

## *Expression Atlas: exploring expression data*

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This practical will introduce you to the data content and functionality of Expression Atlas. More information can be found on the dedicated help page: <https://www.ebi.ac.uk/gxa/help/index.html> and on the Expression Atlas FAQ section: <https://www.ebi.ac.uk/gxa/FAQ.html>



### *Exercise 2*

#### *Differential Expression – Find differentially expressed genes in patients with hepatocellular carcinoma*

##### *Scenario*

After reading the paper about regulation of gene expression in liver cancer patients you would like to find what are the results (if any) in other datasets studying the same topic. So, you decide to check if there is any dataset in Expression Atlas related to hepatocellular carcinoma (liver cancer).

##### *Tasks – Differential expression results*

Use the **Condition query search box** on Expression Atlas home page to search for hepatocellular carcinoma. Start typing the first characters of hepatocellular carcinoma and you will see a list of terms including it. As you want to explore the results in human you can be more specific in your search selecting Homo sapiens as organism.

As you are interested in finding differentially expressed genes in liver cancer patients, let's have a look at **Differential expression results**. You will see a table with a maximum of 1,000 genes differentially expressed in each of the comparisons that involve hepatocellular carcinoma.

Can you find any dataset that compares liver tumor samples vs. liver samples from healthy individuals? What about comparing liver tumor samples from a patient vs. adjacent non-tumor liver tissues? What samples are considered as “reference” or control group?

*Hint:* When you mouse over the title of each comparison you will see more details about the samples compared.

## Tasks – Differential experiment page

Let's have a look at the experiment '*Transcriptome sequencing of human hepatocellular carcinoma*'.

1. What is the gene with the highest up-regulation? What is the more down-regulated one?
2. Are both genes the result of the same comparison? How many comparisons does this experiment involve?
3. How many patients were studied? *Hint:* Explore the **Experimental Design** tab
4. How many genes are differentially expressed in that experiment. How many are up-regulated? And down-regulated?
5. What is the criterion for considering a gene as differentially expressed?
6. How many genes are differentially expressed with a more stringent criteria of absolute value of log<sub>2</sub>-fold change > 2 and adjusted p-value < 0.01?
7. Are there any pathways enriched in the list of differentially expressed genes? Or more specifically, is there any Gene Ontology, InterPro or Reactome term statistically over-represented in the set of genes that are differentially expressed? *Hint:* Explore the **Plots** tab.