



## Expression Atlas : Quick tour

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## PRESENTATION



## Expression Atlas



# Expression Atlas



Expression Atlas(<http://www.ebi.ac.uk/gxa>) is an added value database that provides information about gene and protein expression in different species and contexts, such as tissue, developmental stage, disease or cell type.

Expression Atlas aims

- To serve a wide research community by providing data sets from different organisms, including plants and metazoans.
- To help answer questions such as 'where is a certain gene expressed?' or 'how does its expression change in a disease?'.



**Figure 1.** Expression Atlas includes data curation, analysis, search and visualisation of gene expression experiments

Expression Atlas contains thousands of selected **microarray and RNA-sequencing** (RNA-seq) experiments **from public repositories such as...**

- ArrayExpress
- European Nucleotide Archive(ENA) at EMBL-EBI
- Gene Expression Omnibus(GEO) at NCBI.

**Controlled access datasets** such as...

- The European Phenome-Genome Archive(EGA)
- The database of Genotypes and Phenotypes(dbGAP)

Current **criteria for selection and inclusion of a gene expression dataset** in Expression Atlas are:

- The study must be of general interest
- It must be performed on a species from which a good quality reference genome build is available
- For microarray data, it must be possible to re-annotate the array design against Ensembl
- The study must include at least three biological replicates
- Clear experimental variables must be available



The data sets in Expression Atlas are classified either as **baseline** or **differential**.

Search Gene set enrichment

Gene / Gene properties Enter gene query...  
Examples: REG1B, zinc finger, Q14777 (UniProt), GO:0010468 (regulation of gene expression)

Species Any

Biological conditions Enter condition query...  
Examples: lung, leaf, valproic acid, cancer

Search Clear

Animals Plants Fungi

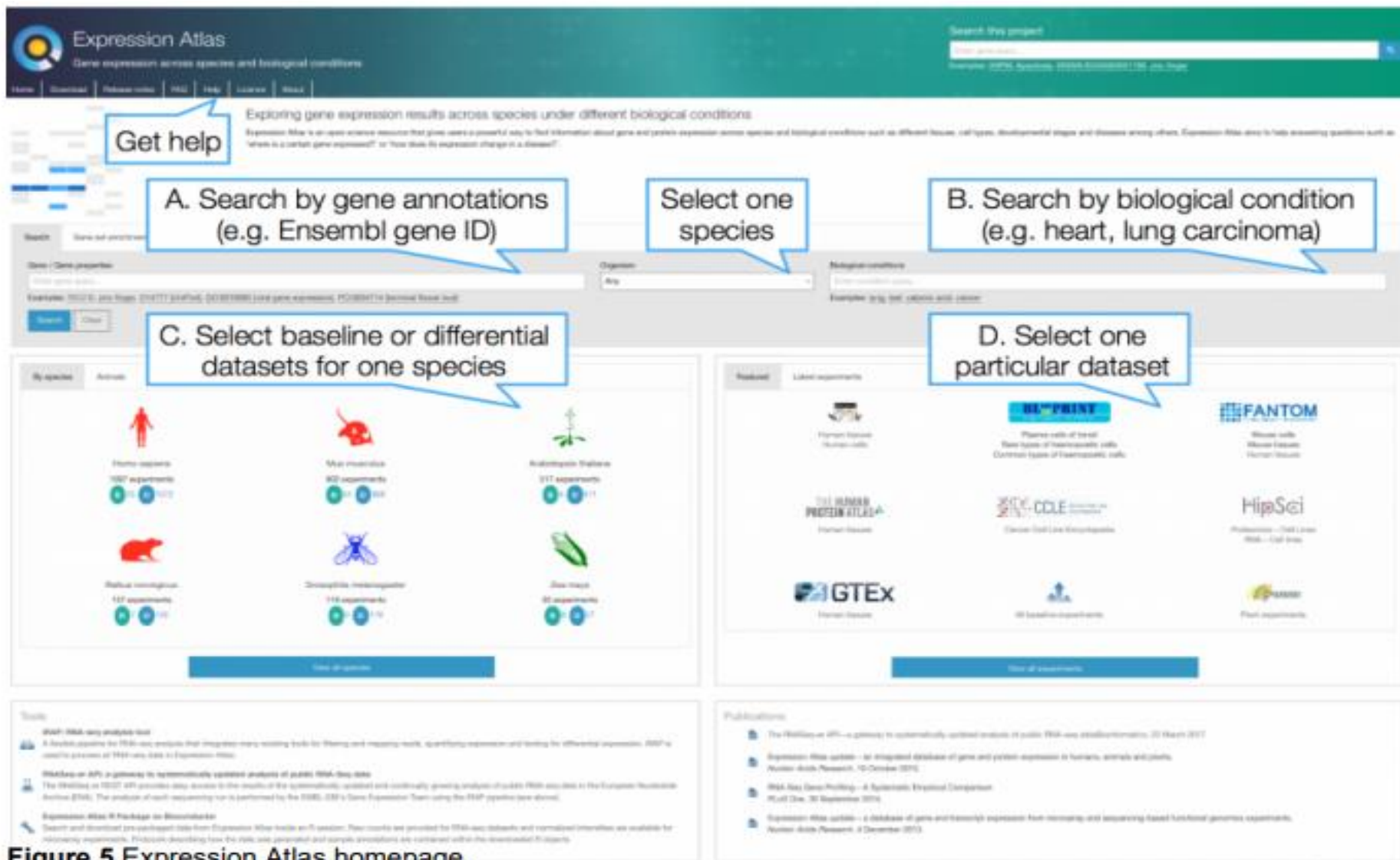
Species	Experiments	Baseline	Differential
Homo sapiens	1403 experiments	57	1346
Mus musculus	1137 experiments	45	1092
Rattus norvegicus	150 experiments	3	147
Drosophila melanogaster	138 experiments	2	136
Gallus gallus	36 experiments	3	33
Caenorhabditis elegans	28 experiments	1	27

Baseline Differential

Show experiments of all species

**The baseline data** sets report transcript or protein abundance typically in constitutive conditions, such as healthy tissues, cell types, developmental stages or cell lines. Baseline data sets are sourced from selected, high-quality RNA-Seq data sets, and in addition, several proteomics data sets have also been included recently.

**Differential** studies report changes in expression between two different conditions, such as healthy and diseased tissue



**Figure 5** Expression Atlas homepage.

