

## *Expression Atlas: exploring expression results*

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This practical will introduce you to the data content and functionality of Expression Atlas ([www.ebi.ac.uk/gxa/home](http://www.ebi.ac.uk/gxa/home)) at EMBL-EBI.

More information can be found on:

- Expression Atlas: Quick tour: <https://www.ebi.ac.uk/training/online/course/expression-atlas-quick-tour-1>
- Expression Atlas help page: <https://www.ebi.ac.uk/gxa/help/index.html>
- Expression Atlas FAQ section: <https://www.ebi.ac.uk/gxa/FAQ.html>



### *Exercise 1*

*Baseline Expression - Look up expression of **TNNI3** gene in normal human tissues*

#### *Scenario*

Imagine you are reading a manuscript about regulation of gene expression in liver cancer patients. In the paper, authors presented evidence that one gene, *TNNI3*, is down-regulated in cancer patients when compared to healthy controls.

*TNNI3* stands for “troponin I3, cardiac type”. You vaguely remember that troponins are responsible for muscle contraction, and since there is no muscle in liver, you are sceptical about the authors’ findings in liver. So, you decide **to look up *TNNI3* in Expression Atlas to see in which tissues the gene is expressed in healthy individuals.**

#### *Tasks – Gene search*

Use the **Gene / Gene properties search box** on Expression Atlas home page to search for *TNNI3* gene. Start typing the first characters of *TNNI3* gene and you will see a list of suggested genes including it. As you want to explore the results in human you can be more specific in your search selecting *Homo sapiens* as organism.

The Baseline Expression results will display all tissues (columns) studied in different experiments (rows) in which *TNNI3* gene is expressed above minimum expression level. By default we display expression data for different tissues but you can use the filters to explore *TNNI3* expression in other conditions such as cell lines, cell types...

### Tasks – Baseline expression results

1. Is *TNNI3* gene expressed in liver? Do the experiments agree on this? Also the proteomics ones?  
*Hint:* In order to see gene expression in liver, you can either select a section of the heatmap to zoom in or use the **Filters** button above the heatmap to select the organ you are interested in.
2. In which tissues *TNNI3* gene is highly expressed?  
*Hint:* You can sort the heatmap results by '**gene expression rank**' using one of the buttons above the heatmap.
3. Where do we find the highest levels of *TNNI3* protein?

### Tasks – Gene annotations

4. Can you find more information about *TNNI3* gene function?  
*Hint:* Try the **TNNI3 information** tab.
5. Do you think the *TNNI3* expression pattern correlated well with *TNNI3* gene function?

### Tasks – Baseline experiment page

6. Let's have a look at the data from the Genotype-Tissue Expression (GTEx) Project by clicking on the particular dataset "GTEx" in the **Baseline expression results**. In which tissue is *TNNI3* highest expressed in that experiment? What is the expression level in that tissue?
7. Can you find more data about variation of *TNNI3* gene expression among biological replicates in that tissue? How many biological replicates were tested for that particular tissue? What is the maximum expression value among them?  
*Hint:* Click on **Switch to boxplot view**
8. Now, let's find more information about *TNNI3* gene. How many transcripts does this gene have? On which chromosome would you find them?  
*Hint:* click on 'Select genome browser to view tracks' button above the heatmap, select '**Ensembl genome browser**' and click on a cell of the heatmap (e.g. the

tissue with the highest expression value) to see *TNNI3* gene expression in the context of the genomic location of the gene.

9. We can also find the subset of genes that are most specifically expressed in liver. According to GTEx experiment, what is the most specifically expressed gene in liver? What is the expression level of that gene in liver?

*Hint:* If you want to see gene expression results not only for *TNNI3* gene, you have to remove it from the Genes search box and click Apply. Now you can use the **Organism parts** select button to sort the heatmap results and select to see genes highly specifically expressed just in one tissue, e.g. liver.

10. What is the expression of that gene in the rest of the tissues?

*Hint:* Use the **Genes search box** to see its gene expression across tissues.

11. What is the gene with the highest expression in liver? What is the expression level of that gene in liver?

*Hint:* try unchecking **Most specific option**.

12. What is the expression of that gene in the rest of the tissues?

*Hint:* Use the **Genes search box** to see its gene expression across tissues.

In this exercise we have used Expression Atlas to find out in which conditions (tissues in that example) is a particular gene expressed. To answer this kind of questions we use the Gene /Gene properties search box on the home page.

We can also use Expression Atlas in a baseline context to answer questions such as what genes are expressed in a particular condition? For example, what genes are expressed in human kidney? To answer this kind of questions we use the Biological condition search box on the home page.