

# Data mining with Ensembl Biomart (answers to questions)

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# Start using Ensembl/BioMart

- Go to Ensembl website <http://www.ensembl.org/index.html>
- Scroll down a bit and click on View in archive site
- Click on Ensembl 85 : Dec 2016

View in archive site

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Help topics

- Frequently Asked Questions
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The following archives are available for this page:



- [Ensembl GRCh37](#): Full Feb 2014 archive with BLAST, VEP and BioMart
- [Ensembl 89: May 2017](#) (GRCh38.p10) - patched/updated gene set Jan 2017
- [Ensembl 88: Mar 2017](#) (GRCh38.p10)
- [Ensembl 87: Dec 2016](#) (GRCh38.p7)
- [Ensembl 86: Oct 2016](#) (GRCh38.p7)
- [Ensembl 85: Jul 2016](#) (GRCh38.p7) - patched/updated gene set Jun 2016
- [Ensembl 84: Mar 2016](#) (GRCh38.p5)

- Click on BioMart in the top menu

Archive! Ensembl | BioMart | Tools | Downloads | Help & Documentation | Blog

- CHOOSE DATABASE : select “Ensembl Genes 85”
- CHOOSE DATASET : select “Homo sapiens genes (GRCh38.p7)”



# Exercise 1: get annotations of a gene

- 1.
  - Click on Filters (left panel),
  - Expand the “GENE” section
  - Select “Input external references ID list”, select “HGNC symbol(s) in the drop down list and enter IDH1.
  - Click on Count in the top left panel  . You should get **Dataset 1 / 63333 Genes**
  - Click on Attributes (left menu)
  - Select “Features” (selected by default)
  - Select Gene ID, Transcript ID and associated Gene Name
  - Click on Results (top left menu) 



Gene ID	Transcript ID	Associated Gene Name
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000345146</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000446179</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000415913</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000484575</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000415282</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000462386</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000417583</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000451391</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000481557</a>	<a href="#">IDH1</a>

- 9 transcripts are found




# Exercise 1: get annotations of a gene

- 2.
  - You can leave the Dataset and Filters the same, and go directly to the Attributes section
  - Click on Attributes (left panel)
  - Select “Sequences”
  - Expand the SEQUENCES section
  - Select Exon sequences
  - Expand “Header Information”
  - Unselect “Gene ID” (Gene Information)
  - Select Associated gene name (Gene Information), transcript IDs (Transcript Information) and Exon IDs (Exon Information).
  - Click on Results 
- 3.
  - You can leave the Dataset and Filters the same, and go directly to the Attributes section
  - Click on Attributes (left panel)
  - In the SEQUENCES section
  - select Coding sequence
  - “Header Information”: unselect Associated gene name (Gene Information) and select transcript ID (Transcript Information) and Exon IDs (Exon Information).
  - Click on Results 


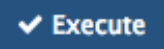
# Exercise 1: get annotations of a gene

- 4.
  - You can leave the Dataset and Filters the same, and go directly to the Attributes section
  - Click on Attributes (left panel)
  - Select “Features” (selected by default)
  - In the GENE section: Gene ID, Transcript ID and Associated Gene Name should be selected
  - Expand the EXTERNAL section
  - Select GO Term Name, GO domain and GO Term Accession
  - Click on Results 
- 5.
  - You can leave the Dataset and Filters the same, and go directly to the Attributes section
  - Click on Attributes (left panel)
  - Select “Variant (Germline)”
  - In the GENE section: Gene ID, Transcript ID and Associated Gene Name should be selected
  - Expand the GERMLINE VARIANT INFORMATION section
  - Select Variant Name, Variant Alleles, Minor allele frequency, Chromosome/scaffold name, Chromosome /scaffold position start (bp), Chromosome/scaffold position end (bp), Variant Consequence 
  - Click on Results


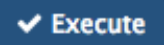
## Exercise 2: get annotations for a set of genes

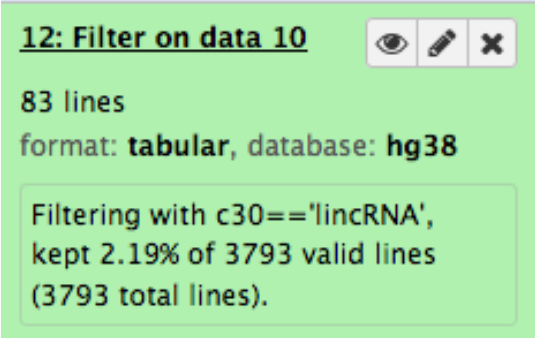
- 2.
  - In Ensembl/BioMart, create a new request (see slide 2.)
  - Click on Filters (left panel)
  - Expand the GENE section
  - Select “Input external references ID list” and select “Gene ID(s)” in the drop down list
  - Click on “Browse” and select the file siMitfvssiLuc.up.txt
  - Click on “Count” (top left button)  **Count**. You should have the number of genes you have in your file generated by SARTools: 3792
  - Click on Attributes (left panel)
  - Select “Features” (selected by default), select Ensembl Gene ID, Chromosome/scaffold name, Gene Start (bp), Gene End (bp), Strand, Associated Gene Name and Gene type.
  - Click on Results  **Results**
  - Select Compressed file (.gz) in the drop down menu. Click on Go  **Go** to download the resulting file.




## Exercise 2: get annotations for a set of genes

- 3.
  - Go to GalaxEast (<http://use.galaxeast.fr>)
  - Open the upload utility: click on  in top of the tool panel and drag and drop your files (siMitfvssiLuc.up.txt and mart\_export.txt.gz) into the opened window
  - Click on Start
- 4.
  - Run the tool “Join Two Datasets”
    - Join: siMitfvssiLuc.up.txt
    - Using column: Column: 1
    - With: mart\_export.txt
    - And column: Column: 1
    - Keep lines of first input that do not join with second input: No
    - Keep lines of first input that are incomplete: No
    - Fill empty columns: No
    - Click on Execute 

## Exercise 2: get annotations for a set of genes

- 5.
  - Click on the button  of the dataset you've just generated “join two datasets on (...)”
  - In the “Attributes” tab, enter siMitfvssiLuc.up.annot.txt in the text box “Name”.
  - Click on Save
- 6.
  - Run the tool “**Filter** data on any column using simple expressions” with the following parameters
    - Filter: siMitfvssiLuc.up.annot.txt
    - With following condition: c30=="lincRNA"
    - Number of header lines to skip: 1
    - Click on Execute 



**12: Filter on data 10**   

83 lines  
format: **tabular**, database: **hg38**

Filtering with c30=='lincRNA',  
kept 2.19% of 3793 valid lines  
(3793 total lines).



## Exercise 2: get annotations for a set of genes

- 7.
  - Don't change Dataset and Filters – simply click on Attributes.
  - Click on Attributes (left panel)
  - Select “Sequences”
  - Expand the SEQUENCES section
  - Select Flank (Transcript) and enter 2000 in the Upstream flank text box
  - Expand the Header information section
  - Select, in addition to the default selected attributes, Description and Associated Gene Name
  - Note: Flank (Transcript) will give the flanks for all transcripts of a gene with multiple transcripts. Flank (Gene) will give the flanks for one possible transcript in a gene (the most 5' coordinates for upstream flanking)

## Exercise 3: get annotations in the genome

- 1.
  - In Ensembl/BioMart, create a new request (see slide 2.)
  - Click on Filters (left panel)
  - Expand the REGION section
  - Select “Multiple Chromosomal Regions” and enter 2:208226227:208276270 in the text box
  - Click on count. **4 genes are found.**
- 2.
  - In Ensembl/BioMart, create a new request (see slide 2.)
  - Click on Filters (left panel)
  - Expand the REGION section
  - Select “Chromosome” and multiple select 1 -> MT (click and drag). This corresponds to 57992 / 63305 Genes
  - Click on Attributes (left panel)
  - Select “Features” (selected by default)
  - In GENE, select Gene ID, Chromosome/scaffold name, Gene Start (bp), Gene End (bp), strand and associated Gene Name
  - Click on Results 