide microarrays. Reference RNA was a pool of RNA isolated from five independently grown 50ml DMA cultures of E. coli K-12 MG1655 Seq (CGSC7740). RNA was isolated from three independently grown 50ml DMA cultures ... [Expand](#)


[View fepB/EG10294 gene profile across 9 experiments](#) 

[Download gene expression data in PCL format](#)

Effect of the global regulators RpoS and cyclic-AMP/CRP on the transcriptome of Escherichia coli K12 during carbon- and energy-limited growth

Franchini, AG, Ihssen J, and Egli T ()

The faecal indicator bacterium Escherichia coli K12 was used to study the effects of the global regulators RpoS and cAMP at the transcription level using microarray technology during short-term (physiological) adaptation to slow growth under limited nutrient supply. Effects due to the absence of one global regulator were assessed by comparing the mRNA levels isolated from rpoS or cya mutants under glucose-limited ... [Expand](#)

[View fepB/EG10294 gene profile across 6 experiments](#) 

[Download gene expression data in PCL format](#)

The PurR regulon in Escherichia coli K-12 MG1655.

Cho BK, et al. (2011) Nucleic Acids Res 39(15):6456-64

5) Gene profile displaying the log₂ expression ratios across 15 samples.

a) Heat map for the entire experiment. Use the '+' and '-' buttons to resize the display.

b) Sample names

c) The zoom window shows the profile for *fepB*.

d) Additional tools

portal for *E. coli* research

Home About Portal Gene Expression Genetics/Phenotypes EcoWiki EcoCyc Community Databases & Downloads Help/Tutorials

Search Create Gene List (Beta) Cluster My Genes Gene Profiles Samples & Conditions Download Data Publications

Hover mouse over elements in zoom window to see more information here Search for [] go Show Quick Help gene explorer Help

Gene Profiles Ito A, et al. (2009) Appl Environ Microbiol 75(12):4093-100

Most similar (orange) and dissimilar (gray) expression patterns for: *fepB* / EG10294

K-12 MG1655, Planktonic cells in exponential phase, rep. 1
K-12 MG1655, Planktonic cells in exponential phase, rep. 2
K-12 MG1655, Planktonic cells in exponential phase, rep. 3
K-12 MG1655, Biofilm-attachment stage, rep. 1
K-12 MG1655, Biofilm-attachment stage, rep. 2
K-12 MG1655, Biofilm-attachment stage, rep. 3
K-12 MG1655, Biofilm-colony stage, rep. 1
K-12 MG1655, Biofilm-colony stage, rep. 2
K-12 MG1655, Biofilm-colony stage, rep. 3
K-12 MG1655, Biofilm-maturation stage, rep. 1
K-12 MG1655, Biofilm-maturation stage, rep. 2
K-12 MG1655, Biofilm-maturation stage, rep. 3
K-12 MG1655, Planktonic cells in stationary phase, rep. 1
K-12 MG1655, Planktonic cells in stationary phase, rep. 2
K-12 MG1655, Planktonic cells in stationary phase, rep. 3

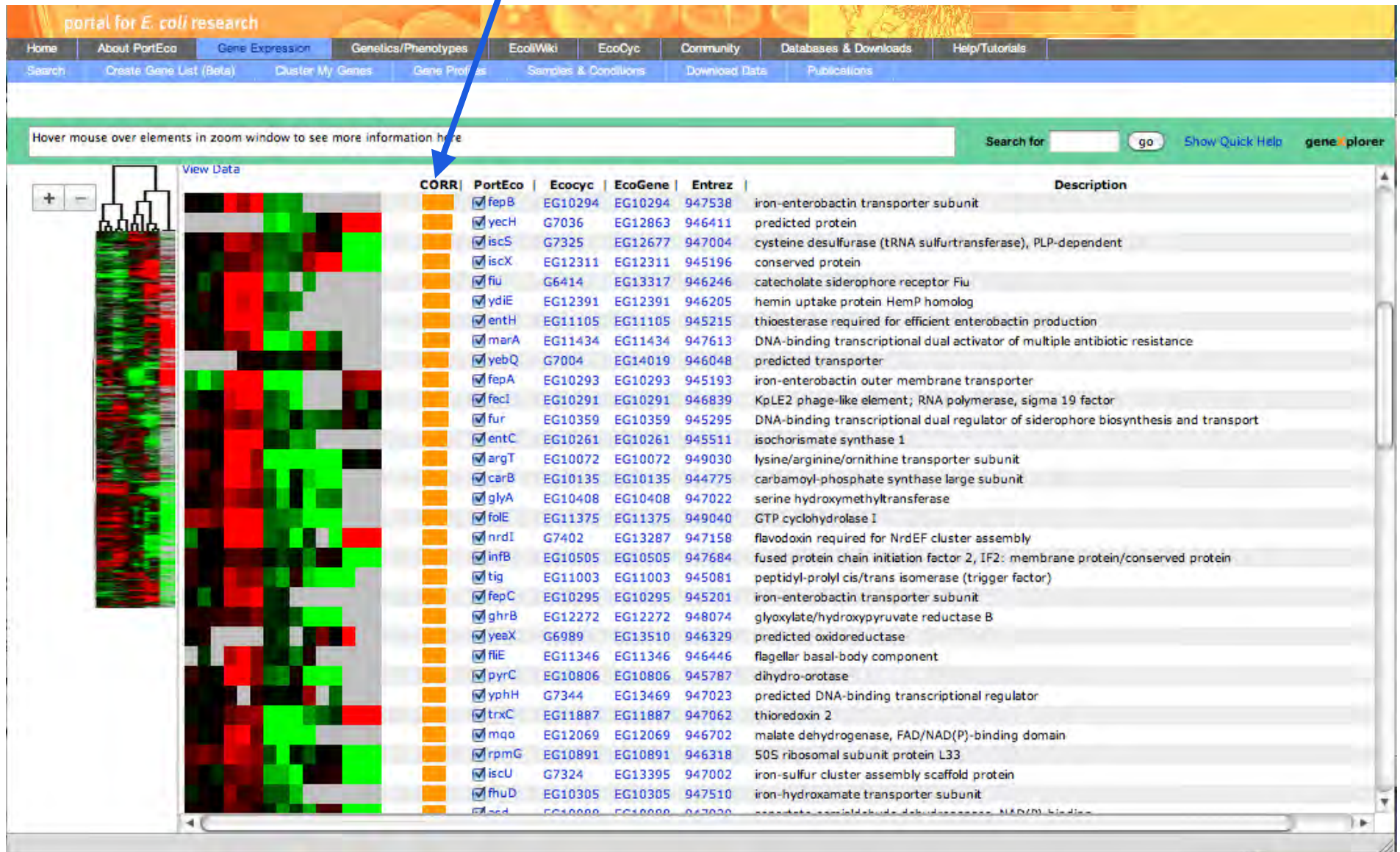
Log (base 2) ratio
< -1.9 < -1.6 < -1.4 < -1.2 1:1 > 1.2 > 1.4 > 1.6 > 1.9

View Data

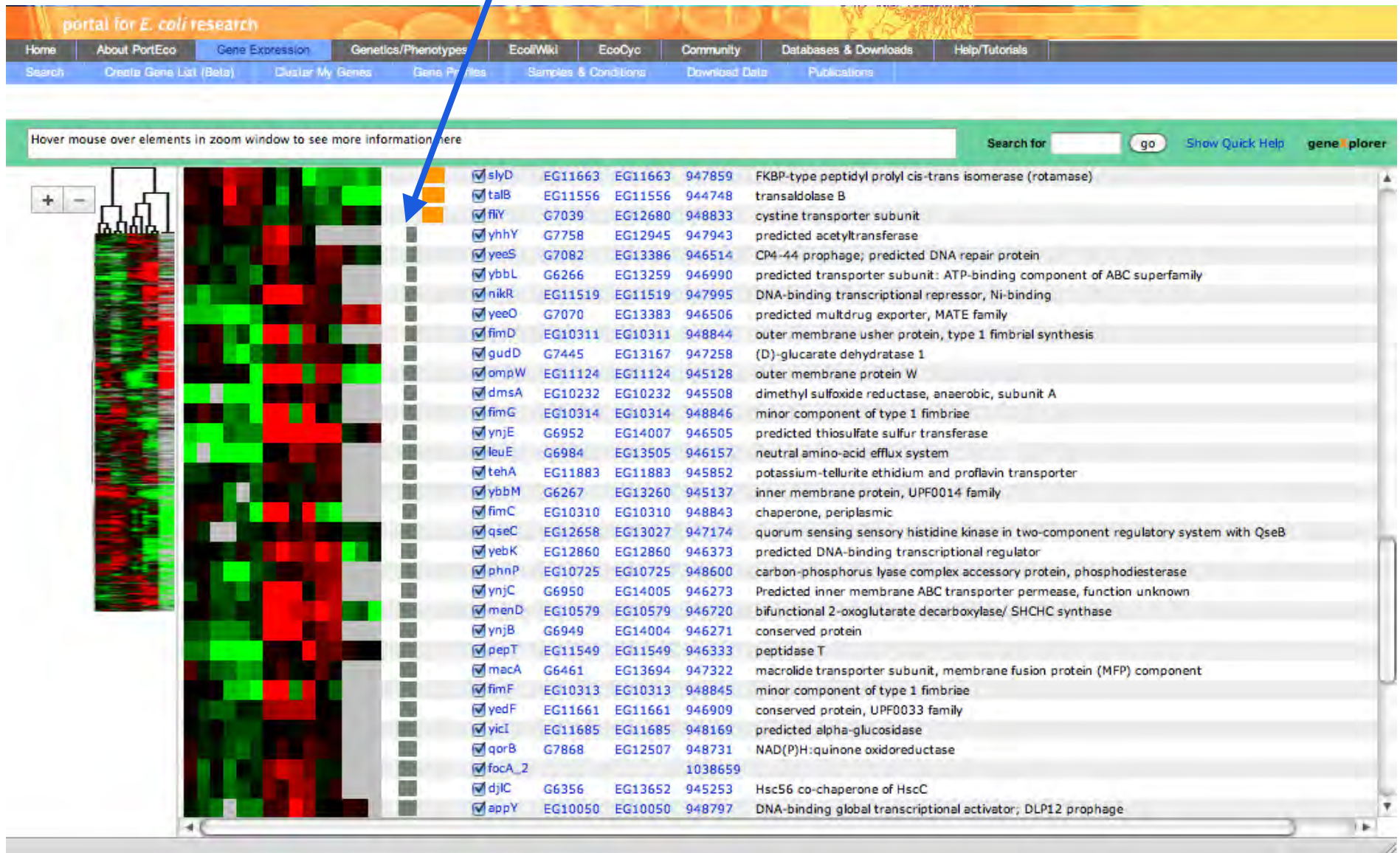
CORR	PortEco	EcoCyc	EcoGene	Entrez	Description
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	iron-enterobactin transporter subunit
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	predicted protein
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	cysteine desulfurase (tRNA sulfurtransferase), PLP-dependent
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	conserved protein
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	catecholeate siderophore receptor Fiu
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	hemin uptake protein HemP homolog
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	thioesterase required for efficient enterobactin production
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	DNA-binding transcriptional dual activator of multiple antibiotic resistance

Show Pathways
Create EcoCyc Group
PANTHER Overrepresentation Tool
Create Gene List (Beta)
GO Term Finder

6) This display also shows the \log_2 expression ratios for genes whose expression is correlated (this page) or anticorrelated (next page) with *fepB*. Mouse over the orange (or gray) box in the Correlation column to see the correlation coefficient.



7) Genes whose expression profile is anticorrelated with that of *fepB* are marked by gray boxes.



8) The correlated and anticorrelated genes can be examined further using one of the tools highlighted below. The next slide shows the result of clicking the 'GO Term Finder'.

portal for *E. coli* research

Home About PortEco Gene Expression Genetics/Phenotypes EcoWiki EcoCyc Community Databases & Downloads Help/Tutorials

Search Create Gene List (Beta) Cluster My Genes Gene Profiles Samples & Conditions Download Data Publications

Hover mouse over elements in zoom window to see more information here Search for go Show Quick Help gene explorer Help

Gene Profiles : Ito A, et al. (2009) Appl Environ Microbiol 75(12):4093-100

Most similar (orange) and dissimilar (gray) expression patterns for: *fepB* / EG10294

Depending on the tool to be used, you can select all or only a subset of the samples to look at.

Log (base 2) ratio

< 1/1.9 < 1/1.6 < 1/1.4 < 1/1.2 1:1 > 1.2 > 1.4 > 1.6 > 1.9

View Data

CORR	PortEco	EcoCyc	EcoGene	Entrez	Description
Orange	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<i>fepB</i> , EG10294, 947538 iron-enterobactin transporter subunit
Orange	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<i>yecH</i> , G7036, EG12863, 946411 predicted protein
Orange	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<i>iscS</i> , G7325, EG12677, 947004 cysteine desulfurase (trna sulfurtransferase), PLP-dependent
Orange	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<i>iscX</i> , EG12311, EG12311, 945196 conserved protein
Orange	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<i>fiu</i> , G6414, EG13317, 946246 catechololate siderophore receptor Fiu
Orange	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<i>ydiE</i> , EG12391, EG12391, 946205 hemin uptake protein HemP homolog
Orange	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<i>entH</i> , EG11105, EG11105, 945215 thioesterase required for efficient enterobactin production
Orange	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<i>marA</i> , EG11434, EG11434, 947612 DNA-binding transcriptional dual activator of multiple antibiotic resistance

Additional tools

- Show Pathways
- Create EcoCyc Group
- PANTHER Overrepresentation Tool
- Create Gene List (Beta)
- GO Term Finder

9) The group of genes including *fepB* and genes expressed like *fepB* is enriched for the biological process of 'iron ion homeostasis'.

portal for *E. coli* research

Home About PortEco Gene Expression Genetics/Phenotypes EcolWiki EcoCyc Community Databases & Downloads Help/Tutorials

Search Create Gene List (Beta) Cluster My Genes Gene Profiles Samples & Conditions Download Data Publications

Check input data...

You entered 101 Gene_Symbols.

Process ontology term finder...

Get associated annotation data -> Get term finder background information ->

88 Gene_Symbol(s) have been associated with an ontology in our database.
13 Gene_Symbol(s) have not been associated with an ontology in our database.

Get ontology data -> Get ontology term finder

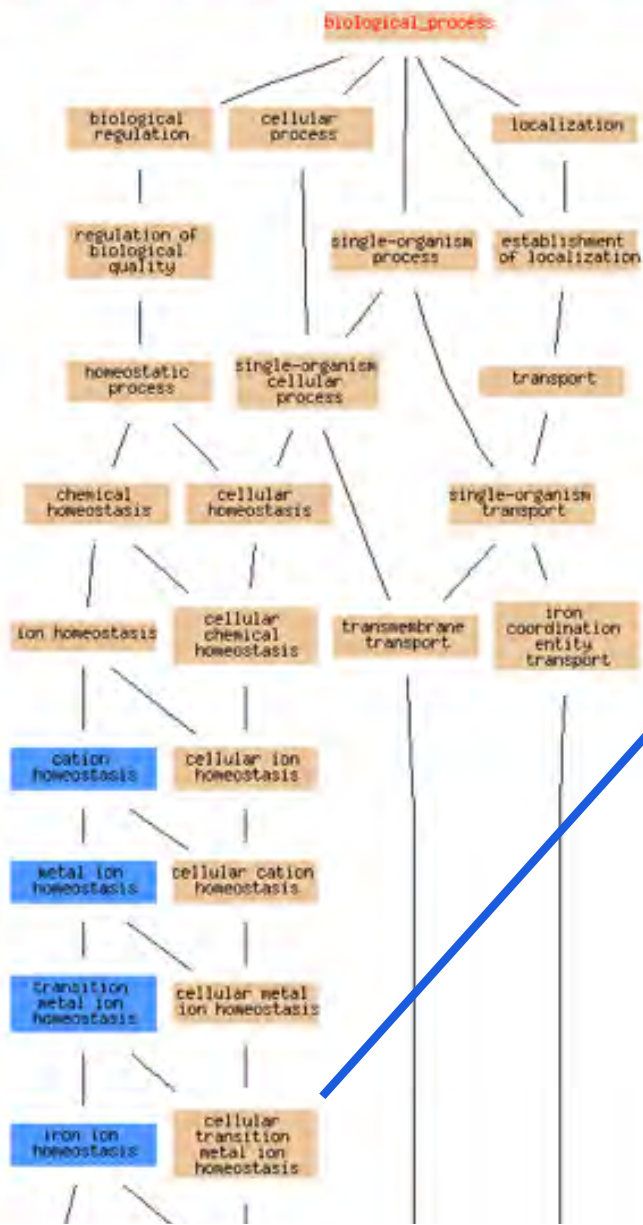
Terms from the **biological_process** ontology with a Corrected P-value more significant than .05

pvalue: <=1e-10 1e-10 to 1e-8 1e-8 to 1e-6 1e-6 to 1e-4 1e-4 to 1e-2 >0.01

```
graph TD;
    bp[biological_process] --> br[biological regulation];
    bp --> cp[cellular process];
    bp --> loc[localization];
    br --> rbq[regulation of biological quality];
    cp --> sop[single-organism process];
    loc --> el[establishment of localization];
    rbq --> hp[homeostatic process];
    sop --> socp[single-organism cellular process];
    el --> tr[transport];
```

The complete results are shown on the next slide.

value: <1e-10 1e-10 to 1e-8 1e-8 to 1e-6 1e-6 to 1e-4 1e-4 to 1e-2 >0.01



pvalue: <1e-10 1e-10 to 1e-8 1e-8 to 1e-6 1e-6 to 1e-4 1e-4 to 1e-2 >0.01

